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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 11:31:12 ; Search time 14294.3 Seconds
(without alignments)
-497.697 Million cell updates/sec

Title: US-09-026-459A-36_COPY_7_2349
Perfect score: 2343
Sequence: 1 ATGTCAAGACTGTTGAAGAA.....CCTCAAACAAGGAAGAGAAA 2343

Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

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46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2343	100.0	4597	5	I05311	I05311 Sequence 1
2	2343	100.0	3232	5	I18496	I18496 Sequence 1
c 3	2343	100.0	3232	5	I18497	I18497 Sequence 2
4	2343	100.0	2994	5	I81465	I81465 Sequence 2
5	2343	100.0	4839	10	HUMRB1MRNA	L41870 Homo sapien
6	2343	100.0	4600	10	HUMRBA1RA	M33647 Human retin
7	2343	100.0	2994	10	HUMRBSA	M28419 Human retin
8	2292	97.8	4597	5	I09369	I09369 Sequence 1
9	2139	91.3	4740	10	HUMRBS	M15400 Human retin
10	1420	60.6	4580	5	A01444	A01444 H.sapiens D
11	207	8.8	480	9	HUMRBSY79	M19701 Human mutat
12	198	8.5	693	5	I09384	I09384 Sequence 17
13	198	8.5	693	9	HUMRBS15	M27858 Human retin
14	198	8.5	180388	9	HUMRETBLAS	L11910 Human retin
15	196	8.4	340	10	HUMRB1501V	L49220 Homo sapien
16	167	7.1	555	10	HUMRB4MU2	L41904 Homo sapien
17	165	7.0	935	5	I09389	I09389 Sequence 22
18	165	7.0	935	9	HUMRBS20	M27863 Human retin
19	165	7.0	420	10	HUMRB23EX	L41910 Homo sapien
20	163	7.0	252	10	HUMRB1777L	L49230 Homo sapien
21	160	6.8	426	11	AF043224	AF043224 Homo sapi
22	155	6.6	555	10	HUMRB17MU2	L41924 Homo sapien
23	148	6.3	717	5	I09387	I09387 Sequence 20
24	148	6.3	717	9	HUMRBS18	L35147 Human retin
25	148	6.3	717	15	M27861	M27861 Figure 2. R
26	147	6.3	224	10	HUMRB1SDDL	L49225 Homo sapien
27	146	6.2	650	5	I09386	I09386 Sequence 19
28	146	6.2	650	9	HUMRBS17	M27860 Human retin
29	145	6.2	609	5	I09377	I09377 Sequence 10
30	145	6.2	609	9	HUMRBS08	L35146 Human retin
31	145	6.2	316	10	HUMRB08EX	L41896 Homo sapien
32	144	6.1	1310	9	HUMRBS22	M27865 Human retin
33	144	6.1	625	10	HUMRB25EX	L41912 Homo sapien
34	132	5.6	224	10	HUMRB1610K	L49223 Homo sapien
35	131	5.6	317	10	HUMRB17MUT	L41999 Homo sapien
36	125	5.3	350	10	HUMRB20MUU	L41996 Homo sapien
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38	122	5.2	589	5	I09385	I09385 Sequence 18
39	122	5.2	589	9	HUMRBS16	M27859 Human retin
40	122	5.2	224	10	HUMRB1646F	L49224 Homo sapien
41	122	5.2	222	10	HUMRB18EX	L41905 Homo sapien
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43	117	5.0	584	5	I09382	I09382 Sequence 15
44	117	5.0	584	9	HUMRBS13	M27856 Human retin
45	116	5.0	202	10	HUMRB1604E	L49222 Homo sapien

ALIGNMENTS

RESULT 1
I05311
LOCUS I05311 4597 bp PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent EP 0259031.
ACCESSION I05311
VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN

  Query Match           100.0%;  Score 2343;  DB 5;  Length 4597;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
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Db     442 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 501

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
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Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
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Db     562 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 621

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
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Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     682 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 741

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
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Db     742 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 801

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
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Db     802 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 861

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
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Db     862 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 921

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
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Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
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Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
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Db    1102 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1161

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
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Db    1162 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1221

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
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Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
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Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
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Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
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Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
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Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
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Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
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Db    1702 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1761

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
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Qy    1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
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Db    1942 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2001

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Qy    1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
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Qy    1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
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Qy    1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
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Qy    1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
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Db    2362 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2421

Qy    1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
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Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
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Qy   2341 AAA 2343
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Db   2782 AAA 2784


RESULT   2
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LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


  Query Match           100.0%;  Score 2343;  DB 5;  Length 3232;
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Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
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Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
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Db    244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
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Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
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Db    364 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 423

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
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Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
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Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
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Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
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Db    904 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 963

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
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Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1083

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1143

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1383

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1443

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1503
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Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1563

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1683

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1743

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1803

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1863

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1923

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1983

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463

Qy   2341 AAA 2343
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Db   2464 AAA 2466
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RESULT   3
I18497/c
LOCUS       I18497       3232 bp    DNA              PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN
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Query Match 100.0%; Score 2343; DB 5; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3113 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 3054

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3053 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 2994

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2993 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 2934

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2933 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 2874

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2873 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 2814

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2813 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 2754

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2753 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 2694

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 2634

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 2574

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 2514

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 2454

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 2394

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 2334
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Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2333 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 2274

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 2214

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2213 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 2154

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2153 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 2094

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2093 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 2034

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2033 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1974

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1973 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1914

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1913 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1853 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1794

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1793 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1733 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1674

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1673 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1614

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1613 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1554

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1494

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1434

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1374

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1314

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1254

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1194

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1134

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 1074

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 1014

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 954

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 894

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 834

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 774

Qy   2341 AAA 2343
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Db    773 AAA 771
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RESULT   4
I81465
LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
                     /organism="unknown"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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Query Match 100.0%; Score 2343; DB 5; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759
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Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

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Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
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Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
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Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
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Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
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Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
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Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
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Qy   2341 AAA 2343
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        |||
Db   2920 AAA 2922


RESULT   5
HUMRB1MRNA
LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
FEATURES             Location/Qualifiers
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Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
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Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
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Db    1719 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1778

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
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Db   1779 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1838

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
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Db   1839 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1898

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
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Db   1899 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1958

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
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Db   1959 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2018

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
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Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
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Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
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Db   2139 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2198

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
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Db   2259 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2318

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
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Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
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Db   2379 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2438

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
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Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
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Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2559 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2618

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2619 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2678

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
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Db   2679 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2738

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
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Db   2739 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2798

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
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Db   2799 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2858

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
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Db   2859 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2918

Qy   2341 AAA 2343
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Db   2919 AAA 2921
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RESULT   6
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
            provided by S.H.Friend, 10-FEB-1988.
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                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDAR
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                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1489 a    842 c    815 g   1454 t
ORIGIN
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  Query Match             100.0%;  Score 2343;  DB 10;  Length 4600;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 504
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Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 564

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 624

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 684

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 744

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 804

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
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Db    805 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 864

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
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Db    865 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 924

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
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Db    925 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 984

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
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Db    985 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1044

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
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Db   1045 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1104

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
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Db   1105 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1164

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
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Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
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Db   1285 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1344

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
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Db   1345 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1404

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
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Db   1405 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1464

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
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Db   1465 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1524

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Db   1525 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1584

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
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Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
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Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
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Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
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Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
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Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
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Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
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Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
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Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
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Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
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Qy    2341 AAA 2343
           |||
Db    2785 AAA 2787


RESULT   7
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDAR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


  Query Match           100.0%;  Score 2343;  DB 10;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
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Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
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Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
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Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
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Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
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Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
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Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2341 AAA 2343
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Db   2920 AAA 2922


RESULT   8
I09369
LOCUS       I09369       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


  Query Match             97.8%;  Score 2292;  DB 5;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2342;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 501

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 561

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 621

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    622 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 681

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    682 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 741

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    742 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 801

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    802 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 861

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 921

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
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Db    922 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 981

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
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Db    982 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1041

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1101

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
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Db   1102 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1161

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
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Db   1162 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1221

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1222 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1281

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1282 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1341

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1342 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1401

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1402 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1461

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1462 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1521

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1522 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1581

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1582 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1641

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1642 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1701

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1702 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1761

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1762 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1821

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1822 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1881

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
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Db   1942 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2001

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
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Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
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Db   2062 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2121

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
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Db   2122 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2181

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2301

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2361

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2421

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2422 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2481

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2482 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2541

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2542 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2601

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   2602 CCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGAAGGATCAGATGAAGCAGATGGA 2661

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2662 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2721

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2722 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2781

Qy   2341 AAA 2343
          |||
Db   2782 AAA 2784
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RESULT   9
HUMRBS
LOCUS       HUMRBS      4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
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            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
     source          1. .4740
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                     /db_xref="taxon:9606"
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                     /dev_stage="foetus"
                     /tissue_type="retina"
                     /map="13q14.2"
     mRNA            <1. .4740
                     /note="rbs mRNA"
     gene            139. .2925
                     /gene="RB1"
     CDS             139. .2925
                     /gene="RB1"
                     /note="retinoblastoma susceptibility protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA69807.1"
                     /db_xref="GI:190959"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
                     IFIARVDLDEMSFTLLSYRKTYEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.

  Query Match           91.3%;  Score 2139;  DB 10;  Length 4740;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 2339;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     880 GGTTCACCTCGAACACGCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     541 AATAAAGATCTAGATGGAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATCGAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 ATAATTCCTCCACACAGTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     841 GAGAAATTTGCTAAAGGTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGGTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019
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Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
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Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
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Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
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Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
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Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
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Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
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Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
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Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
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Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy   2341 AAA 2343
          |||
Db   2920 AAA 2922
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RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g    1451 t      1 others
ORIGIN
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Query Match 60.6%; Score 1420; DB 5; Length 4580;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Qy    325 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 384
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    385 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    445 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 504
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    505 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 564
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy    565 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 624
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy    625 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 684
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy    685 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 744
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy    745 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 804
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy    805 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 864
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy    865 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 924
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy    925 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 984
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy    985 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1044
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1045 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1104
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Db    1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy    1105 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1164
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Db    1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy    1165 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1224
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Db    1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy    1225 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1284
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Db    1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy    1285 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1344
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Db    1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy    1345 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1404
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy    1405 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1464
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Db    1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy    1465 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1524
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Qy    1525 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1584
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Db    1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy    1585 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1644
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Db    2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy    1645 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1704
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Db    2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy    1705 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 1764
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Db    2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy    1765 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 1824
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Db    2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy    1825 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 1884
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy    1885 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 1944
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy    1945 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2004
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Db    2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy    2005 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2064
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy    2065 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2124
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Db    2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy    2125 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2184
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Db    2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy    2185 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2244
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Db    2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy    2245 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2304
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Db    2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy    2305 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2343
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Db    2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768


RESULT  11
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
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     CDS             139. .300
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                     /codon_start=1
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                     /db_xref="GI:190968"
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     misc_recomb     275. .276
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                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


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  Best Local Similarity   100.0%;  Pred. No. 4.2e-100;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     165 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy     225 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 284
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 393

Qy     285 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 344
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Db    394 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 453

Qy    345 GATAGCAAAACAACTAGAAAATGATAC 371
          ||||||||||||||||||||||||||||
Db    454 GATAGCAAAACAACTAGAAAATGATAC 480


RESULT  12
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


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  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1058 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1118 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1177
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Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1178 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1238 CCCTTGCATGGCTCTCAG 1255
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  13
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
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     exon            250. .446
                     /note="retinoblastoma susceptibility gene"
                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             8.5%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1058 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1117
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Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1118 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1177
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Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1178 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1237
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1238 CCCTTGCATGGCTCTCAG 1255
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  14
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
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REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
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                     /db_xref="GI:292421"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
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                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
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     intron       160835. .161996
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     exon         161997. .162110
                  /number=22
     intron       162111. .162203
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     exon         162204. .162367
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                  /number=23

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  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1058 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1117
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Qy    1118 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1177
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RESULT  15
HUMRB1501V
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
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  Best Local Similarity   100.0%;  Pred. No. 3.5e-94;
  Matches  196;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    1120 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1179
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Qy    1180 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1239
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Db     186 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 245

Qy    1240 CTTGCATGGCTCTCAG 1255
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Search completed: February 13, 2000, 11:36:02
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Date: Feb 13, 2000  8:12 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
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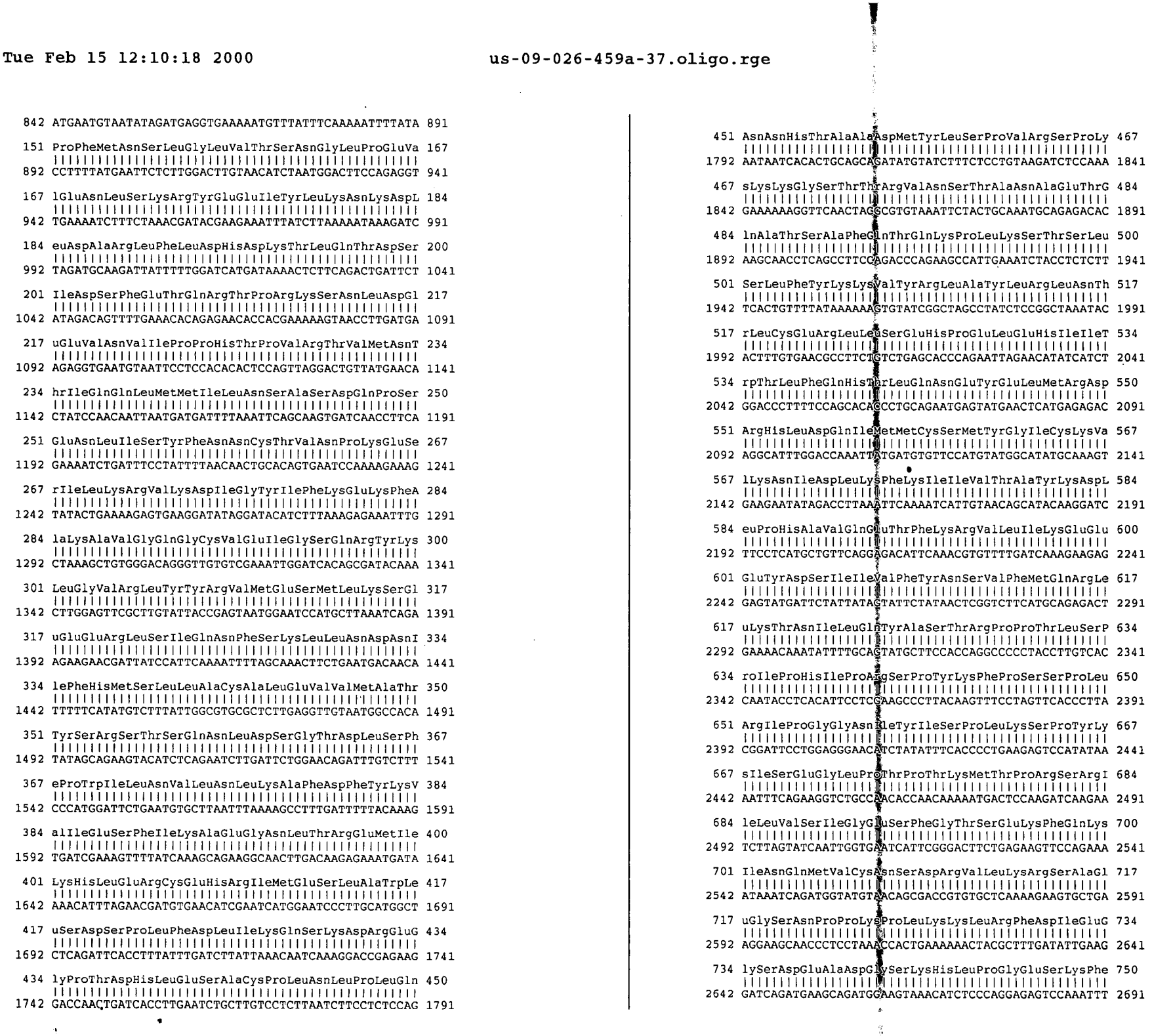
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  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
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     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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seq_documentation_block:
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DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


alignment_scores:
            Quality:  781.00             Length:    781
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x I18497/rev   ..

 Align seg 1/1  to reverse of: I18497  from: 1  to: 3232

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      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
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    3063 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 3014

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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VERSION     I81465.1  GI:3209762
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            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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ACCESSION   L41870
VERSION     L41870.1  GI:793994
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SOURCE      Homo sapiens cDNA to mRNA.
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
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SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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            [published erratum appears in Proc Natl Acad Sci U S A 1988
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COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
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ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
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  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
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  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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VERSION     M15400.1  GI:190958
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  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
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  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


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            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


alignment_scores:
            Quality:  286.00             Length:    522
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 Percent Similarity:  99.617   Percent Identity: 99.617

alignment_block:
 US-09-026-459A-37 x A01444   ..

 Align seg 1/1  to: A01444  from: 1  to: 4580

     192 HisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnAr 208
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1001 CATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAG 1050

     208 gThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProH 225
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1051 AACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCAC 1100

     225 isThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIle 241
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1101 ACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1150

     242 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 258
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1151 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAA 1200

     258 nAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspI 275
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1201 CAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATA 1250

     275 leGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCys 291
         |||||||||||||||||||||||||||||||||   ||||||||||||

    1251 TAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT.GGACAGGGTTGT 1299

     292 ValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrAr 308
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1300 GTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCG 1349

     308 gValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnA 325
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1350 AGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAA 1399

     325 snPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla 341
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    1400 ATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1449

     342 CysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAs 358
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    1450 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAA 1499

     358 nLeuAspSerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuA 375
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     375 snLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAla 391
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    1550 ATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCA 1599

     392 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHi 408
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1600 GAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACA 1649

     408 sArgIleMetGluSerLeu.AlaTrpLeuSerAspSerProLeuPheAsp 424
         |||||||||||||   ||| ||||||||||||||||||||||||||||||
    1650 TCGAATCATGGAATC.CTTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1698

     425 LeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSe 441
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     441 rAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspM 458
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     458 etTyrLeuSerProValArgSerProLysLysLysGlySerThrThrArg 474
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1799 TGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1848

     475 ValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnTh 491
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    1849 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1898

     491 rGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValT 508
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    1899 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGT 1948

     508 yrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 524
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    1949 ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1998

     525 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 541
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     541 uGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetM 558
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     558 etCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhe 574
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2099 TGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2148

     575 LysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluTh 591
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2149 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2198
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     591 rPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValP 608
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    2199 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGT 2248

     608 heTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr 624
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2249 TCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 2298

     625 AlaSerThrArgProProThrLeuSerProIleProHisIleProArgSe 641
         ||||||||||||||||||||||   ||||||||||||||||||||||||
    2299 GCTTCCACCAGGCCCCCTACCTTGCA.CCAATACCTCACATTCCTCGAAG 2347

     641 rProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleT 658
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     658 yrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThr 674
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2398 ATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2447

     675 ProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSe 691
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2448 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2497

     691 rPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnS 708
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2498 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACA 2547

     708 erAspArgValLeu 712
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    2548 GCGACCGTGTGCTC 2561

seq_name: gb_pat:E12560

seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
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            FT   source          1. .4591
            FT                   /organism='Mus musculus'
            FT                   /cell_type='B-cell precursor' FT
                /cell_line='70Z-3'
            FT   5'UTR           1. .98
            FT   CDS             99. .2864
            FT                   /product='Rb protein'
            FT   3'UTR           2865. .4591.
FEATURES              Location/Qualifiers
     source           1. .4591
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN


alignment_scores:
           Quality:   72.00            Length:     72
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x E12560   ..

 Align seg 1/1  to: E12560  from: 1  to: 4591

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     663 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 680
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     680 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 696
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     697 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 713
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    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     713 sArgSerAlaGluGly 718
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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES              Location/Qualifiers
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                      /strain="BALB/c"
                      /sub_species="domesticus"
                      /db_xref="taxon:10090"
                      /cell_line="70Z/3"
                      /cell_type="pre B-lymphocyte"
     CDS              99. .2864
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                      /product="pp105 Rb protein"
                      /protein_id="AAA39964.1"
                      /db_xref="GI:200453"
                      /translation="MPPKAPRRAAAAEPPPPPPPPPREDDPAQDSGPEELPLARLEFE
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                  DLDEMPFTFTELQKSIETSVYKFFDLLKEIDTSTKVDNAMSRLLKKYNVLCALYSKLE
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                  YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
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                  KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
                  NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
                  MESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTLQHLDSGTDLSF
                  PWILNVLNLKAFDFYKVIESFIKVEANLTREMIKHLERCEHRIMESLAWLSDSPLFDL
                  IKQSKDGEGPDNLEPACPLSLPLQGNHTAADMYLSPLRSPKKRTSTTRVNSAANTETQ
                  AASAFHTQKPLKSTSLALFYKKVYRLAYLRLNTLCARLLSDHPELEHIIWTLFQHTLQ
                  NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                  EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
                  ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
                  EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
                  VSNKEEK"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


alignment_scores:
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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x MUSPP105RB   ..

 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

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     663 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 680
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    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     680 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 696
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    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     697 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 713
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    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     713 sArgSerAlaGluGly 718
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seq_name: gb_pr1:HUMRBSY79

seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.

FEATURES             Location/Qualifiers
     source          1. .480
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                     /db_xref="taxon:9606"
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     gene            139. .300
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     CDS             139. .300
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                     /note="mutated retinoblastoma protein"
                     /codon_start=1
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                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


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            Quality:   68.00             Length:     68
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x HUMRBSY79   ..

 Align seg 1/1  to: HUMRBSY79  from: 1  to: 480

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     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

      72 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 89
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      89 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 105
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     106 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 122
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     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     122 nAsp 123
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     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
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                     /cell_type="leukocyte"
                     /map="13q14.2"
     gene            1. .340
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     intron          <1. .64
                     /gene="RB1"
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                     /number=16
     exon            65. .260
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
     CDS             <65. .120
                     /gene="RB1"
                     /note="exon 17"
                     /codon_start=3
                     /db_xref="GDB:G00-118-734"
                     /product="retinoblastoma suspectibility protein"
                     /protein_id="AAA82549.1"
                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
                     /gene="RB1"
                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
     intron          261. .>340
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                     /note="G00-118-734"
                     /number=17
BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN


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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x HUMRB1501V   ..

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     369 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 386
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     386 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 402
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seq_documentation_block:
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DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
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Date: Feb 13, 2000  8:05 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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     18 uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
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            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
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  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
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  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
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            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
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  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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     102 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLe 118
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SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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ORIGIN


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  ORGANISM  Unknown.
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  AUTHORS   Dryja,T.P. and Friend,S.
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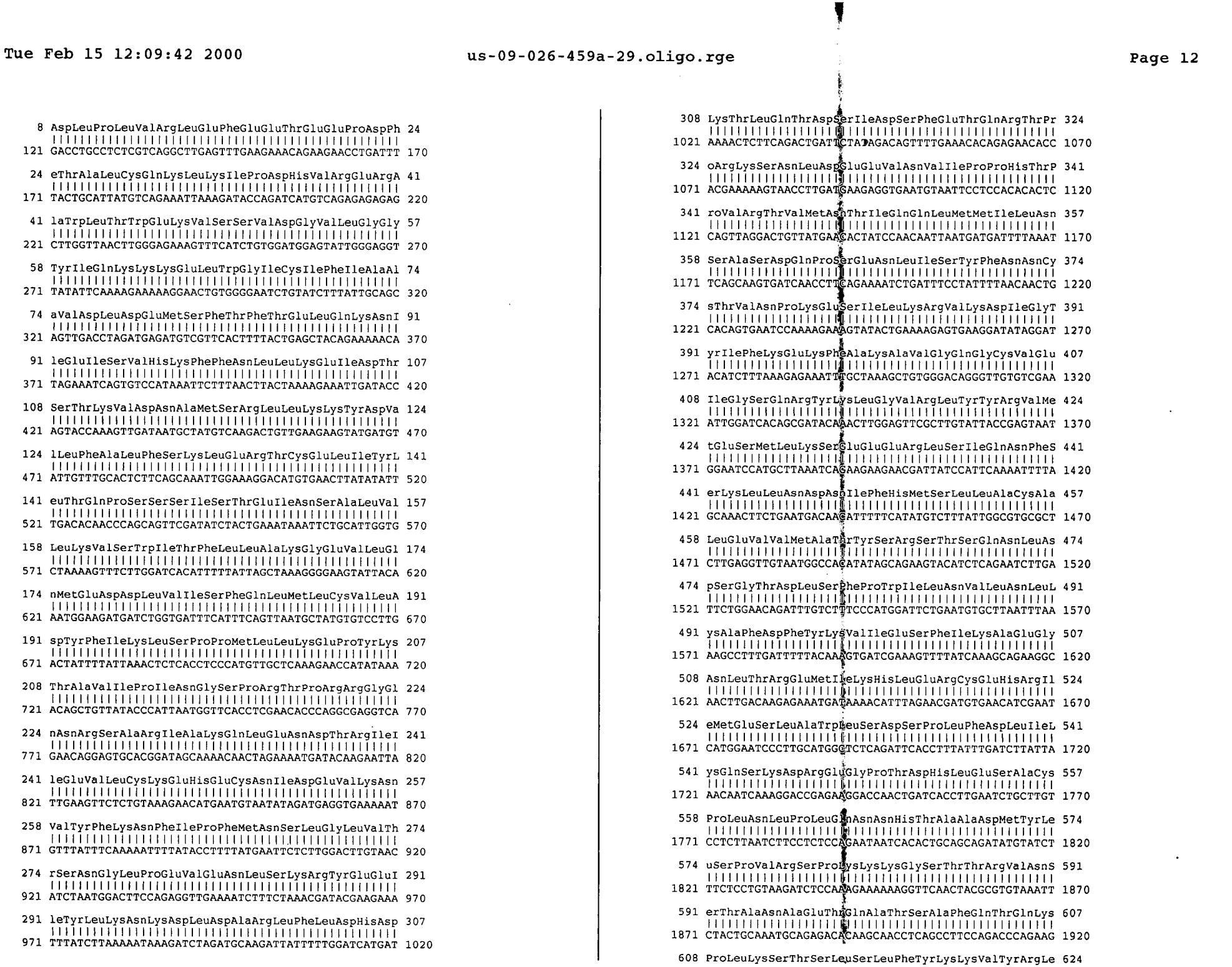
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REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
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871 GTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAAC 920
274 rSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluI 291
921 ATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAA 970
291 leTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 307
971 TTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
308 LysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPr 324
1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACC 1070
324 oArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrP 341
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358 SerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCy 374
1171 TCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTG 1220
374 sThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyT 391
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441 erLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAla 457
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1471 CTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGA 1520
474 pSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuL 491
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seq_documentation_block:
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DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


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     92 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 109
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    109 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 125
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    107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

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    142 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 159
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    159 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 175
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    292 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 309
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 359 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 375
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 426 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 442
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VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
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VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma; susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
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  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
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REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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   642 GluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGl 658
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  2161 GAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGA 2210

   658 uTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerM 675
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2211 GTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCA 2260

   675 etTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIle 691
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   692 ValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysAr 708
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   708 gValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnS 725
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  2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACT 2410

   725 erValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThr 741
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   742 ArgProProThrLeuSerProIleProHisIleProArgSerProTyrLy 758
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  2461 AGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAA 2510

   758 sPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerP 775
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   775 roLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLys 791
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   825 alLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLys 841
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ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
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ORIGIN


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    356 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 372
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    372 nAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspI 389
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   1201 CAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATA 1250

    389 leGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCys 405
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   1251 TAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT.GGACAGGGTTGT 1299

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        ||||||||||||||||||||||||||||||||||||||||||||||||||
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 506 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHi 522
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 522 sArgIleMetGluSerLeu.AlaTrpLeuSerAspSerProLeuPheAsp 538
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1650 TCGAATCATGGAATC.CTTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1698

 539 LeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSe 555
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 555 rAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspM 572
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 605 rGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValT 622
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 622 yrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 638
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1949 ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1998

 639 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 655
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 655 uGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetM 672
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 689 LysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluTh 705
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2149 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2198

 705 rPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValP 722
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2199 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGT 2248

 722 heTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr 738
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 805 rPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnS 822
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
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      72 eAlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnL 89
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      89 ysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIle 105
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DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
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seq_documentation_block:
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DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
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           provided by R.Bernards, 21-JUL-1989.
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                     NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
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                     EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
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BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN       Chromosome 14.


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 Percent Similarity: 100.000   Percent Identity: 100.000

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     777 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 794
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    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     794 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 810
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     811 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 827
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     827 sArgSerAlaGluGly 832
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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_pr1:HUMRBSY79

seq_documentation_block:
LOCUS        HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION   Human mutated retinoblastoma susceptibility (RB) mRNA, complete
             cds.
ACCESSION    M19701 J03809
VERSION      M19701.1  GI:190967
KEYWORDS     retinoblastoma susceptibility.
SOURCE       Human (patient with a maternal family history of retinoblastoma)
             retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 480)
  AUTHORS    Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
             Lee,W.H.
  TITLE      Molecular mechanism of retinoblastoma gene inactivation in
             retinoblastoma cell line Y79
  JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE    88320373
COMMENT      Draft entry and computer-readable sequence for [1] kindly provided
             by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
             normal gene.
FEATURES             Location/Qualifiers
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                     /map="13q14.2"
     gene            139. .300
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     CDS             139. .300
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                     /codon_start=1
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                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN       Chromosome 13q14.1-q14.2.


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: HUMRBSY79  from: 1  to: 480

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     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     186 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     203 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     220 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 236
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     236 nAsp 237
         ||||
     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS        HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
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     intron          <1. .64
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                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
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                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
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ORIGIN


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     483 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     500 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 516
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     517 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 532
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260
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Date: Feb 13, 2000  8:07 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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gb_ro:MUSPP105RB      +   72.00  1324.93  8.9e-66   4591  ! M26391 Mouse retinoblastoma su
gb_pr1:HUMRBSY79      +   68.00  1264.91  2.0e-62   480   ! M19701 Human mutated retinoblas
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ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
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      18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 35
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     216 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 265

      35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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      52 AlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     316 GCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAA 365

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      85 spThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
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     416 ATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 465

     102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     466 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTAT 515

     118 eTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaL 135
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 202 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrAr 218
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 218 gIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGluValL 235
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 252 ValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGl 268
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 268 uGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspH 285
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 966 AGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATC 1015

 285 isAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 301
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1016 ATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065

 302 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHi 318
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 318 sThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleL 335
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  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


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seq_documentation_block:
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
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ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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susceptibility gene
JOURNAL Gene 80 (1), 119-128 (1989)
MEDLINE 90006771
REFERENCE 2 (sites)
AUTHORS Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
TITLE Detection of heterozygous mutations in the RB1 gene in retinoblastoma patients using single-strand conformation polymorphism analysis and polymerase chain reaction sequencing
JOURNAL Oncogene 7 (7), 1445-1451 (1992)
MEDLINE 92319557
REFERENCE 3 (sites)
AUTHORS Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
TITLE Oncogenic point mutations in exon 20 of the RB1 gene in families showing incomplete penetrance and mild expression of the retinoblastoma phenotype
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
MEDLINE 92335261
REFERENCE 4 (sites)
AUTHORS Onadim,Z., Hogg,A. and Cowell,J.K.
TITLE Mechanisms of oncogenesis in patients with familial retinoblastoma
JOURNAL Br. J. Cancer 68 (5), 958-964 (1993)
MEDLINE 94031584
REFERENCE 5 (sites)
AUTHORS Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
TITLE Molecular mechanisms of oncogenic mutations in tumors from patients with bilateral and unilateral retinoblastoma
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
MEDLINE 93348271
REFERENCE 6 (sites)
AUTHORS Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J., Cowell,J.K. and Kaye,F.J.
TITLE Partial inactivation of the RB product in a family with incomplete penetrance of familial retinoblastoma and benign retinal tumors
JOURNAL Oncogene 9 (5), 1321-1326 (1994)
MEDLINE 94203660
COMMENT Mutation data provided by Dr. B.L.Gallie,
Hospital for Sick Children
555 Univ. Ave.
Toronto ONT W5G 1X8
Canada
Ph: 416 813-5868
FAX: 416 813-4989
E-mail: brenda@hafiz.eric.on.ca.

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      18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     219 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 268

      35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
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      52 AlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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      68 sAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleA 85
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     369 AAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTG 418

      85 spThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     419 ATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 468

     102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     469 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTAT 518

     118 eTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaL 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     519 ATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCAT 568

     135 euValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluVal 151
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ACCESSION   M28419
VERSION     M28419.1  GI:190962
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SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
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REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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ORIGIN


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VERSION     I09369.1  GI:587899
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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BASE COUNT     1489 a    841 c    813 g   1454 t
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REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
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 657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

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 305 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVa 321
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seq_documentation_block:
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DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


alignment_scores:
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Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x I18497/rev   ..

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      71 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 88
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    3180 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 3131

      88 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 104
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    3130 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 3081

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
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    838 roGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArg 854
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DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


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DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
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  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
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ORIGIN


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      335 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 351
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   601 yrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 617
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  1949 ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1998

   618 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 634
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  1999 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 2048

   634 uGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetM 651
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2049 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGA 2098

   651 etCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhe 667
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2099 TGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2148

   668 LysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluTh 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2149 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2198

   684 rPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValP 701
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2199 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGT 2248

   701 heTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr 717
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2249 TCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 2298

   718 AlaSerThrArgProProThrLeuSerProIleProHisIleProArgSe 734
     ||||||||||||||||||||||||   ||||||||||||||||||||||||
  2299 GCTTCCACCAGGCCCCCTACCTTGCA.CCAATACCTCACATTCCTCGAAG 2347

   734 rProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleT 751
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2348 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2397

   751 yrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThr 767
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2398 ATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2447

   768 ProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSe 784
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2448 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2497

   784 rPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnS 801
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
  2498 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACA 2547

   801 erAspArgValLeu 805
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  2548 GCGACCGTGTGCTC 2561

seq_name: gb_pr3:AF043224

seq_documentation_block:
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
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                     /gene="RB1"
                     /number=5
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                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
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                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
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                     /gene="RB1"
                     /number=3
     exon            193. .312
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                     /number=4
     exon            313. .350
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alignment_block:
 US-09-026-459A-31 x AF043224   ..

 Align seg 1/1  to: AF043224  from: 1  to: 426

     35 GlyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIl 51
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
     76 GGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTAT 125
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      51 eAlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnL 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     126 TGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGA 175

      68 ysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIle 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     176 AAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATT 225

      85 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTy 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     226 GATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTA 275

     101 rAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuI 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     276 TGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTA 325

     118 leTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAla 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     326 TATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 375

     135 LeuValLeuLysValSerTrpIleThrPheLeuLeu 146
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     376 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 411
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seq_name: gb_pat:E12560

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seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
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            FT                   /organism='Mus musculus'
            FT                   /cell_type='B-cell precursor' FT
               /cell_line='70Z-3'
            FT   5'UTR           1. .98
            FT   CDS             99. .2864
            FT                   /product='Rb protein'
            FT   3'UTR           2865. .4591.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT     1395 a    969 c    898 g   1329 t
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 Percent Similarity: 100.000   Percent Identity: 100.000

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 US-09-026-459A-31 x E12560   ..

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     756 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 773
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     773 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 789
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     790 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 806
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     806 sArgSerAlaGluGly 811
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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
     CDS             99. .2864
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                     /product="pp105 Rb protein"
                     /protein_id="AAA39964.1"
                     /db_xref="GI:200453"
                     /translation="MPPKAPRRAAAAEPPPPPPPPREDDPAQDSGPEELPLARLEFE
                     EIEEPEFIALCQKLKVPDHVRERAWLTWEKVSSVDGILEGYIQKKKELWGICIFIAAV
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                     RTCELIYLTQPSSALSTEINSMLVLKISWITFLLAKGEVLQMEDDLVISFQLMLCVVD
                     YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
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                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                     EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
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BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


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 Percent Similarity: 100.000   Percent Identity: 100.000

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     756 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 773
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     773 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 789
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    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     790 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 806
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    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     806 sArgSerAlaGluGly 811
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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_pr1:HUMRBSY79

seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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     gene            139. .300
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     CDS             139. .300
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                     /note="mutated retinoblastoma protein"
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                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
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     misc_recomb     275. .276
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                     /organism="Homo sapiens"
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ORIGIN      Chromosome 13q14.1-q14.2.


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     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     165 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 182
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     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     182 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 198
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     199 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     215 nAsp 216
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     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
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     gene            1. .340
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                    /gene="RB1"
                    /note="G00-118-734"
                    /number=17
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                    /note="exon 17"
                    /codon_start=3
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                    /product="retinoblastoma suspectibility protein"
                    /protein_id="AAA82549.1"
                    /db_xref="GI:1088309"
                    /translation="VHLRILILEQICLSHGF"
     mutation       66. .67
                    /gene="RB1"
                    /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                    premature stop at AA 518; G00-118-734"
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BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN


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      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     462 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 479
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     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     479 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 495
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     496 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 511
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 11:15:20 ; Search time 14294.3 Seconds
(without alignments)
-556.962 Million cell updates/sec

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Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

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2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
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14: gb_sy:*
15: gb_un:*
16: gb_vi:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vi:*
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37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2619	99.9	4597	5	I05311	I05311 Sequence 1
2	2619	99.9	2994	5	I81465	I81465 Sequence 2
3	2619	99.9	4839	10	HUMRB1MRNA	L41870 Homo sapien
4	2619	99.9	4600	10	HUMRBA1RA	M33647 Human retin
5	2619	99.9	2994	10	HUMRBSA	M28419 Human retin
6	2568	97.9	4597	5	I09369	I09369 Sequence 1
7	2460	93.8	3232	5	I18496	I18496 Sequence 1
c 8	2460	93.8	3232	5	I18497	I18497 Sequence 2
9	2208	84.2	4740	10	HUMRBS	M15400 Human retin
10	1420	54.2	4580	5	A01444	A01444 H.sapiens D
11	338	12.9	426	11	AF043224	AF043224 Homo sapi
12	207	7.9	480	9	HUMRBSY79	M19701 Human mutat
13	198	7.6	693	5	I09384	I09384 Sequence 17
14	198	7.6	693	9	HUMRBS15	M27858 Human retin
15	198	7.6	180388	9	HUMRETBLAS	L11910 Human retin
16	196	7.5	340	10	HUMRB1501V	L49220 Homo sapien
17	167	6.4	555	10	HUMRB4MU2	L41904 Homo sapien
18	165	6.3	935	5	I09389	I09389 Sequence 22
19	165	6.3	935	9	HUMRBS20	M27863 Human retin
20	165	6.3	420	10	HUMRB23EX	L41910 Homo sapien
21	163	6.2	252	10	HUMRB1777L	L49230 Homo sapien
22	155	5.9	555	10	HUMRB17MU2	L41924 Homo sapien
23	148	5.6	717	5	I09387	I09387 Sequence 20
24	148	5.6	717	9	HUMRBS18	L35147 Human retin
25	148	5.6	717	15	M27861	M27861 Figure 2. R
26	147	5.6	224	10	HUMRB1SDDL	L49225 Homo sapien
27	146	5.6	650	5	I09386	I09386 Sequence 19
28	146	5.6	650	9	HUMRBS17	M27860 Human retin
29	145	5.5	609	5	I09377	I09377 Sequence 10
30	145	5.5	609	9	HUMRBS08	L35146 Human retin
31	145	5.5	316	10	HUMRB08EX	L41896 Homo sapien
32	144	5.5	1310	9	HUMRBS22	M27865 Human retin
33	144	5.5	625	10	HUMRB25EX	L41912 Homo sapien
34	132	5.0	224	10	HUMRB1610K	L49223 Homo sapien
35	131	5.0	317	10	HUMRB17MUT	L41999 Homo sapien
36	125	4.8	350	10	HUMRB20MUU	L41996 Homo sapien
37	124	4.7	444	10	HUMRB04MUT	L41892 Homo sapien
38	124	4.7	483	10	HUMRB19MUT	L41906 Homo sapien
39	123	4.7	570	5	I09373	I09373 Sequence 6
40	123	4.7	570	9	HUMRBS04	M27848 Human retin
41	122	4.7	589	5	I09385	I09385 Sequence 18
42	122	4.7	589	9	HUMRBS16	M27859 Human retin
43	122	4.7	224	10	HUMRB1646F	L49224 Homo sapien
44	122	4.7	222	10	HUMRB18EX	L41905 Homo sapien
45	119	4.5	323	10	HUMRB1D18	L49221 Homo sapien

ALIGNMENTS

RESULT 1
I05311
LOCUS I05311 4597 bp PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent EP 0259031.
ACCESSION I05311
VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN

  Query Match             99.9%;  Score 2619;  DB 5;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
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Db     166 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 225

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
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Db     226 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 285

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
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Db     286 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 345

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
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Db     346 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 405

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGAGTGTTGAAGAAGTAT 303
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Db     406 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGAGTGTTGAAGAAGTAT 465

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAAGTTATATATTTGACA 363
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Db     466 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAAGTTATATATTTGACA 525

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
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Qy     424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
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Qy     484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
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Qy     544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
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Qy     604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
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Db     766 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 825

Qy     664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
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Db     826 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 885

Qy     724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
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Db     886 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 945

Qy     784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
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Db     946 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1005

Qy     844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
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Db    1006 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065

Qy     904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
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Db    1066 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1125

Qy     964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
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Db    1126 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1185

Qy    1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
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Db    1186 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1245

Qy    1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
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Db    1246 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1305

Qy    1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
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Db    1306 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1365

Qy    1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
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Db    1366 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1425

Qy    1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
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Qy    1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
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Db    1726 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1785

Qy    1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
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Qy    1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
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Qy    1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
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Qy    1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
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Qy    1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
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Qy    1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
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Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
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Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
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RESULT   2
I81465
LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


  Query Match             99.9%;  Score 2619;  DB 5;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
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Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
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Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
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Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
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Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
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Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
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Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
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Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
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Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
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Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
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Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
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Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
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Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
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Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
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Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
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Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
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Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
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RESULT   3
HUMRB1MRNA
LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
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  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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Db   1443 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1502

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1503 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1562

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
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Db   1563 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1622

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
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Db   1623 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1682

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
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Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
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Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
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Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
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Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
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Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
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Db   2103 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2162

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
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Db   2163 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2222

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2223 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2282
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Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
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Db   2283 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2342

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
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Db   2343 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2402

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
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Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
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Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
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Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
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Db   2583 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2642

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
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Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
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Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
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Db   2823 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2882

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
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RESULT   4
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
            provided by S.H.Friend, 10-FEB-1988.
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                     KMNDSMDTSNKEEK"
BASE COUNT     1489 a    842 c    815 g    1454 t
ORIGIN


  Query Match             99.9%;  Score 2619;  DB 10;  Length 4600;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 228

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
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Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
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Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
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Db    409 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 468

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
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Db    469 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 528

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
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Db    529 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 588

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Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 708

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
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Db    709 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 768

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663

Db    769 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 828

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723

Db    829 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 888

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783

Db    889 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 948

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843

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Db   1129 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1188

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083

Db   1189 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1248

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143

Db   1249 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1308

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTGGCTTGTATTACCGA 1203

Db   1309 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTGGCTTGTATTACCGA 1368

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Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443

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Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683

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Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863

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Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043

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Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103

Db   2209 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2268

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163

Db   2269 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2328

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223

Db   2329 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2388

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283

Db   2389 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2448

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343

Db   2449 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2508

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403

Db   2509 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2568

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463

Db   2569 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2628

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523

Db   2629 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2688

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583

Db   2689 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2748

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622

Db   2749 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2787


RESULT   5
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
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KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
            phosphoprotein associated with DNA binding activity
  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
FEATURES             Location/Qualifiers
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                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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  Query Match           99.9%;  Score 2619;  DB 10;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy     424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy     484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy     544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy     604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy     664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy     724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy     784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy     844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy     904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy     964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy    1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy    1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy    1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy    1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy    1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy    1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
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Db    1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683
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Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
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Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
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Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
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Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
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Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
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Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
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Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACGACTGAAAAAACTA 2463
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Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
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Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
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Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
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Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   6
I09369
LOCUS       I09369       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


  Query Match             97.9%;  Score 2568;  DB 5;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2618;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     166 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 225

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     226 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 285

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     286 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 345

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     346 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 405

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     406 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 465

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     466 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 525

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     526 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 585

Qy     424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     586 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 645

Qy     484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     646 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 705
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Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
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Db    706 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 765

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
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Db    766 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 825

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 885

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 945

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1005

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1125

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1185

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1245

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1305

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1365

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1425

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1485

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
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Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
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Db   1546 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1605

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
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Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
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Db   1666 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1725

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1785

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
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Db   1786 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1845

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1905

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1965

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1966 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2025

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2085

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2145

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
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Db   2146 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2205

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
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Db   2206 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2265

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2325

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2385

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2445

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2505

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2506 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2565

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2625

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CGCTTTCATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2685

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2745

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2746 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784


RESULT   7
I18496
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
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VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN
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Query Match 93.8%; Score 2460; DB 5; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    163 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy    223 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy    283 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy    343 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy    403 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy    463 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy    523 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy    583 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy    643 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy    703 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy    763 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy    823 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy    883 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy    943 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy   1003 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy   1063 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy   1123 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy   1183 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy   1243 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy   1303 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy   1363 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1423 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1483 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy   1543 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy   1603 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy   1663 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy   1723 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1783 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy   1843 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1903 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   1963 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   2023 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2082
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Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   2083 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2142

Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2143 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2202

Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2203 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2262

Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2263 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2322

Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2323 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2382

Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2383 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2442

Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2443 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2502

Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2503 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2562

Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2563 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622

Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466


RESULT   8
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


  Query Match             93.8%;  Score 2460;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    163 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 222

Db   3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy    223 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 282

Db   3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy    283 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 342

Db   3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy    343 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 402

Db   3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy    403 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 462

Db   2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy    463 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 522

Db   2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy    523 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 582

Db   2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy    583 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 642

Db   2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy    643 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 702

Db   2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy    703 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 762

Db   2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy    763 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 822

Db   2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy    823 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 882

Db   2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy    883 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 942

Db   2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy    943 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1002

Db   2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy   1003 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1062

Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy   1063 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1122

Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy   1123 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1182

Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy   1183 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1242

Db   2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy   1243 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1302

Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy   1303 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1362

Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031
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Qy   1363 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1423 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1483 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1543 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1603 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy   1663 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy   1723 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1782
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Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1783 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1842
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Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy   1843 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1902
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Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1903 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1962
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Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy   1963 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   2023 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2082
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Qy   2083 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2142
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Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2143 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTGACATTCCTCGAAGC 2202
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Qy   2203 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2262
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Qy   2263 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2322
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Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2323 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2382
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Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2383 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2443 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2502
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Qy   2503 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2563 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
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                     /gene="RB1"
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                     IFIARVDLDEMSFTLLSYRKTYEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
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                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
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                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
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                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
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```

KMNDSMDTSNKEEK"
BASE COUNT 1508 a 887 c 862 g 1483 t
ORIGIN 1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.

Query Match 84.2%; Score 2208; DB 10; Length 4740;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2408; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    211 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 570

Qy    271 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 630

Qy    331 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690

Qy    391 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 750

Qy    451 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 810

Qy    511 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 870

Qy    571 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 930

Qy    631 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990

Qy    691 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 1050

Qy    751 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 1110

Qy    811 TATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAG 870
          ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
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Qy    871 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    931 GAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 990
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    991 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1050
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Qy   1051 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1110
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Db   1351 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1410

Qy   1111 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1470

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1530

Qy   1231 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1590

Qy   1291 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1350
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Db   1591 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1650

Qy   1351 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1410
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Db   1651 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1710

Qy   1411 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1470
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Db   2071 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 2130

Qy   1831 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 1890
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Db   2131 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 2190

Qy   1891 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 1950
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Db   2191 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2250

Qy   1951 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2010
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Db   2251 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2310

Qy   2011 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2070
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Db   2311 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2370

Qy   2071 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2130
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Qy   2131 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2190
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Db   2431 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2490

Qy   2191 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2250
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Qy   2251 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2310
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Db   2731 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2790

Qy   2491 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2550

Db   2791 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2850

Qy   2551 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2610

Db   2851 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2910

Qy   2611 AAGGAAGAGAAA 2622

Db   2911 AAGGAAGAGAAA 2922


RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
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                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match             54.2%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663

Db    752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723

Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783

Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843

Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903

Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963

Db   1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023

Db   1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083

Db   1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143

Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203

Db   1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263

Db   1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323

Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383

Db   1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443

Db   1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503

Db   1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563

Db   1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623

Db   1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683

Db   1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743

Db   1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803

Db   1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863

Db   1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923

Db   2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070
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Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
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Db   2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
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Db   2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
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Db   2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
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Db   2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
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Db   2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
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Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
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Db   2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
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Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
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Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
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Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
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Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
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LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
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FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
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                     mice"
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     exon            <1. .7
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                     /number=5
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                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
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                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
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                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
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     exon            8. .76
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                     /number=3
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     exon            351. .418
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     exon            419. .>426
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BASE COUNT      145 a     61 c     82 g    138 t
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Qy    102 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 161
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Db     75 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 134

Qy    162 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 221
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Db    135 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 194

Qy    222 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 254

Qy    282 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 314

Qy    342 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 374

Qy    402 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 439
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Db    375 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 412
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RESULT  12
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
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                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
                     /note="mutated retinoblastoma protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
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ORIGIN      Chromosome 13q14.1-q14.2.


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  Best Local Similarity   100.0%;  Pred. No. 9.3e-98;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    444 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 503
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Db    274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy    504 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 393

Qy    564 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 453

Qy    624 GATAGCAAAACAACTAGAAAATGATAC 650
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Db    454 GATAGCAAAACAACTAGAAAATGATAC 480


RESULT  13
I09384
LOCUS       I09384        693 bp                  PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 5.1e-93;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1337 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1396
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Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1397 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1456
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Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1457 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1516
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1517 CCCTTGCATGGCTCTCAG 1534
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  14
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
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     exon            250. .446
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                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.6%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-93;
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Qy   1337 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1396
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Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1397 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1456
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Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1457 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1516
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1517 CCCTTGCATGGCTCTCAG 1534
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  15
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891

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     source          1. .180388
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                     /evidence=experimental
     protein_bind    1866. .1872
                     /bound_moiety="ATF"
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     exon            <2060. .2196
                     /number=1
     CDS             join(2060. .2196,5424. .5550,39446. .39561,41926. .42045,
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                     177005. .177078)
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                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAA53483.1"
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                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDAR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSA
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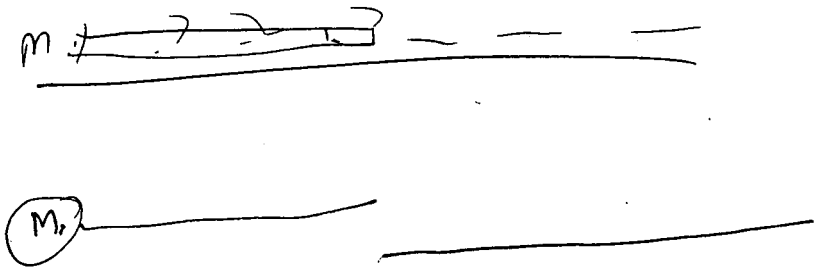
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
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Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
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Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
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Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
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RESULT   2
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LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


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  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
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Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
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Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
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Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
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Db    610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
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Db    670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
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Db    730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
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Db    790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
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Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
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Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
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Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
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Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
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Db   1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
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Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
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Db   1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

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Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
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Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
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Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
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Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTGATGCTGTTCAGGAG 1923
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Db   2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

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LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
FEATURES             Location/Qualifiers
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Db    489 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 548
Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
Db    549 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 608
Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
Db    609 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 668
Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
Db    669 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 728
Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
Db    729 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 788
Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
Db    789 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 848
Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
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Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
Db    909 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 968
Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
Db    969 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1028
Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
Db   1029 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1088
Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
Db   1089 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1148
Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
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Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
Db   1269 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1328
Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
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Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
Db   1629 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1688
Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
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Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
Db   2049 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2108
Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
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Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
Db   2169 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2228
Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
Db   2229 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2288
Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
Db   2289 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2348
Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
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Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
Db   2409 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2468
Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
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Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
Db   2529 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2588
Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
Db   2589 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2648
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Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
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Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
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Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
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Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
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Db   2889 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2921
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RESULT   4
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
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                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
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                     KMNDSMDTSNKEEK"
BASE COUNT     1489 a    842 c    815 g    1454 t
ORIGIN
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  Query Match             99.9%;  Score 2493;  DB 10;  Length 4600;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
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Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
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Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
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Db    595 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 654

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
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Db    655 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 714

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
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Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    775 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 834

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    835 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 894

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    895 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 954

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    955 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1014

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
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Db   1015 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1074

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
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Db   1075 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1134

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
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Db   1135 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1194

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
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Db   1195 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1254

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023

Db   1255 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1314

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083

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Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143

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Db   1495 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1554

Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323

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Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383

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Db   1735 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1794

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563

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Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683

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Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743

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Db   2095 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2154

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923

Db   2155 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2214

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983

Db   2215 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2274

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043

Db   2275 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2334

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103

Db   2335 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2394

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163

Db   2395 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2454

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223

Db   2455 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2514

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283

Db   2515 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2574

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343

Db   2575 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2634

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403

Db   2635 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2694

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463

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Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496

Db   2755 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2787
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RESULT   5
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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VERSION     I18496.1  GI:1598851
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SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
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Qy   2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
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Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226
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Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
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Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT   7
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN
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  Query Match             98.6%;  Score 2460;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy     97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy    157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy    217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy    277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy    337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy    397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy    457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
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Db   2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751
Qy    517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
Db   2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691
Qy    577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
Db   2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631
Qy    637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
Db   2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571
Qy    697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
Db   2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511
Qy    757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
Db   2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451
Qy    817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
Db   2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391
Qy    877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331
Qy    937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271
Qy    997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCAGAGCGATACAAACTT 1056
Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCAGAGCGATACAAACTT 2211
Qy   1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
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Qy   1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091
Qy   1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031
Qy   1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971
Qy   1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911
Qy   1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851
Qy   1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791
Qy   1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
Qy   1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671
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Qy   1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
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Qy   1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551
Qy   1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491
Qy   1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431
Qy   1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371
Qy   1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311
Qy   1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251
Qy   2017 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
Db   1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191
Qy   2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131
Qy   2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071
Qy   2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011
Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951
Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
Db    950 CCTAAACCACTGAAAAAACTAGCGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891
Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831
Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
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I09369
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DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
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  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN
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Query Match 97.8%; Score 2442; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2492; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
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Db     292 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 351

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 411

Qy     124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 471

Qy     184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 531

Qy     244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 591

Qy     304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 651

Qy     364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 711

Qy     424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
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Db     772 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 831

Qy     544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 891

Qy     604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     892 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 951

Qy     664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     952 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1011

Qy     724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1012 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1071

Qy     784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1072 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1131

Qy     844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1132 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1191

Qy     904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1192 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1251

Qy     964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1252 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1311

Qy    1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1312 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1371

Qy    1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1372 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1431

Qy    1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
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Db    1432 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1491

Qy    1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1492 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1551

Qy    1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1552 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1611

Qy    1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
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Db    1612 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1671

Qy    1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
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Db    1672 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1731

Qy    1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
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Db    1732 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1791

Qy    1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
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Db    1792 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1851

Qy    1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1852 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1911

Qy    1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1912 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1971

Qy    1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1972 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2031

Qy    1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
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Db    2032 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2091

Qy    1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2092 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2151

Qy    1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2152 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2211

Qy    1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2212 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2271
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Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2272 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2331

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
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Db   2332 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2391

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2392 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2451

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2452 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2511

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2512 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2571

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2572 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2631

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2632 CATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2691

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2692 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2751

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2752 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
     source          1. .4740
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                     /dev_stage="foetus"
                     /tissue_type="retina"
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     mRNA            <1. .4740
                     /note="rbs mRNA"
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                     /gene="RB1"
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                     /codon_start=1
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                     /protein_id="AAA69807.1"
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                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g    1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.
```

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  Query Match             88.5%;  Score 2208;  DB 10;  Length 4740;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2408;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     85 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 570

Qy    145 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 630

Qy    205 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690

Qy    265 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 324
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 750

Qy    325 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 384
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 810

Qy    385 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 870

Qy    445 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 504
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 930

Qy    505 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 564
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990

Qy    565 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 624
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Db    991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 1050

Qy    625 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 684
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 1110
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Qy    685 TATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAG 744
          ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db   1111 TATCTTAAAAATAAAGATCTAGATCGAAGATTATTTTTGGATCATGATAAAACTCTTCAG 1170

Qy    745 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 804
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 1230

Qy    805 GAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 864
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 GAGGTGAATATAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1290

Qy    865 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 924
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1291 TTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1350

Qy    925 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 984
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1410

Qy    985 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1044
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1470

Qy   1045 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1104
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1530

Qy   1105 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1164
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1590

Qy   1165 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1224
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1650

Qy   1225 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1284
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1710

Qy   1285 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1770

Qy   1345 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1830

Qy   1405 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1464
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Db   1831 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1890

Qy   1465 CACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1524
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Qy   1525 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 1584
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Db   1951 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 2010

Qy   1585 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 1644
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Qy   1645 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 1704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 2130

Qy   1705 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 1764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 2190

Qy   1765 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 1824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2250

Qy   1825 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 1884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2310

Qy   1885 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 1944
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2370

Qy   1945 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2430

Qy   2005 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2064
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Db   2431 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2490

Qy   2065 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2124
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Db   2491 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2550

Qy   2125 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2184
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Db   2551 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2610

Qy   2185 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2244
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Db   2611 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2670

Qy   2245 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2304
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Db   2731 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2790

Qy   2365 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2850

Qy   2425 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2910

Qy   2485 AAGGAAGAGAAA 2496
          ||||||||||||
Db   2911 AAGGAAGAGAAA 2922
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RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1477 a 840 c 811 g 1451 t 1 others
ORIGIN

Query Match 56.9%; Score 1420; DB 5; Length 4580;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Qy   478 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 537
Db   752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy   538 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 597
Db   812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy   598 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 657
Db   872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy   658 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 717
Db   932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy   718 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 777
Db   992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy   778 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 837
Db  1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy   838 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 897
Db  1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy   898 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATGCAAAAGAAAGTATA 957
Db  1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATGCAAAAGAAAGTATA 1231

Qy   958 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1017
Db  1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy  1018 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTGGCTTGTATTACCGA 1077
Db  1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTGGCTTGTATTACCGA 1350

Qy  1078 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTGAAAATTTTAGCAAA 1137
Db  1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTGAAAATTTTAGCAAA 1410

Qy  1138 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTGTTGAGGTTGTAATG 1197
Db  1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTGTTGAGGTTGTAATG 1470

Qy  1198 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1257
Db  1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy  1258 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1317
Db  1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy  1318 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1377
Db  1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy  1378 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1437
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Qy  1438 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1497
Db  1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy  1498 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1557
Db  1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy  1558 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1617
Db  1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy  1618 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1677
Db  1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy  1678 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1737
Db  1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy  1738 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1797
Db  2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy  1798 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1857
Db  2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy  1858 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 1917
Db  2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy  1918 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 1977
Db  2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy  1978 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2037
Db  2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy  2038 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2097
Db  2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy  2098 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2157
Db  2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy  2158 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2217
Db  2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy  2218 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2277
Db  2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy  2278 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2337
Db  2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy  2338 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2397
Db  2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy  2398 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2457
Db  2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy  2458 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
Db  2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
AF043224
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
     exon            <1. .7
                     /gene="RB1"
                     /number=5
     CDS             <1. .137
                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
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     exon            8. .76
                     /gene="RB1"
                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
                     /gene="RB1"
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     exon            351. .418
                     /gene="RB1"
                     /number=6
     exon            419. .>426
                     /gene="RB1"
                     /number=7
BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 1.7e-153;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
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Db     103 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 162

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 222

Qy     124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     223 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 282

Qy     184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     283 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 342

Qy     244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     343 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 402

Qy     304 TTTTTATTAG 313
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Db     403 TTTTTATTAG 412


RESULT  12
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
                     /note="mutated retinoblastoma protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


  Query Match             8.3%;  Score 207;  DB 9;  Length 480;
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  Best Local Similarity   100.0%;  Pred. No. 9.6e-99;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    318 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy    378 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 393

Qy    438 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 453

Qy    498 GATAGCAAAACAACTAGAAAATGATAC 524
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Db    454 GATAGCAAAACAACTAGAAAATGATAC 480


RESULT  13
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.9%;  Score 198;  DB 5;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-94;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1211 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1271 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1331 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1390
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1391 CCCTTGCATGGCTCTCAG 1408
          ||||||||||||||||||
Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  14
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
                     /number=16
     exon            250. .446
                     /note="retinoblastoma susceptibility gene"
                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.9%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-94;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1211 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1271 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1330
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Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1331 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1390
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1391 CCCTTGCATGGCTCTCAG 1408
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  15
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
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REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
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     protein_bind    1858. .1863
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     exon            <2060. .2196
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                     61730. .61807,64330. .64439,65364. .65441,70242. .70329,
                     73753. .73869,76430. .76486,76889. .76920,77001. .77077,
                     78083. .78279,149998. .150116,153208. .153353,156693. .156838,
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                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSA
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                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
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                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
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     intron          2197. .5423
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     intron          5551. .39445
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     intron          44707. .45798
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     intron     156839. .160729
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     exon       160730. .160834
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  Best Local Similarity   100.0%;  Pred. No. 5.4e-94;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1211 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1270
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Db   78083 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 78142

Qy    1271 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78143 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 78202

Qy    1331 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1390
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78203 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 78262

Qy    1391 CCCTTGCATGGCTCTCAG 1408
           ||||||||||||||||||
Db   78263 CCCTTGCATGGCTCTCAG 78280


Search completed: February 13, 2000, 11:31:12
Job time: 17168 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:55:55 ; Search time 9092.07 Seconds
(without alignments)
1156.112 Million cell updates/sec

Title: US-09-026-459A-50_COPY_7_2790
Perfect score: 2784
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2784

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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3: em_est3:*
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103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		476	17.1	572	64	AL120941	AL120941 DKFZp762D
c 2		352	12.6	415	51	AI745644	AI745644 tr24b06.x
c 3		348	12.5	411	51	AI745643	AI745643 tr24b05.x
4		257	9.2	285	33	AA382103	AA382103 EST95270
5		204	7.3	304	32	AA361277	AA361277 EST70529
c 6		181	6.5	571	41	AI074792	AI074792 oy03a06.s
c 7		161	5.8	329	36	AA664676	AA664676 nu64f09.s

	8	156	5.6	456	30	AA210875 AA210875 zr88f11.r
c	9	132	4.7	171	38	AA765882 AA765882 oa14a06.s
	10	114	4.1	386	24	N25402 N25402 yx40c12.r1
	11	113	4.1	457	24	N41391 N41391 yw70g06.r1
	12	89	3.2	152	22	R57845 R57845 F6142 Fetal
	13	82	2.9	525	30	AA258255 AA258255 zr59g04.r
c	14	53	1.9	349	20	T24020 T24020 seq2177 3HF
	15	48	1.7	397	22	R70325 R70325 yj81b10.r1
	16	48	1.7	522	28	AA072780 AA072780 mm76a05.r
	17	42	1.5	986	89	AQ901300 AQ901300 HS_5234_A
	18	38	1.4	472	46	AA955457 AA955457 UI-R-A1-e
c	19	35	1.3	914	38	AA763411 AA763411 vw54a04.r
c	20	35	1.3	871	38	AA763485 AA763485 vw54h01.r
	21	34	1.2	427	37	AA709628 AA709628 vv41c11.r
c	22	33	1.2	462	48	AI606529 AI606529 vb27g08.y
	23	33	1.2	832	49	AI646038 AI646038 vw54a10.x
	24	33	1.2	709	49	AI646097 AI646097 vw54h07.x
	25	33	1.2	575	49	AI662832 AI662832 vb27g08.x
	26	31	1.1	284	59	AV111279 AV111279 AV111279
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	28	29	1.0	615	40	AA959836 AA959836 vw54h01.s
c	29	26	0.9	405	39	AA861150 AA861150 ak36a12.s
	30	26	0.9	529	40	AA959709 AA959709 vw54a04.s
	31	25	0.9	356	41	AI020392 AI020392 ub17a05.r
c	32	24	0.9	492	33	AA396353 AA396353 vb27g08.r
c	33	22	0.8	440	33	AA440741 AA440741 LD15614.5
c	34	22	0.8	332	44	AI259982 AI259982 LP03562.5
	35	22	0.8	586	59	AI770926 AI770926 606063D04
c	36	21	0.8	640	38	AA752076 AA752076 96AS1023
	37	21	0.8	219	38	AA752355 AA752355 96GS0852
c	38	21	0.8	501	74	AV391000 AV391000 AV391000
c	39	20	0.7	439	21	R12275 R12275 yf40f10.r1
c	40	20	0.7	424	21	R21339 R21339 yg50d05.r1
c	41	20	0.7	372	21	R21352 R21352 yg50f05.r1
c	42	20	0.7	351	21	T78368 T78368 yc99g02.r1
c	43	20	0.7	478	22	H06003 H06003 yl76c05.r1
c	44	20	0.7	299	36	AA618388 AA618388 nq18h09.s
	45	20	0.7	574	103	AQ498524 AQ498524 HS_5120_B

ALIGNMENTS

RESULT 1
AL120941
LOCUS AL120941 572 bp mRNA EST 27-SEP-1999
DEFINITION DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762D143 5', mRNA sequence.
ACCESSION AL120941
VERSION AL120941.1 GI:5926942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948410.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.
No sl sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES Location/Qualifiers
source 1. .572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762D143"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 180 a 128 c 98 g 166 t
ORIGIN

Query Match 17.1%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 3.9e-204;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1468 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1527
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1528 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1588 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1648 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1707
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1708 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1767
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Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1768 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1827
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Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1828 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1887
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Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1888 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1943
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT 2
AI745644/c
LOCUS AI745644 415 bp mRNA EST 21-JUN-1999
DEFINITION tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI745644
VERSION AI745644.1 GI:5113932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137189.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

```
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             12.6%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-148;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2138 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 2197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy    2198 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy    2258 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2317
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Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy    2318 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2377
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Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy    2378 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2437
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Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy    2438 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2489
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


  Query Match             12.5%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-146;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2142 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy    2202 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy    2262 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy    2322 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy    2382 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2441
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Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy    2442 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2489
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .285
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):107475"
                      /db_xref="taxon:9606"
                      /clone_lib="Activated T-cells II"
                      /cell_type="T-lymphocyte"
                      /dev_stage="adult"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             9.2%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-105;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1932 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1991
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy    1992 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 2051
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy    2052 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 2111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy    2112 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy    2172 TGTAACAGCATACAAGG 2188
           ||||||||||||||||
Db     241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             7.3%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 2e-81;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy    1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1981 CGGCTAAATACACTT 1995
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AI074792/c
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


  Query Match             6.5%;  Score 181;  DB 41;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 4e-71;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     85 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 309

Qy    145 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 249

Qy    205 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 189

Qy    265 G 265
          |
Db    188 G 188


RESULT   7
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             5.8%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-62;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1536 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1596 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1656 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1696
          |||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   8
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             5.6%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 8e-60;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2629 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCGAGGAGAGTCCAAA 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCGAGGAGAGTCCAAA 84

Qy   2689 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2749 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||||||||||||||
Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   9
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             4.7%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 7e-49;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1331 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy   1391 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1451 TGTCTTTATTGG 1462
          ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT  10
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.1%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2584 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60

Qy   2644 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  11
N41391
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g     128 t
ORIGIN


  Query Match             4.1%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-40;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2520 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2580 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2632
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329
```

```
RESULT  12
R57845
LOCUS       R57845         152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.2%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-29;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2354 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy    2414 ATATTTCACCCCTGAAGAGTCCATATAAA 2442
           |||||||||||||||||||||||||||||
Db      61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  13
AA258255
LOCUS       AA258255       525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             2.9%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-26;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2703 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2762
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2763 TACCTCAAACAAGGAAGAGAAA 2784
           |||||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  14
T24020/c
LOCUS       T24020         349 bp    mRNA            EST       01-AUG-1994
DEFINITION  seq2177 3HFLSK20 Homo sapiens cDNA clone 3HFLSK20-63 3', mRNA
            sequence.
ACCESSION   T24020
VERSION     T24020.1  GI:520260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   Soares,M.B.
  TITLE     Human infant brain library b4HB3MA cDNAs
```

```
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Bento Soares
            Columbia University
            Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
            10032
            Tel: 2129602313
            Fax: 2127813577
            Email: cuc@cuccfa.ccc.columbia.edu
            antisense Kanamycin
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="3HFLSK20-63"
                     /clone_lib="3HFLSK20"
                     /lab_host="E. coli"
                     /note="Vector: Lafmid K; Site_1: Not I; Site_2: EcoR I;
                     cDNA from polyA+ RNA from human fetal liver + spleen. 20
                     weeks post-conception "
BASE COUNT       98 a     73 c     59 g    118 t      1 others
ORIGIN
```

```
  Query Match             1.9%;  Score 53;  DB 20;  Length 349;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-13;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    213 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 297
```

```
RESULT  15
R70325
LOCUS       R70325         397 bp    mRNA            EST       01-JUN-1995
DEFINITION  yj81b10.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:155131 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   R70325
VERSION     R70325.1  GI:843842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 803
            High quality sequence stops: 324
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 803   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1. .397
                     /organism="Homo sapiens"
                     /db_xref="GDB:569832"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155131"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      130 a     47 c     71 g    147 t      2 others
ORIGIN
```

```
  Query Match             1.7%;  Score 48;  DB 22;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-11;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    136 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 183
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 334
```

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Search completed: February 13, 2000, 16:56:05
Job time: 15547 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:54:38 ; Search time 9092.07 Seconds
(without alignments)
1088.838 Million cell updates/sec

Title: US-09-026-459A-30_COPY_7_2628
Perfect score: 2622
Sequence: 1 ATGGATTTTACTGCATTATG.....CCTCAAACAAGGAAGAGAAA 2622

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
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24: gb_est5:*
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37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
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41: gb_est22:*
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45: gb_est26:*
46: gb_est27:*
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50: gb_est31:*
51: gb_est32:*
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53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match %	Length	DB	ID	Description
1		476	18.2	572	64	AL120941	AL120941 DKFZp762D
c 2		352	13.4	415	51	AI745644	AI745644 tr24b06.x
c 3		348	13.3	411	51	AI745643	AI745643 tr24b05.x
4		257	9.8	285	33	AA382103	AA382103 EST95270
5		204	7.8	304	32	AA361277	AA361277 EST70529
c 6		161	6.1	329	36	AA664676	AA664676 nu64f09.s
7		156	5.9	456	30	AA210875	AA210875 zr88f11.r

c	8	132	5.0	171	38	AA765882 AA765882 oa14a06.s
	9	114	4.3	386	24	N25402 N25402 yx40c12.r1
	10	113	4.3	457	24	N41391 N41391 yw70g06.r1
c	11	100	3.8	571	41	AI074792 AI074792 oy03a06.s
	12	89	3.4	152	22	R57845 R57845 F6142 Fetal
	13	82	3.1	525	30	AA258255 AA258255 zr59g04.r
c	14	53	2.0	349	20	T24020 T24020 seq2177 3HF
	15	48	1.8	522	28	AA072780 AA072780 mm76a05.r
	16	42	1.6	986	89	AQ901300 AQ901300 HS_5234_A
	17	38	1.4	472	46	AA955457 AA955457 UI-R-A1-e
c	18	35	1.3	914	38	AA763411 AA763411 vw54a04.r
c	19	35	1.3	871	38	AA763485 AA763485 vw54h01.r
	20	34	1.3	427	37	AA709628 AA709628 vv41c11.r
c	21	33	1.3	462	48	AI606529 AI606529 vb27g08.y
	22	33	1.3	832	49	AI646038 AI646038 vw54a10.x
	23	33	1.3	709	49	AI646097 AI646097 vw54h07.x
	24	33	1.3	575	49	AI662832 AI662832 vb27g08.x
	25	31	1.2	284	59	AV111279 AV111279
	26	31	1.2	174	72	AV302462 AV302462
	27	29	1.1	615	40	AA959836 AA959836 vw54h01.s
	28	26	1.0	397	22	R70325 R70325 yj81b10.r1
c	29	26	1.0	405	39	AA861150 AA861150 ak36a12.s
	30	26	1.0	529	40	AA959709 AA959709 vw54a04.s
	31	25	1.0	356	41	AI020392 AI020392 ub17a05.r
c	32	24	0.9	492	33	AA396353 AA396353 vb27g08.r
c	33	20	0.8	439	21	R12275 R12275 yf40f10.r1
c	34	20	0.8	424	21	R21339 R21339 yg50d05.r1
c	35	20	0.8	372	21	R21352 R21352 yg50f05.r1
c	36	20	0.8	351	21	T78368 T78368 yc99g02.r1
c	37	20	0.8	478	22	H06003 H06003 yl76c05.r1
c	38	20	0.8	299	36	AA618388 AA618388 nq18h09.s
	39	20	0.8	405	38	AA774885 AA774885 ae83f10.s
	40	20	0.8	175	39	AA825220 AA825220 oc66f12.s
	41	20	0.8	446	40	AA926650 AA926650 om28c01.s
	42	20	0.8	453	44	AI309208 AI309208 qo70d01.x
c	43	20	0.8	188	71	AV320612 AV320612
	44	20	0.8	548	81	B72527 B72527 RPCI11-9E12
	45	20	0.8	574	103	AQ498524 AQ498524 HS_5120_B

ALIGNMENTS

```
RESULT   1
AL120941
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


  Query Match           18.2%;  Score 476;  DB 64;  Length 572;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-225;
  Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1306 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1366 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1426 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1486 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1546 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1606 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1666 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1726 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1781
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476


RESULT   2
AI745644/c
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
```

Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco.

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FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN
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  Query Match             13.4%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-163;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1976 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 2035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy   2036 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2095
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy   2096 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy   2156 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy   2216 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy   2276 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2327
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64
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RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN
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  Query Match             13.3%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-161;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1980 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy   2040 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy   2100 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy   2160 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy   2220 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy   2280 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2327
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64
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RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .285
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):107475"
                      /db_xref="taxon:9606"
                      /clone_lib="Activated T-cells II"
                      /cell_type="T-lymphocyte"
                      /dev_stage="adult"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             9.8%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-116;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1770 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy   1830 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy   1890 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy   1950 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy   2010 TGTAACAGCATACAAGG 2026
          ||||||||||||||||
Db    241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277       304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             7.8%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 3.2e-90;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1579 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy   1639 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1699 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1758
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1759 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1819 CGGCTAAATACACTT 1833
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.1%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-69;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1374 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1434 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1494 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1534
          |||||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   7
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             5.9%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-66;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2467 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2527 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2587 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||
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Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   8
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.0%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-54;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1169 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCGATGCTTAAATCAG 1228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCGATGCTTAAATCAG 112

Qy   1229 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1289 TGTCTTTATTGG 1300
           ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT   9
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.3%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-45;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2422 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60
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Qy   2482 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  10
N41391
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


  Query Match             4.3%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-45;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2358 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2418 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2470
          |||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329


RESULT  11
AI074792/c
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


  Query Match             3.8%;  Score 100;  DB 41;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-39;
  Matches  100;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 228

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 103
          |||||||||||||||||||||||||||||||||||||||
Db    227 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 188


RESULT  12
R57845
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
```

```
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN
```

```
  Query Match             3.4%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-33;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2192 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCGTGGAGGGAACATCT 2251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCGTGGAGGGAACATCT 60

Qy   2252 ATATTTCACCCCTGAAGAGTCCATATAAA 2280
          |||||||||||||||||||||||||||||
Db     61 ATATTTCACCCCTGAAGAGTCCATATAAA 89
```

```
RESULT  13
AA258255
LOCUS       AA258255      525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN
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  Query Match             3.1%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-30;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2541 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy   2601 TACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||
Db     61 TACCTCAAACAAGGAAGAGAAA 82
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RESULT  14
T24020/c
LOCUS       T24020        349 bp    mRNA            EST       01-AUG-1994
DEFINITION  seq2177 3HFLSK20 Homo sapiens cDNA clone 3HFLSK20-63 3', mRNA
            sequence.
ACCESSION   T24020
VERSION     T24020.1  GI:520260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   Soares,M.B.
  TITLE     Human infant brain library b4HB3MA cDNAs
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Bento Soares
            Columbia University
            Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
            10032
            Tel: 2129602313
            Fax: 2127813577
            Email: cuc@cuccfa.ccc.columbia.edu
```

```
            antisense Kanamycin
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .349
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="3HFLSK20-63"
                      /clone_lib="3HFLSK20"
                      /lab_host="E. coli"
                      /note="Vector: Lafmid K; Site_1: Not I; Site_2: EcoR I;
                      cDNA from polyA+ RNA from human fetal liver + spleen. 20
                      weeks post-conception "
BASE COUNT       98 a     73 c     59 g    118 t      1 others
ORIGIN


  Query Match             2.0%;  Score 53;  DB 20;  Length 349;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-15;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 103
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 297


RESULT  15
AA072780
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES              Location/Qualifiers
     source           1. .522
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:534320"
                      /clone_lib="Stratagene mouse macrophage (#937306)"
                      /tissue_type="macrophage"
                      /dev_stage="WEHI-3 cell line"
                      /lab_host="SOLR (kanamycin resistant)"
                      /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                      Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                      Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                      3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


  Query Match             1.8%;  Score 48;  DB 28;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-13;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2167 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2214
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     207 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 254


Search completed: February 13, 2000, 16:54:46
Job time: 15468 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 12:36:58 ; Search time 9092.07 Seconds
(without alignments)
1227.123 Million cell updates/sec

Title: US-09-026-459A-28_COPY_7_2961
Perfect score: 2955
Sequence: 1 ATGCAGGACAGCGGCCCGGA.....TGTTTCCTCTTCCAAAGTAA 2955

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
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16: em_est16:*
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69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
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89: gb_gss7:*
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101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	476	16.1	572	64	AL120941	AL120941 DKFZp762D
2	352	11.9	525	30	AA258255	AA258255 zr59g04.r
c 3	352	11.9	415	51	AI745644	AI745644 tr24b06.x
c 4	348	11.8	411	51	AI745643	AI745643 tr24b05.x
5	257	8.7	285	33	AA382103	AA382103 EST95270
6	204	6.9	304	32	AA361277	AA361277 EST70529
7	203	6.9	456	30	AA210875	AA210875 zr88f11.r

c	8	190	6.4	457	42	AI093215 AI093215 qb04a02.x
	9	188	6.4	430	24	N32668 N32668 yx77d10.r1
c	10	182	6.2	447	42	AI082179 AI082179 ox75e04.x
c	11	164	5.5	571	41	AI074792 AI074792 oy03a06.s
c	12	161	5.4	329	36	AA664676 AA664676 nu64f09.s
c	13	151	5.1	370	38	AA766463 AA766463 oa32f12.s
c	14	132	4.5	171	38	AA765882 AA765882 oa14a06.s
	15	114	3.9	386	24	N25402 N25402 yx40c12.r1
	16	113	3.8	457	24	N41391 N41391 yw70g06.r1
	17	89	3.0	152	22	R57845 R57845 F6142 Fetal
c	18	53	1.8	349	20	T24020 T24020 seq2177 3HF
	19	48	1.6	397	22	R70325 R70325 yj81b10.r1
	20	48	1.6	522	28	AA072780 AA072780 mm76a05.r
	21	42	1.4	986	89	AQ901300 AQ901300 HS_5234_A
	22	38	1.3	472	46	AA955457 AA955457 UI-R-A1-e
c	23	35	1.2	914	38	AA763411 AA763411 vw54a04.r
c	24	35	1.2	871	38	AA763485 AA763485 vw54h01.r
	25	34	1.2	427	37	AA709628 AA709628 vv41c11.r
c	26	33	1.1	462	48	AI606529 AI606529 vb27g08.y
	27	33	1.1	832	49	AI646038 AI646038 vw54a10.x
	28	33	1.1	709	49	AI646097 AI646097 vw54h07.x
	29	33	1.1	575	49	AI662832 AI662832 vb27g08.x
	30	31	1.0	284	59	AV111279 AV111279 AV111279
	31	31	1.0	174	72	AV302462 AV302462 AV302462
	32	29	1.0	615	40	AA959836 AA959836 vw54h01.s
c	33	26	0.9	405	39	AA861150 AA861150 ak36a12.s
	34	26	0.9	529	40	AA959709 AA959709 vw54a04.s
	35	25	0.8	356	41	AI020392 AI020392 ub17a05.r
c	36	24	0.8	492	33	AA396353 AA396353 vb27g08.r
c	37	20	0.7	439	21	R12275 R12275 yf40f10.r1
c	38	20	0.7	424	21	R21339 R21339 yg50d05.r1
c	39	20	0.7	372	21	R21352 R21352 yg50f05.r1
c	40	20	0.7	351	21	T78368 T78368 yc99g02.r1
c	41	20	0.7	478	22	H06003 H06003 yl76c05.r1
c	42	20	0.7	255	30	AA247197 AA247197 csg0286.s
c	43	20	0.7	299	36	AA618388 AA618388 nq18h09.s
	44	20	0.7	405	38	AA774885 AA774885 ae83f10.s
	45	20	0.7	574	103	AQ498524 AQ498524 HS_5120_B

ALIGNMENTS

RESULT 1
AL120941
LOCUS AL120941 572 bp mRNA EST 27-SEP-1999
DEFINITION DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762D143 5', mRNA sequence.
ACCESSION AL120941
VERSION AL120941.1 GI:5926942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948410.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES Location/Qualifiers
source 1. .572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762D143"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 180 a 128 c 98 g 166 t
ORIGIN

Query Match 16.1%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.9e-226;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1369 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1429 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1489 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1549 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1609 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1669 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1729 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1789 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT 2
AA258255
LOCUS AA258255 525 bp mRNA EST 06-AUG-1997
DEFINITION zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA258255
VERSION AA258255.1 GI:1893417
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 525)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1393412.
Contact: Wilson RK
Washington University School of Medicine

```
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES              Location/Qualifiers
     source           1. .525
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:667734"
                      /clone_lib="Soares_NhHMPu_S1"
                      /tissue_type="Pooled human melanocyte, fetal heart, and
                      pregnant uterus"
                      /lab_host="DH10B"
                      /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; Equal amounts of plasmid DNA from three
                      normalized libraries (melanocyte 2NbHM, pregnant uterus
                      NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                      were made in vitro. Following HAP purification, this DNA
                      was used as tracer in a subtractive hybridization
                      reaction. The driver was PCR-amplified cDNAs from pools of
                      5,000 clones made from the same 3 libraries. The pools
                      consisted of I.M.A.G.E. clones 260232-265223,
                      340488-345479, and 484488-489479."
BASE COUNT      150 a      89 c     107 g     179 t
ORIGIN


  Query Match             11.9%;  Score 352;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-164;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2604 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2663
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy   2664 TACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCT 2723
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCT 120

Qy   2724 CTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCC 2783
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCC 180

Qy   2784 ACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGT 2843
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGT 240

Qy   2844 GATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTG 2903
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTG 300

Qy   2904 TAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 352


RESULT   3
AI745644/c
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             11.9%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-164;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2039 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 2098
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy   2099 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy   2159 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2218
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy   2219 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy   2279 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2338
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy   2339 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2390
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
```

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            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN
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```
  Query Match             11.8%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-162;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy    2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy    2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy    2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy    2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy    2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2390
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64
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```
RESULT   5
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN
```

```
  Query Match             8.7%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-117;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1833 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1892
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy    1893 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1952
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120
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Qy   1953 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 2012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy   2013 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2072
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy   2073 TGTAACAGCATACAAGG 2089
          ||||||||||||||||
Db    241 TGTAACAGCATACAAGG 257
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RESULT   6
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN
```

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  Query Match             6.9%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-90;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1642 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy   1702 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169

Qy   1762 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1821
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1822 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1882 CGGCTAAATACACTT 1896
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304
```

```
RESULT   7
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
```

```
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.9%;  Score 203;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-90;
  Matches  203;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2753 TGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGG 2812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGG 310

Qy   2813 ATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCA 2872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 ATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCA 370

Qy   2873 TTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCA 2932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 TTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCA 430

Qy   2933 GATTGTTTCCTCTTCCAAAGTAA 2955
          |||||||||||||||||||||||
Db    431 GATTGTTTCCTCTTCCAAAGTAA 453


RESULT   8
AI093215/c
LOCUS       AI093215      457 bp    mRNA            EST       05-OCT-1998
DEFINITION  qb04a02.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
            IMAGE:1695242 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   AI093215
VERSION     AI093215.1  GI:3432191
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Feb 17, 1998 this sequence version replaced gi:2150873.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 670   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1695242"
                     /clone_lib="Soares_pregnant_uterus_NbHPU"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pT7T3 Pac; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization.  Library
                     constructed by M. Fatima Bonaldo."
BASE COUNT      174 a     78 c     75 g    130 t
ORIGIN


  Query Match             6.4%;  Score 190;  DB 42;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-84;
  Matches  190;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2766 CAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGC 2825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 CAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGC 398

Qy   2826 AGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATAC 2885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 AGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATAC 338

Qy   2886 AAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCT 2945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 AAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCT 278

Qy   2946 TCCAAAGTAA 2955
          ||||||||||
Db    277 TCCAAAGTAA 268


RESULT   9
N32668
LOCUS       N32668        430 bp    mRNA            EST       10-JAN-1996
DEFINITION  yx77d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:267763 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N32668
VERSION     N32668.1  GI:1153067
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 430)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Jan 25, 1995 this sequence version replaced gi:637756.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 297
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 495   Std Error: 0.00
            Seq primer: T7
            High quality sequence stop: 297.
FEATURES             Location/Qualifiers
     source          1. .430
                     /organism="Homo sapiens"
                     /db_xref="GDB:3877405"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:267763"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
```

the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT 113 a 70 c 81 g 158 t 8 others
ORIGIN

Query Match 6.4%; Score 188; DB 24; Length 430;
Best Local Similarity 100.0%; Pred. No. 9.3e-83;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   2768 GGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAG 2827
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAG 60

Qy   2828 ATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAA 2887
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAA 120

Qy   2888 GATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTC 2947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTC 180

Qy   2948 CAAAGTAA 2955
          ||||||||
Db    181 CAAAGTAA 188
```

RESULT 10
AI082179/c
LOCUS AI082179 447 bp mRNA EST 24-SEP-1998
DEFINITION ox75e04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662174 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI082179
VERSION AI082179.1 GI:3418971
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044361.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 663 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 439.
FEATURES Location/Qualifiers
source 1. .447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1662174"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
BASE COUNT 171 a 76 c 73 g 127 t
ORIGIN

Query Match 6.2%; Score 182; DB 42; Length 447;
Best Local Similarity 100.0%; Pred. No. 9e-80;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   2774 GTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAA 2833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447 GTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAA 388

Qy   2834 TTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGA 2893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    387 TTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGA 328

Qy   2894 AAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGT 2953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    327 AAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGT 268

Qy   2954 AA 2955
          ||
Db    267 AA 266
```

RESULT 11
AI074792/c
LOCUS AI074792 571 bp mRNA EST 24-SEP-1998
DEFINITION oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1664722 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32 repetitive element ;, mRNA sequence.
ACCESSION AI074792
VERSION AI074792.1 GI:3401436
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 571)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2043761.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 644 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 359.
FEATURES Location/Qualifiers
source 1. .571
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1664722"
/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 126 a 147 c 143 g 153 t 2 others
ORIGIN

Query Match 5.5%; Score 164; DB 41; Length 571;
Best Local Similarity 100.0%; Pred. No. 7.6e-71;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    351 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 292

Qy     63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    291 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 232

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 166
          |||||||||||||||||||||||||||||||||||||||||||
Db    231 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 188
```

RESULT 12
AA664676/c
LOCUS AA664676 329 bp mRNA EST 13-FEB-1998
DEFINITION nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497 similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA664676
VERSION AA664676.1 GI:2619289
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 329)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1400955.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 303.

```
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert size 600 bp. Reference: Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t  .
ORIGIN
```

Query Match 5.4%; Score 161; DB 36; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1437 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1497 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1557 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1597
          |||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135
```

RESULT 13
AA766463/c
LOCUS AA766463 370 bp mRNA EST 08-FEB-1998
DEFINITION oa32f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306703 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA766463
VERSION AA766463.1 GI:2817701
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 370)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2045900.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1313 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

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FEATURES             Location/Qualifiers
     source          1. .370
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1306703"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      145 a     65 c     58 g    102 t
```

```
ORIGIN

  Query Match             5.1%;  Score 151;  DB 38;  Length 370;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-64;
  Matches  151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2805 TTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAAT 2864
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAAT 292

Qy    2865 GTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAG 2924
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 GTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAG 232

Qy    2925 TTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
           ||||||||||||||||||||||||||||||
Db     231 TTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 201


RESULT  14
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN

  Query Match             4.5%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 1e-54;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1232 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy    1292 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy    1352 TGTCTTTATTGG 1363
           ||||||||||||
Db      51 TGTCTTTATTGG 40


RESULT  15
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
```

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

BASE COUNT 114 a 78 c 87 g 96 t 11 others
ORIGIN

Query Match 3.9%; Score 114; DB 24; Length 386;
Best Local Similarity 100.0%; Pred. No. 7.1e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2485 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGGTTTGATATTGAAGGA 2544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGGTTTGATATTGAAGGA 60

Qy   2545 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114
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Search completed: February 13, 2000, 16:54:38
Job time: 15460 sec

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OM of: US-09-026-459A-2_COPY_370_928 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 13, 2000  7:10 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171029_15755/app_query.fasta.1
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=seq2.rng -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-2_COPY_370_928
Query length: 559
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 39.630000



score_list:
Sequence              Strd Orig    ZScore    EScore Len  ! Documentation  ..
N_Geneseq_36:Q04713    +  2890.00 4957.46  1.6e-268  2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545    +  2890.00 4957.46  1.6e-268  2994  ! Retinoblastoma gene. Method of
N_Geneseq_36:Q70536    +  2890.00 4952.44  3.0e-268  4597  ! Human retinoblastoma gene. Dia
N_Geneseq_36:Q72690    +  2890.00 4956.56  1.8e-268  3233  ! Retinoblastoma 94kD therapeuti
N_Geneseq_36:Q90059    +  2890.00 4957.46  1.6e-268  2995  ! Retinoblastoma tumour suppress
N_Geneseq_36:V58447    +  2890.00 4955.76  1.9e-268  3461  ! Modified retinoblastoma tumour
N_Geneseq_36:V58448    +  2890.00 4956.16  1.8e-268  3347  ! Modified retinoblastoma tumour
N_Geneseq_36:V58449    +  2890.00 4956.82  1.7e-268  3161  ! Modified retinoblastoma tumour
N_Geneseq_36:V58450    +  2890.00 4956.05  1.9e-268  3377  ! Modified retinoblastoma tumour
N_Geneseq_36:V58451    +  2890.00 4956.03  1.9e-268  3383  ! Modified retinoblastoma tumour
N_Geneseq_36:V58452    +  2890.00 4955.45  2.0e-268  3554  ! Modified retinoblastoma tumour
N_Geneseq_36:V58440    +  2890.00 4955.45  2.0e-268  3555  ! Modified retinoblastoma tumour
N_Geneseq_36:V58441    +  2890.00 4955.78  1.9e-268  3455  ! Modified retinoblastoma tumour
N_Geneseq_36:V58442    +  2890.00 4956.00  1.9e-268  3392  ! Modified retinoblastoma tumour
N_Geneseq_36:V58443    +  2890.00 4956.24  1.8e-268  3323  ! Modified retinoblastoma tumour
N_Geneseq_36:V58444    +  2890.00 4956.44  1.8e-268  3266  ! Modified retinoblastoma tumour
N_Geneseq_36:V58445    +  2890.00 4957.00  1.7e-268  3113  ! Modified retinoblastoma tumour
N_Geneseq_36:V58446    +  2890.00 4956.24  1.8e-268  3323  ! Modified retinoblastoma tumour
N_Geneseq_36:V54990    +  2890.00 4955.45  2.0e-268  3555  ! DNA sequence of the specificat
N_Geneseq_36:V54991    +  2890.00 4956.62  1.7e-268  3218  ! DNA sequence of the specificat
N_Geneseq_36:V40004    +  2890.00 4957.46  1.6e-268  2994  ! Retinoblastoma protein RB. New
N_Geneseq_36:X00737    +  2890.00 4957.46  1.6e-268  2995  ! cDNA encoding a retinoblastoma
N_Geneseq_36:N81369    +  2887.00 4947.26  5.8e-268  4597  ! Human retinoblastoma gene Diag
N_Geneseq_36:X04501    +  2883.00 4940.35  1.4e-267  4597  ! Human retinoblastoma gene cDNA
N_Geneseq_36:Q86398    +  2882.00 4943.63  9.2e-268  2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489    +  2856.00 4892.58  6.4e-265  5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261    +  2823.00 4836.72  8.3e-262  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502    +  1369.00 2308.08  5.8e-121 18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490    +  1305.00 2197.57  8.3e-115 18177  ! DNA of human retinoblastoma g
N_Geneseq_36:Q32665    +   646.00 1080.72  1.4e-52   2808  ! Nearly complete p107 cDNA. cDN
N_Geneseq_36:Q82748    +   618.00 1030.63  8.3e-50   3249  ! pRb2 retinoblastoma tumour sup
N_Geneseq_36:V05714    +   498.00  821.61  3.7e-38   3747  ! Maize retinoblastoma gene. Con
N_Geneseq_36:V17081    +   498.00  821.61  3.7e-38   3747  ! Maize retinoblastoma (Rb) prot
N_Geneseq_36:V72860    +   293.50  469.94  1.4e-18   3241  ! Caenorhabditis elegans synMuv
N_Geneseq_36:V35363    +   120.00  165.21  0.1332    4940  ! P. falciparum gp190 DNA. Recom
N_Geneseq_36:Q41228    +   118.00  171.72  0.0579    2110  ! Clone GP22 encoding major surf
N_Geneseq_36:V52162    +   116.50  150.62  0.8663   10254  ! Streptococcus pneumoniae genc
N_Geneseq_36:X20248_04 -   116.50  122.84   30.53  110000  ! Continuation (5 of 10) of
N_Geneseq_36:V21451    +   114.00  154.85  0.5037    4940  ! P. falciparum modified gp190 D
N_Geneseq_36:Q58322    +   110.00  159.99  0.2604    1764  ! GGF2BPP4. Glial growth factor
N_Geneseq_36:Q62841    +   110.00  159.99  0.2604    1764  ! GGF2BPP4. Glial mitogenic poly
N_Geneseq_36:Q74913    +   110.00  159.99  0.2604    1764  ! Bovine glial cell growth fa
N_Geneseq_36:T06732    +   110.00  159.99  0.2604    1764  ! BPP4 glial growth factor 2
N_Geneseq_36:T31002    +   110.00  159.99  0.2604    1764  ! Glial growth factor II codi
N_Geneseq_36:T48089    +   110.00  159.99  0.2604    1764  ! Human neuregulin GGF2BBP4 c

seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


alignment_scores:
            Quality: 2890.00              Length:    559
              Ratio:  5.170                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-2_COPY_370_928 x Q04713   ..

 Align seg 1/1  to: Q04713  from: 1  to: 2994

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    1246 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1295

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1296 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1345

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1346 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1395

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1396 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1445

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1446 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1495

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1496 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1545

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1546 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1595
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 117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1596 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1645

 134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1646 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1695

 151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1696 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1745

 167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1746 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1795

 184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1796 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1845

 201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1846 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1895

 217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1896 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1945

 234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1946 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1995

 251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1996 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGGCTT 2045

 267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2046 CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAA 2095

 284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2096 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGGCTT 2145

 301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2146 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 2195

 317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2196 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 2245

 334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2246 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 2295

 351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2296 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2345

 367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2346 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2395

 384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2396 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2445

 401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2446 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2495

 417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2496 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2545

 434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2546 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2595

 451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2596 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2645

 467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2646 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2695

 484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2696 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2745

 501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2746 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2795

 517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2796 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2845

 534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2846 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2895

 551 MetAspThrSerAsnLysGluGluLys 559
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2896 ATGGATACCTCAAACAAGGAAGAGAAA 2922
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seq_name: N_Geneseq_36:Q41545

seq_documentation_block:

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ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag=  a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
```

```
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality: 2890.00              Length:    559
              Ratio:  5.170                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-2_COPY_370_928 x Q41545   ..

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    1246 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1295

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1296 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1345

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1346 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1395

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1396 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1445

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1446 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1495

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1496 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1545

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1546 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1595

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1596 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1645

     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
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     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1696 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1745

     167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1746 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1795

     184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1796 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1845

     201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1846 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1895

     217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1896 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1945

     234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1946 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1995

     251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1996 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 2045

     267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2046 CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAA 2095

     284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2096 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 2145

     301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2146 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 2195

     317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2196 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 2245

     334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2246 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 2295

     351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2296 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2345

     367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2346 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2395

     384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2396 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2445

     401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2446 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2495

     417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2496 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2545

     434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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    2546 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2595

     451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2596 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2645

     467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2646 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2695

     484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
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    2696 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2745

     501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2796 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2845

     534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
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    2846 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2895

     551 MetAspThrSerAsnLysGluGluLys 559
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    2896 ATGGATACCTCAAACAAGGAAGAGAAA 2922

seq_name: N_Geneseq_36:Q70536

seq_documentation_block:
ID   Q70536 standard; DNA; 4597 BP.
AC   Q70536;
DT   27-MAR-1995  (first entry)
DE   Human retinoblastoma gene.
KW   Retinoblastoma; cancer; detection; diagnosis; protein; neoplasm;
KW   assay; immune complex; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             337. .2787
FT                   /*tag=  a
PN   EP-608004-A.
PD   27-JUL-1994.
PF   11-AUG-1987; 307095.
PR   11-AUG-1986; US-895163.
PA   (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA   (WHED ) WHITEHEAD INST.
PA   BIOMEDICAL RES.
PI   Dryja TP,  Friend S;
DR   WPI; 94-272746/34.
DR   P-PSDB; R58568.
PT   Diagnosing the presence of defective retinoblastoma alleles -
PT   comprises comparing genetic material corresponding to a normal
PT   human retinoblastoma with DNA from a patient.
PS   Example 2(2); Figure 7; 18pp; English.
CC   A method for detecting the presence, in a tumour sample, of a protein
CC   the absence of which is associated with a neoplasm, comprises
CC   producing an antibody to the protein and then contacting the
CC   antibody with the tumour sample.  Immune complexes indicate the
CC   presence of the protein in the sample.  The method may be used in
CC   the detection and treatment of a defective human gene related to
CC   cancer, in particular retinoblastoma.
SQ   Sequence   4597 BP;    1489 A;    841 C;    812 G;    1455 T;


alignment_scores:
            Quality: 2890.00              Length:    559
              Ratio:  5.170                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-2_COPY_370_928 x Q70536   ..

 Align seg 1/1  to: Q70536  from: 1  to: 4597

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    1108 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1157

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1158 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1207

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1208 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1257

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1258 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1307

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1308 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1357

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1358 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1407

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1408 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1457

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1458 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1507

     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
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    1508 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1557

     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
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    1558 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1607

     167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
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    1608 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1657

     184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1708 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1757

     217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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     234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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    1808 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1857

     251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
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    1858 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 1907

     267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
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     284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
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    1958 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 2007

     301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
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    2008 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 2057

     317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2058 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 2107

     334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2108 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 2157

     351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2158 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2207

     367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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  2308 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2357

   417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
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   434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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  2408 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2457

   451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  2458 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2507

   467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
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   484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
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  2558 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2607

   501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
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  2608 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2657

   517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
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   534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
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  2708 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2757

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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;

alignment_scores:
            Quality: 2890.00              Length:    559
              Ratio:  5.170                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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     790 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 839

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     840 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 889

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     890 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 939

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     940 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 989

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     990 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1039

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1040 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1089

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1090 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1139

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
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     184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
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    1340 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1389

     201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
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     217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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1540 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 1589

 267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
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 284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
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1690 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 1739

 317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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1740 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAGCAAA 1789

 334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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1790 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 1839

 351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1840 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 1889

 367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1890 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 1939

 384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
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1940 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 1989

 401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1990 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2039

 417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
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2040 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2089

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     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2090 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2139

 451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2140 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2189

 467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2190 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2239

 484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2240 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2289

 501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2290 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2339

 517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2340 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2389

 534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2390 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2439

 551 MetAspThrSerAsnLysGluGluLys 559
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2440 ATGGATACCTCAAACAAGGAAGAGAAA 2466
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seq_name: N_Geneseq_36:Q90059

seq_documentation_block:

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ID   Q90059 standard; DNA; 2995 BP.
AC   Q90059;
DT   28-NOV-1995  (first entry)
DE   Retinoblastoma tumour suppressor gene.
KW   Recombinant; adenovirus; expression vector; TSG; small lung cancer;
KW   hepatocarcinoma; melanoma; retinoblastoma; sarcoma; sickle cell;
KW   anaemia; Tay-Sach's disease; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag=  a
PN   WO9511984-A.
PD   04-MAY-1995.
PF   25-OCT-1994; U12235.
PR   25-OCT-1993; US-142669.
PR   19-MAY-1994; US-246007.
PA   (CANJ-) CANJI INC.
PI   Gregory RJ,  Maneval DC,  Wills KN;
DR   WPI; 95-178876/23.
DR   P-PSDB; R74271.
PT   Adenoviral vector with deletion of viral protein IX contains
PT   foreign gene - esp. encoding tumour suppressor protein for gene
PT   therapy of tumours, reduces contamination by wild type adenovirus
PS   Disclosure; Fig 3; 92pp; English.
CC   The sequence is that of the DNA sequence encoding a retinoblastoma
CC   tumour protein.  The gene can be used in a novel method involving a
CC   recombinant adenovirus expression vector to treat diseases
CC   associated with the ansence of the TSg or the presence of a mutated
CC   TSG, e.g. many forms of carcinoma, sickle cell anaemia or Tay-Sach's
CC   disease.
CC   See also Q90060-5.
SQ   Sequence   2995 BP;    975 A;    617 C;    594 G;    809 T;
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alignment_scores:

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           Quality: 2890.00              Length:    559
             Ratio:  5.170                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

US-09-026-459A-2_COPY_370_928 x Q90059 ..

Align seg 1/1 to: Q90059 from: 1 to: 2995

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    1 ProProHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMe 17
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 1246 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1295

   17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1296 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1345

   34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1346 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1395

   51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1396 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1445

   67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1446 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1495

   84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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1496 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1545

 101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1546 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1595

 117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1596 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1645

 134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1646 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1695

 151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1696 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1745

 167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1746 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1795

 184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
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1796 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1845

 201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
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1846 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1895

 217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1896 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1945

 234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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1946 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1995

 251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
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1996 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 2045

 267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2046 CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAA 2095

 284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
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2096 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 2145

 301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2146 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 2195

 317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2196 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 2245

 334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2246 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 2295

 351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2296 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2345

 367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2346 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2395

 384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
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2396 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2445

 401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2446 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2495

 417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2496 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2545

 434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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2546 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2595

 451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2596 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2645

 467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2646 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2695

 484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2696 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2745

 501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2746 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2795

 517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2796 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2845

 534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2846 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2895

 551 MetAspThrSerAsnLysGluGluLys 559
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2896 ATGGATACCTCAAACAAGGAAGAGAAA 2922
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:

ID V58447 standard; DNA; 3461 BP.
AC V58447;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2700
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69371.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 188-192; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3461 BP; 1141 A; 675 C; 627 G; 1018 T;

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alignment_scores:
           Quality: 2890.00              Length:    559
             Ratio:  5.170                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58447  from: 1  to: 3461

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    1021 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1070

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1071 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1120

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1121 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1170

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1171 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1220

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1221 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1270

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1271 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1320

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1321 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1370

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1371 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1420

     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1421 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1470

     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1471 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1520

     167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
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    1521 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1570

     184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1571 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1620

     201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
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    1621 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCAGCT 1670

     217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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    1671 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1720

     234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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    1721 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1770

     251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
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    1771 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 1820

     267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1821 CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAA 1870

     284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1871 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 1920

     301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1921 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 1970

     317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1971 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 2020

     334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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     351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2071 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2120

     367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2121 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2170

     384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2171 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2220

     401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2221 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2270

     417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
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    2271 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2320

     434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2321 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2370

     451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2371 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2420

     467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2421 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2470

     484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2471 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2520

     501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2521 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2570

     517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2571 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2620

     534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2621 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2670

     551 MetAspThrSerAsnLysGluGluLys 559
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seq_name: N_Geneseq_36:V58448

seq_documentation_block:
ID   V58448 standard; DNA; 3347 BP.
AC   V58448;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2586
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69372.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 196-200; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3347 BP;    1096 A;    650 C;    617 G;    984 T;


alignment_scores:
            Quality: 2890.00              Length:    559
              Ratio:  5.170                Gaps:      0
 Percent Similarity: 100.000    Percent Identity: 100.000

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     907 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 956

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     957 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1006

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1007 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1056

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1057 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1106

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1107 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1156

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1157 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1206

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1207 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1256

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1257 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1306

     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1307 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1356

     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1357 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1406

     167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1407 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1456

     184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
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    1457 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1506

     201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1507 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1556

     217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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    1557 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1606

     234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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    1607 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1656

     251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
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    1707 CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAA 1756

     284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1757 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 1806

     301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1807 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 1856

     317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1857 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 1906

     334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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    1907 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 1956

     351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1957 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2006

     367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2007 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2056

     384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2057 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2106

     401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
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    2107 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2156
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     417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
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    2157 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2206

     434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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    2207 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2256

     451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2257 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2306

     467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2307 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2356

     484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2357 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2406

     501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2407 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2456

     517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2457 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2506

     534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2556

     551 MetAspThrSerAsnLysGluGluLys 559
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    2557 ATGGATACCTCAAACAAGGAAGAGAAA 2583

seq_name: N_Geneseq_36:V58449

seq_documentation_block:
ID   V58449 standard; DNA; 3161 BP.
AC   V58449;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2400
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69373.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 203-207; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3161 BP;    1037 A;    619 C;    586 G;    919 T;


alignment_scores:
            Quality: 2890.00            Length:    559
              Ratio:  5.170              Gaps:      0
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     771 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 820

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     821 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 870

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     871 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 920

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     921 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 970

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     971 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1020

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1021 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1070

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1071 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1120

     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1121 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1170

     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1171 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1220

     167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1221 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1270

     184 ysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeu 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1271 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1320

     201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1321 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1370

     217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1371 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1420

     234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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    1421 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1470

     251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1471 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 1520

     267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
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 1521 CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAA 1570

  284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
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 1571 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 1620

  301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1621 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 1670

  317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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 1671 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 1720

  334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1721 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 1770

  351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1771 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 1820

  367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1821 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 1870

  384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1871 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 1920

  401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1921 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 1970

  417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1971 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2020

  434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2021 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2070

  451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2071 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2120

  467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2121 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2170

  484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2171 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2220

  501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2221 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2270

  517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2271 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2320

  534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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seq_name: N_Geneseq_36:V58450

seq_documentation_block:

ID   V58450 standard; DNA; 3377 BP.
AC   V58450;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2616
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69374.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 210-215; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3377 BP;    1113 A;    654 C;    626 G;    984 T;


alignment_scores:
            Quality: 2890.00              Length:    559
              Ratio:  5.170                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-2_COPY_370_928 x V58450   ..

 Align seg 1/1  to: V58450  from: 1  to: 3377

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      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     987 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1036

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
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    1037 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1086

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1087 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1136

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1137 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1186

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1187 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1236

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    1237 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1286

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
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    1287 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1336
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 151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
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1387 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1436

 167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1437 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1486

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 217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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 234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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 251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
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 317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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 334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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 351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
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 401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
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 417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
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 434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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 467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
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 517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
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 534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
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seq_name: N_Geneseq_36:V58451

seq_documentation_block:
ID V58451 standard; DNA; 3383 BP.
AC V58451;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2622
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69375.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 218-222; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3383 BP; 1104 A; 657 C; 623 G; 999 T;

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Quality: 2890.00 Length: 559
Ratio: 5.170 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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     17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
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    993 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1042

     34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
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   1043 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1092

     51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1093 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1142

     67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
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   1143 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1192

     84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
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   1193 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1242

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    117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
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   1343 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1392

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   1393 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1442

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   1543 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1592

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    317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
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KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


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     317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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     334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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     351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
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    2164 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2213

     367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
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    2214 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2263

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    2264 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2313

     401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
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    2314 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2363

     417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2414 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2463

     451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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    2464 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2513

     467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2514 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2563

     484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2564 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2613

     501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2614 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGA 2663

     517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2664 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2713

     534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
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    2714 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2763

     551 MetAspThrSerAsnLysGluGluLys 559
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seq_name: N_Geneseq_36:V58440

seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality: 2890.00             Length:    559
              Ratio:  5.170               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-2_COPY_370_928 x V58440   ..

 Align seg 1/1  to: V58440  from: 1  to: 3555

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    1114 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1163

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1164 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1213

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1214 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1263

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1264 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1313

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1314 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1363

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1364 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1413

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1414 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1463

     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1464 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1513

     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1514 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1563

     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1564 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1613

     167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
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         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1664 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1713

     201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1714 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1763

     217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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    1764 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1813

     234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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    1814 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1863

     251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1864 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 1913

     267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1914 CCAGACCCAGAAGCCATTGAAATCTACCTCTCTCTTTCACTGTTTTATAAAA 1963

     284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1964 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 2013

     301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
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    2014 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 2063
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     317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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     334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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    2114 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 2163

     351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2164 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2213

     367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
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    2214 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTGTATTA 2263

     384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
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    2264 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2313

     401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
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     417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
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    2364 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2413

     434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2414 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2463

     451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
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    2464 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2513

     467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
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     484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2564 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2613

     501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
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    2614 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGGAGA 2663

     517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
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    2664 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2713

     534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID V58441 standard; DNA; 3455 BP.
AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2694
FT /*tag= a

PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification - inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor protein (RTSP) of the invention. The proteins can be used for inhibiting cellular proliferation, when coadministered with a p53 protein. The RTSPs can be used for treating diseases characterised by abnormal cellular proliferation, particularly cancers. The RTSPs have a broader spectrum of activity than wild type RTSPs.
SQ Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 T;

alignment_scores:
Quality: 2890.00 Length: 559
Ratio: 5.170 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: V58441 from: 1 to: 3455

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    1015 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1064

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
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    1065 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1114

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
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    1115 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1164

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
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      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
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      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
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     167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
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 201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
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1615 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1664

 217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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 234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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 251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
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1765 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 1814

 267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
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 284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
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1865 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 1914

 301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
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1915 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 1964

 317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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1965 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 2014

 334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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 351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
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2065 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2114

 367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
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2115 GGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2164

 384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2165 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2214

 401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
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2215 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2264

 417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2265 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2314

 434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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2315 ACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2364

 451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
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 467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
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2415 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2464

 484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
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 517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
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 534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
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2615 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2664

 551 MetAspThrSerAsnLysGluGluLys 559
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
            Quality: 2890.00              Length:    559
              Ratio:  5.170                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-2_COPY_370_928 x V58442   ..

 Align seg 1/1  to: V58442  from: 1  to: 3392

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     952 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 1001

      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1002 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1051
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  34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1052 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1101

  51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1102 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1151

  67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1152 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1201

  84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1202 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1251

 101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1252 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1301

 117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1302 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1351

 134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1352 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1401

 151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
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 167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
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 201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
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1552 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1601

 217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
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 234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
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1652 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1701

 251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
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 267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
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 284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
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 301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
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1852 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCA 1901

 317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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1902 CACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAA 1951

 334 leMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeu 350
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1952 TTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 2001

 351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
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2002 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2051

 367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
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 384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
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 401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
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2152 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2201

 417 oArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGlyA 434
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2202 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2251

 434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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 451 ProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGl 467
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2302 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGG 2351

 467 yGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValC 484
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2352 TGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAT 2401

 484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
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 501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
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 517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
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2502 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2551

 534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
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 551 MetAspThrSerAsnLysGluGluLys 559
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2602 ATGGATACCTCAAACAAGGAAGAGAAA 2628
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seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.

PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification - inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor protein (RTSP) of the invention. The proteins can be used for inhibiting cellular proliferation, when coadministered with a p53 protein. The RTSPs can be used for treating diseases characterised by abnormal cellular proliferation, particularly cancers. The RTSPs have a broader spectrum of activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

alignment_scores:
Quality: 2890.00 Length: 559
Ratio: 5.170 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-2_COPY_370_928 x V58443 ..

Align seg 1/1 to: V58443 from: 1 to: 3323

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      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
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     933 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 982

      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
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     983 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1032

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
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      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
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    1083 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1132

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
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    1133 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1182

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
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     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
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     151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
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     351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
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 501 LysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAs 517
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 517 pGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaG 534
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2433 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2482

 534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
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 551 MetAspThrSerAsnLysGluGluLys 559
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OM of: US-09-026-459A-29 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15917/app_query.fasta.1
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 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
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 -THREADS=1

Search information block:
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Query length: 895
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


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gb_est22:AI074792     -   54.00  989.35  2:4e-46   571  ! AI074792 oy03a06.s1 Soares_sene
gb_est17:AA664676     -   53.00  974.63  1.6e-45   329  ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875     +   52.00  953.32  2.5e-44   456  ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277     +   49.00  899.79  2.4e-41   304  ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882     -   43.00  790.95  2.7e-35   171  ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392     +   42.00  766.60  6.2e-34   356  ! AI020392 ub17a05.r1 Stratagene
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gb_est5:N25402        +   38.00  690.56  1.1e-29   386  ! N25402 yx40c12.r1 Soares melanc
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gb_est11:AA258255     +   27.00  480.82  5.1e-18   525  ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628     +   25.00  444.65  5.3e-16   427  ! AA709628 vv41c11.r1 Soares 2NbM
gb_est21:AA959836     +   24.00  423.06  8.5e-15   615  ! AA959836 vw54h01.s1 Soares mous
gb_est27:AA955457     +   24.00  425.04  6.6e-15   472  ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est30:AI646038     +   24.00  420.79  1.1e-14   832  ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832     +   24.00  423.56  7.9e-15   575  ! AI662832 vb27g08.x1 Soares mous
gb_est21:AA959709     +   23.00  405.33  8.2e-14   529  ! AA959709 vw54a04.s1 Soares mous
gb_est42:AV302462     +   23.00  413.66  2.8e-14   174  ! AV302462 AV302462 RIKEN full-le
gb_est1:T24020        -   17.00  295.29  1.1e-07   349  ! T24020 seq2177 3HFLSK20 Homo sa
gb_est14:AA396353     -   17.00  292.72  1.5e-07   492  ! AA396353 vb27g08.r1 Soares mous
gb_est3:R70325        +   16.00  275.47  1.4e-06   397  ! R70325 yj81b10.r1 Soares breast
gb_est33:AV111279     +   16.00  277.98  1.0e-06   284  ! AV111279 AV111279 Mus musculus
gb_est32:C82304       +   14.00  232.51  0.0003    799  ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300      +   14.00  230.94  0.0004    986  ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est36:AI931087     +   11.00  184.15  0.1718    267  ! AI931087 fc77c03.y1 Zebrafish W
gb_est20:AA861150     -   10.00  162.17  2.88      405  ! AA861150 ak36a12.s1 Soares_test
gb_est16:AA558448     -    9.00  141.17  42.54     539  ! AA558448 nk39a08.s1 NCI_CGAP_GC
gb_est20:AA868515     -    9.00  138.69  58.51     751  ! AA868515 ak43c04.s1 Soares_test
gb_est41:AV280802     +    9.00  147.46  19.01     233  ! AV280802 AV280802 RIKEN full-le
gb_est41:AV316571     +    9.00  146.99  20.18     248  ! AV316571 AV316571 RIKEN full-le
gb_est44:AW182968     -    9.00  139.28  54.24     694  ! AW182968 xj65f07.x1 Soares_NFL_
gb_est44:AW207606     +    9.00  144.32  28.41     354  ! AW207606 UI-H-BI1-afk-h-06-0
gb_gss1:CNS00WI4      +    9.00 *139.00  56.19     720  ! AL093610 Arabidopsis thalian
gb_gss3:B67798        +    9.00  141.47  40.95     518  ! B67798 T24H12TR TAMU Arabido
gb_gss5:AQ821350      +    9.00  140.05  49.12     626  ! AQ821350 HS_5216_B1_F12_T7A
gb_gss10:AQ231238     -    9.00  142.61  35.39     445  ! AQ231238 HS_2058_A1_A04_T7 C
gb_gss14:AQ571705     -    9.00  141.80  39.28     496  ! AQ571705 HS_2119_A1_D03_T7C

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00              Length:    159
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     457 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 473
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     473 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 490
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     490 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 506
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     507 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 523
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     523 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     540 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 556
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     557 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 573
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     573 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 590
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     590 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 606
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     607 LysProLeuLysSerThrSerLeuSer 615
         ||||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
            Quality:  117.00              Length:    117
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     681 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 697
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     697 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 714
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     714 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 730
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     731 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 747
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     747 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 764
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     764 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     781 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 797
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     797 g 797
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
```

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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


alignment_scores:
            Quality:  116.00             Length:    116
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     682 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 698
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     698 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 715
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     715 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 731
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     732 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 748
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     748 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 765
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     765 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 781
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     782 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 797
         |||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a      63 c      52 g      83 t
ORIGIN


alignment_scores:
            Quality:   85.00             Length:     85
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     628 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 645
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     645 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 661
         |||||||||||||||||||||||||||||||||||||||||||||||||
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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     662 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 678
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     678 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 695
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAAGAGCAT 251

     695 yrLys 696
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; 5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:

US-09-026-459A-29 x AA072780   ..

Align seg 1/1  to: AA072780  from: 1  to: 522

     761 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 777
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     777 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 794
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     794 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 810
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     811 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 827
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     827 s 827
         |
     458 A 458

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
```

```
ORIGIN


alignment_scores:
            Quality:   54.00             Length:     54
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

       2 GlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGluGl 18
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     350 CAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGA 301

      18 uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     300 AACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAG 251

      35 spHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerSerVal 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     250 ATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTG 201

      52 AspGlyValLeu 55
         |||||||||||
     200 GATGGAGTATTG 189

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


alignment_scores:
            Quality:   53.00             Length:     53
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     480 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 496
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     496 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 513
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     513 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 529
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     530 TrpLeuSer 532
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
```

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 80 c 90 g 133 t 3 others
ORIGIN

alignment_scores:
Quality: 52.00 Length: 52
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-29 x AA210875 ..

Align seg 1/1 to: AA210875 from: 1 to: 456

844 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 860
25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

860 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 877
75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

877 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 893
125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

894 GluLys 895
175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS AA361277 304 bp mRNA EST 21-APR-1997
DEFINITION EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION AA361277
VERSION AA361277.1 GI:2013596
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 304)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., , Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 12140200
COMMENT On Sep 12, 1996 this sequence version replaced gi:1407493.
Other_ESTs: THC168922
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .304
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165411"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 94 a 79 c 43 g 86 t 2 others
ORIGIN

alignment_scores:
Quality: 49.00 Length: 49
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-29 x AA361277 ..

Align seg 1/1 to: AA361277 from: 1 to: 304

548 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 564
50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

564 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 581
100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

581 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 596
150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS AA765882 171 bp mRNA EST 08-FEB-1998
DEFINITION oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA765882
VERSION AA765882.1 GI:2817120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044576.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

```
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Insert Length: 2415   Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
           Quality:   43.00            Length:     43
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     412 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 428
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     428 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 445
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     445 snAspAsnIlePheHisMetSerLeuLeu 454
         |||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS       AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION  ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AI020392
VERSION     AI020392.1  GI:3234728
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
           Quality:   42.00            Length:     42
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     791 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 807
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     807 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 824
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     824 rgValLeuLysArgSerAlaGluGly 832
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
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     source          1. .914
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AA763411/rev   ..

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     430 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 446
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     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     446 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 463
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     463 laThrTyrSerArgSerThr 469
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     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     829 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 845
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     845 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 862
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

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seq_name: gb_est19:AA763485

seq_documentation_block:
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

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     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     524 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 541
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     541 ysGlnSerLysAsp 545
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     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
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                     /db_xref="GDB:3887236"
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                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


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            Quality:   37.00            Length:     37
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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    824 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 841
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    268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

    841 ysLeuArgPhe 844
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    318 AACTACGCTTT 328
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 11:20:43 ; Search time 14294.3 Seconds
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Title: US-09-026-459A-32_COPY_7_2559
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Searched: 821193 seqs, -1518192014 residues

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Word size : 0

Number of hits that pass the threshold : 1642386

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49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2551	99.9	4597	5	I05311	I05311 Sequence 1
2	2551	99.9	2994	5	I81465	I81465 Sequence 2
3	2551	99.9	4839	10	HUMRB1MRNA	L41870 Homo sapien
4	2551	99.9	4600	10	HUMRBA1RA	M33647 Human retin
5	2551	99.9	2994	10	HUMRBSA	M28419 Human retin
6	2500	97.9	4597	5	I09369	I09369 Sequence 1
7	2460	96.4	3232	5	I18496	I18496 Sequence 1
c 8	2460	96.4	3232	5	I18497	I18497 Sequence 2
9	2208	86.5	4740	10	HUMRBS	M15400 Human retin
10	1420	55.6	4580	5	A01444	A01444 H.sapiens D
11	338	13.2	426	11	AF043224	AF043224 Homo sapi
12	207	8.1	480	9	HUMRBSY79	M19701 Human mutat
13	198	7.8	693	5	I09384	I09384 Sequence 17
14	198	7.8	693	9	HUMRBS15	M27858 Human retin
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16	196	7.7	340	10	HUMRB1501V	L49220 Homo sapien
17	167	6.5	555	10	HUMRB4MU2	L41904 Homo sapien
18	165	6.5	935	5	I09389	I09389 Sequence 22
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22	155	6.1	555	10	HUMRB17MU2	L41924 Homo sapien
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26	147	5.8	224	10	HUMRB1SDDL	L49225 Homo sapien
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33	144	5.6	625	10	HUMRB25EX	L41912 Homo sapien
34	132	5.2	224	10	HUMRB1610K	L49223 Homo sapien
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38	124	4.9	483	10	HUMRB19MUT	L41906 Homo sapien
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ALIGNMENTS

RESULT 1
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LOCUS I05311 4597 bp PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent EP 0259031.
ACCESSION I05311
VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN
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Query Match 99.9%; Score 2551; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     234 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 293

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
Db     294 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 353

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
Db     354 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 413

Qy     183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
Db     414 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 473

Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
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Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
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Qy     363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
Db     594 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 653

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
Db     654 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 713

Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
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Qy     783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
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Qy     903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
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Qy    1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
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Db    1314 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1373

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Qy    1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
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Qy    1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
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Qy    1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
Db    1614 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1673

Qy    1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
Db    1674 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1733

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Qy    1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
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Qy    1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
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Qy    1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
Db    2034 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2093

Qy    1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
Db    2094 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2153

Qy    1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
Db    2154 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2213

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Db   2214 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2273

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
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Db   2274 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2333

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
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Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
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RESULT   2
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ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
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REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
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ORIGIN


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Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
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Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
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Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
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Db    492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
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Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
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Db    612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
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Db    732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
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Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
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Db    852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
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Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
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Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
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Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
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Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
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Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
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Db   1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
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Db   1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
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Db   1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
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Db   1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
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Db   1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
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Db   1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
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Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
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Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
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RESULT   3
HUMRB1MRNA
LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
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ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
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Canada
Ph: 416 813-5868
FAX: 416 813-4989
E-mail: brenda@hafiz.eric.on.ca.

FEATURES Location/Qualifiers

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exon 402. .517
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mutation 506. .509
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exon 518. .637
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mutation 537. .542
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mutation 621. .622
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/note="Tumor GOS537 bilateral frameshift mutation causing premature stop.; G00-118-734"
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exon 638. .676
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exon 745. .855
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/number=7

exon 856. .998
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exon 999. .1076
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/number=9

exon 1077. .1186
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/note="G00-118-734"
/number=10

mutation 1095
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/note="Tumor GOS559 mutation causing premature stop.; G00-118-734"
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mutation 1104
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/note="Tumor GOS563 unilateral mutation causing premature stop; G00-118-734"
/citation=[5]
/replace="t"

exon 1187. .1264
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/note="G00-118-734"
/number=11

mutation 1209
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/note="Tumor GOS159 unilateral mutation causing a premature stop; G00-118-734"
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exon 1265. .1352
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/note="G00-118-734"
/number=12

mutation 1320
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mutation 1352. .1375
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/note="Tumor GOS13 unilateral frameshift mutation resulting in premature stop; Associated with this mutation is a large 13q14.3 sub-band deletion; G00-118-734"
/citation=[5]
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exon 1353. .1469
/gene="RB1"
/note="G00-118-734"
/number=13

mutation 1400. .1401
/gene="RB1"
/note="RBF58 insertion mutation causing premature stop; G00-118-734"
/citation=[4]

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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
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Db     371 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 430

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
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Db     431 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 490

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
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Db     491 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 550

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Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
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Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
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Db     671 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 730

Qy     363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
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Db     731 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 790

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
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Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
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Qy     543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
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Qy     603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
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Db     971 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1030

Qy     663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
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Qy     723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
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Qy     843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
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Db    1211 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1270

Qy     903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
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Qy     963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
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Db    1331 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1390

Qy    1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
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Qy    1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
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Db    1451 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1510

Qy    1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
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Db    1511 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1570

Qy    1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
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Db    1571 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1630

Qy    1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
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Qy    1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
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Qy    1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
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Qy    1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
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Qy    1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
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Db    2111 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2170

Qy    1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
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Db    2171 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2230

Qy    1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2231 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2290

Qy    1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
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Db    2291 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2350

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Db    2411 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2470
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Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
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Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
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Db   2891 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2921
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RESULT   4
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
            provided by S.H.Friend, 10-FEB-1988.
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BASE COUNT     1489 a    842 c    815 g    1454 t
ORIGIN
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  Query Match             99.9%;  Score 2551;  DB 10;  Length 4600;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
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Db    477 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 536

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
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Db    537 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 596

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Db    597 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 656

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Db    657 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 716

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
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Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
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Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
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Db    837 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 896

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
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ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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Query Match 99.9%; Score 2551; DB 10; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
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RESULT   6
I09369
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VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


  Query Match             97.9%;  Score 2500;  DB 5;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2550;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     234 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 293

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 353

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 413

Qy     183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 473

Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     474 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 533

Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     534 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 593

Qy     363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     594 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 653

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
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Db     654 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 713

Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
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Db     714 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 773

Qy     543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
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Db     774 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 833

Qy     603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
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Db     834 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 893

Qy     663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     894 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 953

Qy     723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     954 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1013

Qy     783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1014 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1073
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Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
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Db   1074 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1133

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1134 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1193

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1194 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1253

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1254 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1313

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
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Db   1314 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1373

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1374 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1433

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
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Db   1434 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1493

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
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Db   1494 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1553

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1554 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1613

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
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Db   1614 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1673

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
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Db   1674 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1733

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
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Db   1734 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1793

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
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Db   1794 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1853

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
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Db   1854 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1913

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
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Db   1914 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1973

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1974 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2033

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
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Db   2034 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2093

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
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Db   2094 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2153

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
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Db   2154 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2213

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
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Db   2214 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2273

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2274 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2333

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
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Db   2334 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2393

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2394 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2453

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
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Db   2454 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2513

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
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Db   2514 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2573

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
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Db   2574 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCA 2633

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
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Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
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Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
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RESULT   7
I18496
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN
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Query Match 96.4%; Score 2460; DB 5; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66
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Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
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Db    487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
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Db    547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
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Db    607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
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Db    787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
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Db    907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
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Db    967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
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Db   1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
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Db   1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
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Db   1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
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Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

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Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

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Db   1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
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Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
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Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
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Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
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Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466


RESULT   8
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


  Query Match             96.4%;  Score 2460;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
Db   3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
Db   3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
Db   3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
Db   3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
Db   2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
Db   2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
Db   2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
Db   2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
Db   2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
Db   2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
Db   2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
Db   2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
Db   2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
Db   2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
Db   2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671
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Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2374 CCTAAACCACTGAAAAAACTAGGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771


RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
     source          1. .4740
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                     /dev_stage="foetus"
                     /tissue_type="retina"
                     /map="13q14.2"
     mRNA            <1. .4740
                     /note="rbs mRNA"
     gene            139. .2925
                     /gene="RB1"
     CDS             139. .2925
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                     /note="retinoblastoma susceptibility protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA69807.1"
                     /db_xref="GI:190959"
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                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
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                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
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                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
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                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
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                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g    1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


  Query Match             86.5%;  Score 2208;  DB 10;  Length 4740;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2408;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    142 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 570

Qy    202 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 630

Qy    262 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690

Qy    322 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 750
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Qy    382 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 810

Qy    442 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 870

Qy    502 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 930

Qy    562 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990

Qy    622 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 681
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Db    991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 1050

Qy    682 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 741
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Db   1051 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 1110

Qy    742 TATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAG 801
          ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
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Qy    802 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 861
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Db   1171 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 1230

Qy    862 GAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 921
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 GAGGTGAATATAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1290

Qy    922 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 981
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Db   1291 TTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1350

Qy    982 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1410

Qy   1042 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1470

Qy   1102 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1530

Qy   1162 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1590

Qy   1222 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1650

Qy   1282 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1710

Qy   1342 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1770

Qy   1402 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1830

Qy   1462 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1890

Qy   1522 CACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 CACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1950

Qy   1582 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 1641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 2010

Qy   1642 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 1701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 2070

Qy   1702 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 1761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 2130

Qy   1762 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 1821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 2190

Qy   1822 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 1881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2250

Qy   1882 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 1941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2310

Qy   1942 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2370

Qy   2002 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2430

Qy   2062 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2490

Qy   2122 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2550

Qy   2182 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2610

Qy   2242 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2670

Qy   2302 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2730

Qy   2362 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2790

Qy   2422 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2850

Qy   2482 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2910

Qy   2542 AAGGAAGAGAAA 2553
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          ||||||||||||
Db   2911 AAGGAAGAGAAA 2922


RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match             55.6%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy     535 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 594
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy     595 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 654
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy     655 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 714
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy     715 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 774
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy     775 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 834
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy     835 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 894
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy     895 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 954
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy     955 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1014
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy    1015 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1074
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy    1075 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy    1135 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy    1195 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy    1255 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1314
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy    1315 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy    1375 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy    1435 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1494
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy    1495 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy    1555 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy    1615 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy    1675 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy    1735 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy    1795 TTAGAACATATCATCTGGACCGTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy    1855 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1914
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy    1915 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 1974
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy    1975 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2034
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy    2035 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2094
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy    2095 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2154
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy    2155 CCCTTACGGATTCCTGGAGGGAAGATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2214
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2370 CCCTTACGGATTCCTGGAGGGAAGATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429
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Qy   2215 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2275 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2335 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2394
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2395 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2455 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2515 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||||||||||||
Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
AF043224
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
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                     /db_xref="taxon:9606"
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                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
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                     /gene="RB1"
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     CDS             <1. .137
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                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
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                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
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                     /number=6
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                     /number=3
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     exon            313. .350
                     /gene="RB1"
                     /number=5
     exon            351. .418
                     /gene="RB1"
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     exon            419. .>426
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BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 6.8e-168;
  Matches  338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     33 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     75 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 134

Qy     93 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 194

Qy    153 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 254

Qy    213 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 314

Qy    273 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 374

Qy    333 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 370
          |||||||||||||||||||||||||||||||||||||
Db    375 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 412
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RESULT  12
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
```

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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
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Qy     375 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 434
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Db     274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy     435 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 494
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Db     334 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 393

Qy     495 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 554
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Qy     555 GATAGCAAAACAACTAGAAAATGATAC 581
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Db     454 GATAGCAAAACAACTAGAAAATGATAC 480


RESULT  13
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LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
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ORIGIN


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Qy    1388 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1447
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Db     370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy    1448 CCCTTGCATGGCTCTCAG 1465
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Db     430 CCCTTGCATGGCTCTCAG 447


RESULT  14
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DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
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ORIGIN


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Db     370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy    1448 CCCTTGCATGGCTCTCAG 1465
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RESULT  15
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DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
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VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
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SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
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  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
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About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN


alignment_scores:
           Quality:  850.00              Length:    850
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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seq_name: gb_pat:I81465

seq_documentation_block:
LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


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              Ratio:  1.000                Gaps:      0
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VERSION     L41870.1  GI:793994
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
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  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
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  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
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  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
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  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
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REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
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  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
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            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
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  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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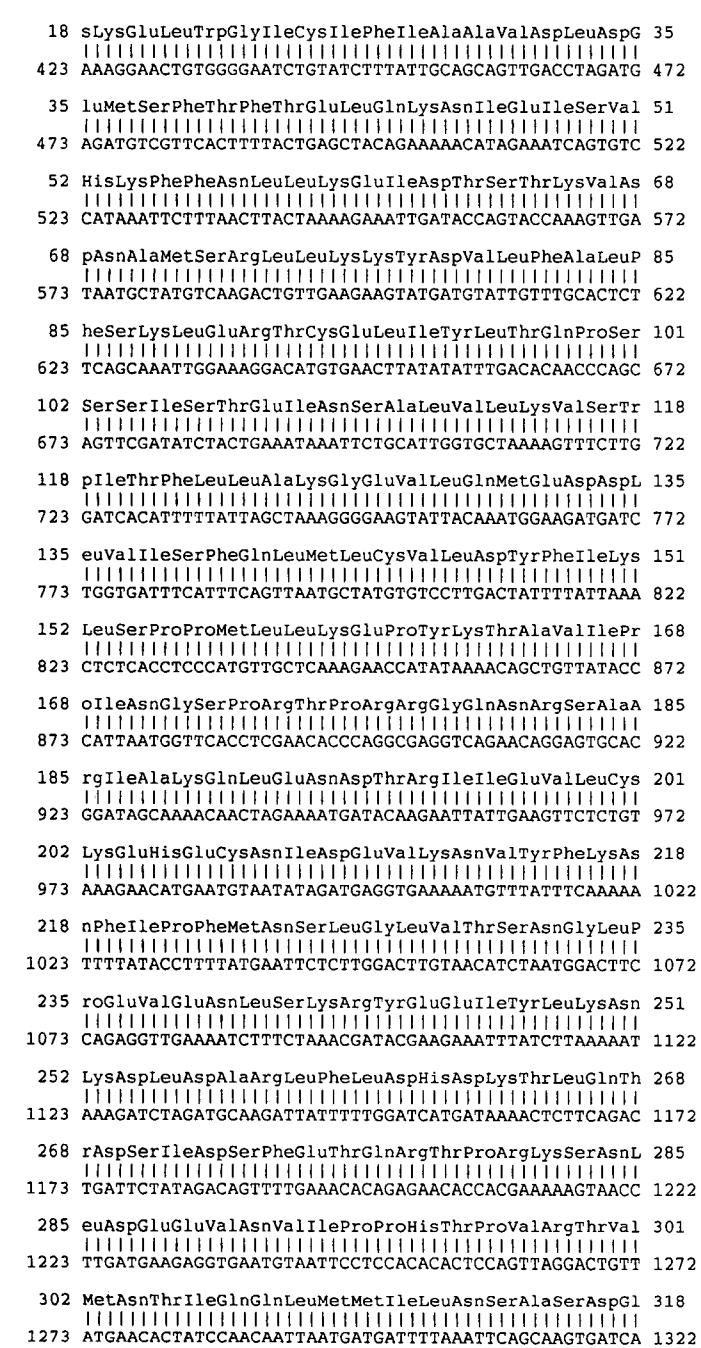
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VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
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  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


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     115 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 131
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DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


alignment_scores:
            Quality:  820.00             Length:    820
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alignment_block:
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seq_documentation_block:
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DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


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1985 TAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACAT 2034

 602 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 618
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 618 tArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleC 635
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 652 LysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLy 668
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 668 sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG 685
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 702 LeuSerProIleProHisIleProArgSerProTyrLysPheProSerSe 718
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seq_documentation_block:
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DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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BASE COUNT     1508 a    887 c    862 g    1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


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         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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seq_documentation_block:
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DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
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SOURCE      human.
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            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
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ORIGIN


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     428 nLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuA 445
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1500 TCTTGATTCAGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTA 1549

     445 snLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAla 461
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1550 ATTTAAAAGCCTTTGATTTTTATAAAAGTGATCGAAAGTTTTATCAAAGCA 1599

     462 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHi 478
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1600 GAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACA 1649

     478 sArgIleMetGluSerLeu.AlaTrpLeuSerAspSerProLeuPheAsp 494
         |||||||||||||   ||| ||||||||||||||||||||||||||||||
    1650 TCGAATCATGGAATC.CTTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1698

     495 LeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSe 511
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1699 CTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1748

     511 rAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspM 528
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1749 TGCTTGTCCTCTTAATCTTCGTCTCCAGAATAATCACACTGCAGCAGATA 1798

     528 etTyrLeuSerProValArgSerProLysLysLysGlySerThrThrArg 544
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1799 TGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1848

     545 ValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnTh 561
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1849 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1898

     561 rGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValT 578
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1899 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGT 1948

     578 yrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 594
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1949 ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1998

     595 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 611
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    1999 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 2048

     611 uGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetM 628
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    2049 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGA 2098

     628 etCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhe 644
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    2099 TGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2148

     645 LysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluTh 661
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2149 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2198

     661 rPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValP 678
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2199 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGT 2248

     678 heTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr 694
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2249 TCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 2298

     695 AlaSerThrArgProProThrLeuSerProIleProHisIleProArgSe 711
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    2299 GCTTCCACCAGGCCCCCTACCTTGCA.CCAATACCTCACATTCCTCGAAG 2347

     711 rProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleT 728
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2348 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2397

     728 yrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThr 744
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  2398 ATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2447

   745 ProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSe 761
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2448 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2497

   761 rPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnS 778
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2498 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACA 2547

   778 erAspArgValLeu 782
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  2548 GCGACCGTGTGCTC 2561

seq_name: gb_pr3:AF043224

seq_documentation_block:
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
     exon            <1. .7
                     /gene="RB1"
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                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
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                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
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                     /number=5
     exon            351. .418
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BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AF043224   ..

 Align seg 1/1  to: AF043224  from: 1  to: 426

     12 GlyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIl 28
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     76 GGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTAT 125

     28 eAlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnL 45
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    126 TGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGA 175

     45 ysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIle 61
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    176 AAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATT 225

     62 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTy 78
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    226 GATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTA 275

     78 rAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuI 95
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    276 TGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTA 325

     95 leTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAla 111
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    326 TATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 375

    112 LeuValLeuLysValSerTrpIleThrPheLeuLeu 123
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    376 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 411

seq_name: gb_pat:E12560

seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
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          strandedness: Double;
          CC   topology: Linear;
          CC   hypothetical: No;
          CC   anti-sense: No;
          FH   Key             Location/Qualifiers
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          FT   source          1. .4591
          FT                   /organism='Mus musculus'
          FT                   /cell_type='B-cell precursor' FT
              /cell_line='70Z-3'
          FT   5'UTR           1. .98
          FT   CDS             99. .2864
          FT                   /product='Rb protein'
          FT   3'UTR           2865. .4591.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN


alignment_scores:
            Quality:   72.00             Length:     72
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x E12560   ..

 Align seg 1/1  to: E12560  from: 1  to: 4591

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     733 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     750 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 766
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     767 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     783 sArgSerAlaGluGly 788
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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
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COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
     CDS             99. .2864
                     /codon_start=1
                     /product="pp105 Rb protein"
                     /protein_id="AAA39964.1"
                     /db_xref="GI:200453"
                     /translation="MPPKAPRRAAAAEPPPPPPPPPREDDPAQDSGPEELPLARLEFE
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                     DLDEMPFTETELQKSIETSVYKFFDLLKEIDTSTKVDNAMSRLLKKYNVLCALYSKLE
                     RTCELIYLTQPSSALSTEINSMLVLKISWITFLLAKGEVLQMEDDLVISFQLMLCVVD
                     YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
                     CNIDEVKNVYFKNFIPFINSLGIVSSNGLPEVESLSKRYEEVYLKNKDLDARLFLDHD
                     KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
                     NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
                     MESMLKSEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTLQHLDSGTDLSF
                     PWILNVLNLKAFDFYKVIESFIKVEANLTREMIKHLERCEHRIMESLAWLSDSPLFDL
                     IKQSKDGEGPDNLEPACPLSLPLQGNHTAADMYLSPLRSPKKRTSTTRVNSAANTETQ
                     AASAFHTQKPLKSTSLALFYKKVYRLAYLRLNTLCARLLSDHPELEHIIWTLFQHTLQ
                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                     EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
                     ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
                     EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
                     VSNKEEK"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x MUSPP105RB   ..

 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

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     733 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 750
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    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     767 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 783
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    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     783 sArgSerAlaGluGly 788
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seq_name: gb_pri:HUMRBSY79

seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
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VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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     CDS             139. .300
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                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
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     misc_recomb     275. .276
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                     /organism="Homo sapiens"
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x HUMRBSY79   ..

 Align seg 1/1  to: HUMRBSY79  from: 1  to: 480

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     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     142 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 159
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     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     159 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 175
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     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     176 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 192
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     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     192 nAsp 193
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     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
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LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
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                     /cell_type="leukocyte"
                     /map="13q14.2"
     gene            1. .340
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                     /number=16
     exon            65. .260
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                     /note="G00-118-734"
                     /number=17
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                     /gene="RB1"
                     /note="exon 17"
                     /codon_start=3
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                     /product="retinoblastoma suspectibility protein"
                     /protein_id="AAA82549.1"
                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
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                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
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      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     439 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 456
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473 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 488
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Date: Feb 13, 2000  8:10 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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  AUTHORS   Dryja,T.P. and Friend,S.
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  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
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DEFINITION  Sequence 2 from patent US 5710255.
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
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  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
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            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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VERSION     M33647.1  GI:190945
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  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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ORIGIN


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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


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DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .4597
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BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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1811 TGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAA 1860

 479 GlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPr 495
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1861 CAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCC 1910

 495 oLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuS 512
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1911 TCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTT 1960

 512 erProValArgSerProLysLysLysGlySerThrThrArgValAsnSer 528
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1961 CTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 2010

 529 ThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPr 545
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2011 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

 545 oLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuA 562
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 562 laTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPro 578
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2111 CCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCA 2160

 579 GluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGl 595
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2161 GAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGA 2210

 595 uTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerM 612
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 612 etTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIle 628
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 629 ValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysAr 645
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 645 gValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnS 662
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 662 erValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThr 678
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 679 ArgProProThrLeuSerProIleProHisIleProArgSerProTyrLy 695
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 695 sPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerP 712
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 712 roLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLys 728
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seq_documentation_block:
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DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
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BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


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Percent Similarity:  99.617   Percent Identity: 99.617

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    259 gThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProH 276
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    276 isThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIle 292
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    293 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 309
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    309 nAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspI 326
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   1201 CAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATA 1250

    326 leGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCys 342
        |||||||||||||||||||||||||||||||||   ||||||||||||
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    343 ValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrAr 359
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    409 nLeuAspSerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuA 426
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    426 snLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAla 442
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    459 sArgIleMetGluSerLeu.AlaTrpLeuSerAspSerProLeuPheAsp 475
        |||||||||||||   ||| |||||||||||||||||||||||||||||
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    492 rAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspM 509
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    526 ValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnTh 542
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    542 rGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValT 559
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    576 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 592
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    592 uGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetM 609
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    609 etCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhe 625
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    626 LysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluTh 642
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    642 rPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValP 659
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    659 heTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr 675
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
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SOURCE      human.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
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DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
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            CC   anti-sense: No;
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seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
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DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
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                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
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                     /cell_type="pre B-lymphocyte"
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                     KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
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BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


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              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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 US-09-026-459A-35 x MUSPP105RB   ..

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     714 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 731
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    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     731 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 747
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     748 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 764
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    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

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    2657 AAGAAGTGCTGAAGGC 2672

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seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
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     misc_recomb     275. .276
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                     /organism="Homo sapiens"
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x HUMRBSY79   ..

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     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     123 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     140 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 156
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     157 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 173
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     173 nAsp 174
         ||||
     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
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     mutation        66. .67
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ORIGIN


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alignment_block:
 US-09-026-459A-35 x HUMRB1501V   ..

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      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     420 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 437
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     437 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 453
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     454 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 469
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 06:45:04 ; Search time 14294.3 Seconds
(without alignments)
-627.697 Million cell updates/sec

Title: US-09-026-459A-28_COPY_7_2961
Perfect score: 2955
Sequence: 1 ATGCAGGACAGCGGCCCGGA.....TGTTTCCTCTTCCAAAGTAA 2955

Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
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11: gb_pr3:*
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13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vi:*
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18: em_hum1:*
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48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2953	99.9	4839	10	HUMRB1MRNA	L41870 Homo sapien
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4	2883	97.6	4597	5	I09369	I09369 Sequence 1
5	2755	93.2	2994	5	I81465	I81465 Sequence 2
6	2755	93.2	2994	10	HUMRBSA	M28419 Human retin
7	2730	92.4	3232	5	I18496	I18496 Sequence 1
c 8	2730	92.4	3232	5	I18497	I18497 Sequence 2
9	2427	82.1	4740	10	HUMRBS	M15400 Human retin
10	1639	55.5	4580	5	A01444	A01444 H.sapiens D
11	341	11.5	2352	5	I09392	I09392 Sequence 25
12	341	11.5	2352	9	HUMRBS23	M27866 Human retin
13	341	11.5	180388	9	HUMRETBLAS	L11910 Human retin
14	338	11.4	426	11	AF043224	AF043224 Homo sapi
15	216	7.3	1815	13	G06460	G06460 human STS W
16	207	7.0	480	9	HUMRBSY79	M19701 Human mutat
17	198	6.7	693	5	I09384	I09384 Sequence 17
18	198	6.7	693	9	HUMRBS15	M27858 Human retin
19	196	6.6	340	10	HUMRB1501V	L49220 Homo sapien
20	167	5.7	555	10	HUMRB4MU2	L41904 Homo sapien
21	165	5.6	935	5	I09389	I09389 Sequence 22
22	165	5.6	935	9	HUMRBS20	M27863 Human retin
23	165	5.6	420	10	HUMRB23EX	L41910 Homo sapien
24	163	5.5	252	10	HUMRB1777L	L49230 Homo sapien
25	155	5.2	555	10	HUMRB17MU2	L41924 Homo sapien
26	148	5.0	717	5	I09387	I09387 Sequence 20
27	148	5.0	717	9	HUMRBS18	L35147 Human retin
28	148	5.0	717	15	M27861	M27861 Figure 2. R
29	147	5.0	224	10	HUMRB1SDDL	L49225 Homo sapien
30	146	4.9	650	5	I09386	I09386 Sequence 19
31	146	4.9	650	9	HUMRBS17	M27860 Human retin
32	145	4.9	609	5	I09377	I09377 Sequence 10
33	145	4.9	609	9	HUMRBS08	L35146 Human retin
34	145	4.9	316	10	HUMRB08EX	L41896 Homo sapien
35	144	4.9	1310	9	HUMRBS22	M27865 Human retin
36	144	4.9	625	10	HUMRB25EX	L41912 Homo sapien
37	132	4.5	224	10	HUMRB1610K	L49223 Homo sapien
38	131	4.4	317	10	HUMRB17MUT	L41999 Homo sapien
39	130	4.4	704	5	I09371	I09371 Sequence 4
40	130	4.4	704	9	HUMRBS02	M27846 Human retin
41	130	4.4	410	10	HUMRB02EX	L41890 Homo sapien
42	125	4.2	350	10	HUMRB20MUU	L41996 Homo sapien
43	124	4.2	444	10	HUMRB04MUT	L41892 Homo sapien
44	124	4.2	483	10	HUMRB19MUT	L41906 Homo sapien
45	123	4.2	570	5	I09373	I09373 Sequence 6

ALIGNMENTS

RESULT 1
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LOCUS HUMRB1MRNA 4839 bp mRNA PRI 05-MAY-1995
DEFINITION Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and mutations.
ACCESSION L41870
VERSION L41870.1 GI:793994
KEYWORDS retinoblastoma protein; retinoblastoma susceptibility.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)
AUTHORS McGee,T.L., Yandell,D.W. and Dryja,T.P.
TITLE Structure and partial genomic sequence of the human retinoblastoma susceptibility gene
JOURNAL Gene 80 (1), 119-128 (1989)
MEDLINE 90006771
REFERENCE 2 (sites)
AUTHORS Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
TITLE Detection of heterozygous mutations in the RB1 gene in retinoblastoma patients using single-strand conformation polymorphism analysis and polymerase chain reaction sequencing
JOURNAL Oncogene 7 (7), 1445-1451 (1992)
MEDLINE 92319557
REFERENCE 3 (sites)
AUTHORS Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
TITLE Oncogenic point mutations in exon 20 of the RB1 gene in families showing incomplete penetrance and mild expression of the retinoblastoma phenotype
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
MEDLINE 92335261
REFERENCE 4 (sites)
AUTHORS Onadim,Z., Hogg,A. and Cowell,J.K.
TITLE Mechanisms of oncogenesis in patients with familial retinoblastoma
JOURNAL Br. J. Cancer 68 (5), 958-964 (1993)
MEDLINE 94031584
REFERENCE 5 (sites)
AUTHORS Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
TITLE Molecular mechanisms of oncogenic mutations in tumors from patients with bilateral and unilateral retinoblastoma
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
MEDLINE 93348271
REFERENCE 6 (sites)
AUTHORS Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J., Cowell,J.K. and Kaye,F.J.
TITLE Partial inactivation of the RB product in a family with incomplete penetrance of familial retinoblastoma and benign retinal tumors
JOURNAL Oncogene 9 (5), 1321-1326 (1994)
MEDLINE 94203660
COMMENT Mutation data provided by Dr. B.L.Gallie,
Hospital for Sick Children
555 Univ. Ave.
Toronto ONT W5G 1X8
Canada
Ph: 416 813-5868
FAX: 416 813-4989
E-mail: brenda@hafiz.eric.on.ca.

FEATURES Location/Qualifiers

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Db     239 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 298

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
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Qy     243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
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Qy     303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
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Db     539 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 598

Qy     363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
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Qy     423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
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Db     719 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 778

Qy     543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
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Db     779 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 838

Qy     603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
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Db     839 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 898

Qy     663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
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Qy     723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
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Qy     783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
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Qy     903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
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Qy     963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
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Qy    1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
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Qy    1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
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Qy    1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
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Db    1439 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1498

Qy    1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
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Qy    1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
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Qy    1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
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Db   1679 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1738

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Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
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Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
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Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
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Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
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Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
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Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
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Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
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Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
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Db   3179 TCTTCCAAAGTAA 3191
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RESULT   2
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
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BASE COUNT     1489 a    842 c    815 g   1454 t
ORIGIN


  Query Match             99.9%;  Score 2953;  DB 10;  Length 4600;
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  Matches 2953;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
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Qy    603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
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Db    885 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 944

Qy    843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1004

Qy    903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1064

Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1124

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1184

Qy   1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1244

Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1304

Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1364

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1424

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
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Db   1425 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1484

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1485 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1544

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
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Db   1545 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1604

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
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Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1665 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1724

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1725 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1784

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1844

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1904

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1964

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
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Db   1965 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2024

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982

Db   2025 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2084

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042

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Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102

Db   2145 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2204

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162

Db   2205 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2264

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222

Db   2265 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2324

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282

Db   2325 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2384

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCGCTGAAGAGTCCATATAA 2342

Db   2385 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCGCTGAAGAGTCCATATAA 2444

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402

Db   2445 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2504

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462

Db   2505 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2564

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522

Db   2565 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2624

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582

Db   2625 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2684

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642

Db   2685 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2744

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702

Db   2745 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2804

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2762

Db   2805 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2864

Qy   2763 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2822

Db   2865 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2924

Qy   2823 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2882

Db   2925 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2984

Qy   2883 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 2942

Db   2985 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 3044

Qy   2943 TCTTCCAAAGTAA 2955
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Db   3045 TCTTCCAAAGTAA 3057


RESULT   3
I05311
LOCUS       I05311       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN


  Query Match             97.6%;  Score 2883;  DB 5;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2933;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     22 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 81

Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy     82 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 141

Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    142 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 201

Db    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    202 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 261

Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    262 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 321

Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    322 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 381

Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    382 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 441

Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    442 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 501

Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy    502 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 561

Db    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy    562 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 621

Db    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy    622 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 681

Db    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy    682 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 741
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Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

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Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    802 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 861

Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    862 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 921

Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

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Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy    982 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1041

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Qy   1102 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1161

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Qy   1162 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1221

Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

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Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy   1282 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1341

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Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

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Qy   1582 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1641

Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1642 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1701

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Db   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1762 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1821

Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy   1822 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1881

Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1882 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 1941

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Qy   2002 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2061

Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2062 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2121

Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2122 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2181

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Qy   2182 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2241

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Qy   2242 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2301

Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2302 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2361

Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

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Qy   2422 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2481

Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2482 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2541

Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640

Qy   2542 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2601

Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

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Qy   2782 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2841

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Qy   2902 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
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Db   3001 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 3054


RESULT   4
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DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


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  Matches 2933;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      22 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy      82 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     142 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 201
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Db     241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy     202 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 261
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Qy     382 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy     442 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy     502 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy     562 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy     622 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy     682 GCACGGATAGCAAAACAAGTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCACGGATAGCAAAACAAGTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy     742 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy     802 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 861
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy     862 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 921
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Qy     922 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 981
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy     982 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1041
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy    1042 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy    1102 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy    1162 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy    1222 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy    1282 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1341
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy    1342 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1401
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy    1402 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy    1462 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1521
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy    1522 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1581
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy    1582 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1641
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy    1642 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy    1702 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
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Qy   1762 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1821
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Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy   1822 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1881
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Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1882 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 1941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   1942 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2002 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2062 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2122 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2182 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2242 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2302 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2362 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Qy   2422 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2482 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGAA 2640

Qy   2542 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2602 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2662 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2820

Qy   2722 CTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2880

Qy   2782 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2940
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Qy   2842 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 2901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 3000

Qy   2902 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 3054


RESULT   5
I81465
LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
                     /organism="unknown"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


  Query Match             93.2%;  Score 2755;  DB 5;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2755;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy     63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy    303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy    363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy    423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy    483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy    543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839
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Qy    603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
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Db    840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy    663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

Qy    723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

Qy    783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy    843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1139

Qy    903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962'
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

Qy   1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
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Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919
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Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 TCCTCTCCAGAATAATCAGACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
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Db   2340 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2399

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
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Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
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Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
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Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
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Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
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Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757
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Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994
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RESULT   6
HUMRBSA
LOCUS       HUMRBSA     2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
            phosphoprotein associated with DNA binding activity
  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
FEATURES             Location/Qualifiers
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                     /tissue_type="retinoblastoma"
                     /map="Xp22.32;Yp11.3"
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     CDS             139. .2925
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                     /note="retinoblastoma suceptibility protein"
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                     /db_xref="GDB:G00-120-184"
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                     /db_xref="GI:190963"
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                     IFIAAVDLDEMSFTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
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                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
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                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
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                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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  Query Match           93.2%;  Score 2755;  DB 10;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2755;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy     123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy     183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy     243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
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Db     480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy     303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy     363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy     423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
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Db     660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy     483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy     543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839

Qy     603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy     663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
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Qy     783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
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Db    1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy     843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
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Qy     903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

Qy     963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy    1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

Qy    1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy    1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy    1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy    1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
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Db   1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
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Db   1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
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Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
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Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
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Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
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Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
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Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
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Db   1920 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
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Db   1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
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Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
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Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
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Db   2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
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Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
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Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
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Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
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Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639
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Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
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Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2703 TGGTGGACACTGTGTACACGTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 TGGTGGACACTGTGTACACGTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994
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RESULT   7
I18496
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN
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  Query Match             92.4%;  Score 2730;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2730;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    226 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 285
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Db      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy    286 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy    346 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 405
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Db    127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy    406 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy    466 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy    526 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 585
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Db    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy    586 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 645
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy    646 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 705
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy    706 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 765
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy    766 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy    826 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy    886 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy    946 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy   1006 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy   1066 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy   1126 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy   1186 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy   1246 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1305
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Db   1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy   1306 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy   1366 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy   1426 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1486 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1546 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy   1606 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy   1666 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy   1726 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1785
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Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1846 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy   1906 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1965
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1966 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   2026 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   2086 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   2146 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2205
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Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2206 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2266 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2326 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2386 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2445
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Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2446 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2506 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2565
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Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2566 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2625
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Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2626 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466

Qy   2686 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2467 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2526
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Qy   2746 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2805
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Db   2527 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2586

Qy   2806 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2587 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2646

Qy   2866 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2647 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2706

Qy   2926 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
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Db   2707 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2736


RESULT   8
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


  Query Match             92.4%;  Score 2730;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2730;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    226 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy    286 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy    346 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy    406 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 465
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Db   3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy    466 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 525
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Db   2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy    526 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 585
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy    586 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 645
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy    646 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 705
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Db   2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy    706 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 765
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy    766 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 825
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Db   2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy    826 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 885
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Db   2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy    886 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 945
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Db   2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy    946 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1005
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Db   2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy   1006 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy   1066 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1125
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Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy   1126 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1185
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Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy   1186 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1245
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Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy   1246 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy   1306 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy   1366 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy   1426 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1486 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1546 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1606 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1666 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1726 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1785
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Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy   1786 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1845
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Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1846 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy   1906 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1965
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1966 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2025
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Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy   2026 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2085
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Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   2086 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2145
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Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311

Qy   2146 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2205
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Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2206 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy   2266 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy   2326 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2386 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2446 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2506 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2566 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2626 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771

Qy   2686 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    770 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 711

Qy   2746 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    710 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 651

Qy   2806 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    650 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 591

Qy   2866 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2925
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Db    590 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 531

Qy   2926 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          ||||||||||||||||||||||||||||||
Db    530 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 501


RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
     source          1. .4740
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RB-[1,5]"
                     /dev_stage="foetus"
                     /tissue_type="retina"
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     mRNA            <1. .4740
                     /note="rbs mRNA"
     gene            139. .2925
                     /gene="RB1"
     CDS             139. .2925
                     /gene="RB1"
                     /note="retinoblastoma susceptibility protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA69807.1"
                     /db_xref="GI:190959"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
                     IFIARVDLDEMSFTLLSYRKTYEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
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ORIGIN 1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.

Query Match 82.1%; Score 2427; DB 10; Length 4740;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2677; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy    274 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 570

Qy    334 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 630

Qy    394 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690

Qy    454 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 750

Qy    514 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 810

Qy    574 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 870

Qy    634 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 930

Qy    694 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990

Qy    754 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 1050

Qy    814 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 1110

Qy    874 TATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAG 933
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   1111 TATCTTAAAAATAAAGATCTAGATCGAAGATTATTTTTGGATCATGATAAAACTCTTCAG 1170

Qy    934 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 1230

Qy    994 GAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1053
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 GAGGTGAATATAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1290

Qy   1054 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1113
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1291 TTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1350

Qy   1114 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1410

Qy   1174 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1470

Qy   1234 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1471 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1530

Qy   1294 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1590

Qy   1354 TCTTTATTGGCGTGCGCTGTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TCTTTATTGGCGTGCGCTGTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1650

Qy   1414 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1473
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Db   1651 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1710

Qy   1474 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1533
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Db   1711 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1770

Qy   1534 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1830

Qy   1594 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1653
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Db   1831 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1890

Qy   1654 CACCTTGAATCTGCTTGTCGTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1713
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Db   1891 CACCTTGAATCTGCTTGTCGTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1950

Qy   1714 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 1773
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Db   1951 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 2010

Qy   1774 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 1833
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Db   2011 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 2070

Qy   1834 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 2130

Qy   1894 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 2190

Qy   1954 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2250

Qy   2014 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2310

Qy   2074 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2370

Qy   2134 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2430

Qy   2194 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2490

Qy   2254 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2550

Qy   2314 TATATTTCACCCCTGAAGAGTGCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2373
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Qy   2374 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2433
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Db   2611 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2670

Qy   2434 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2493
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Qy   2494 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2553
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Db   2731 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2790

Qy   2554 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2614 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2673
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Db   2851 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2910

Qy   2674 AAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCAT 2733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2911 AAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCAT 2970

Qy   2734 TGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATA 2793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2971 TGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATA 3030

Qy   2794 TCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAG 2853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3031 TCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGAGTCCTAAG 3090

Qy   2854 CCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGC 2913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3091 CCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGC 3150

Qy   2914 CATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          |||||||||||||||||||||||||||||||||||||||||||
Db   3151 CATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 3192


RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match           55.5%;  Score 1639;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2279;  Conservative    0;  Mismatches    8;  Indels    2;  Gaps    2;

Qy    667 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    727 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    787 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    847 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy    907 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 966
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy    967 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy   1027 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy   1087 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy   1147 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy   1207 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy   1267 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy   1327 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1387 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1446
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy   1447 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy   1507 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1566
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Db   1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy   1567 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1626
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy   1627 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy   1687 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy   1747 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy   1807 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy   1867 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy   1927 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy   1987 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy   2047 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy   2107 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2166
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy   2167 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy   2227 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2286
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy   2287 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2346
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Db   2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy   2347 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2407 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2467 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2526
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2527 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2587 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2647 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGT 2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGT 2789

Qy   2707 GGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCC 2766
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2790 GGACACTGTGTGCACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCC 2849

Qy   2767 AGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCA 2826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2850 AGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCA 2909

Qy   2827 GATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACA 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2910 GATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACA 2969
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Qy   2887 AGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTT 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2970 AGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTT 3029

Qy   2947 CCAAAGTAA 2955
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Db   3030 CCAAAGTAA 3038


RESULT  11
I09392
LOCUS       I09392       2352 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 25 from Patent WO 8906703.
ACCESSION   I09392
VERSION     I09392.1  GI:587922
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2352)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 25 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .2352
                     /organism="unknown"
BASE COUNT      717 a    399 c    368 g    867 t      1 others
ORIGIN


  Query Match           11.5%;  Score 341;  DB 5;  Length 2352;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-170;
  Matches  341;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2615 CTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 2674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 CTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 250

Qy   2675 AGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATT 2734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 AGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATT 310

Qy   2735 GTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATAT 2794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATAT 370

Qy   2795 CTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGC 2854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGC 430

Qy   2855 CACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCC 2914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 CACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCC 490

Qy   2915 ATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          |||||||||||||||||||||||||||||||||||||||||
Db    491 ATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 531


RESULT  12
HUMRBS23
LOCUS       HUMRBS23     2352 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 27.
ACCESSION   M27866
VERSION     M27866.1  GI:341783
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     23 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 2352)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .2352
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
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                     M27847.1:283. .398,M27848.1:196. .315,M27849.1:294. .332,
                     M27850.1:146. .213,M27851.1:302. .412,L35146.1:270. .412,
                     M27852.1:236. .313,M27853.1:266. .375,M27854.1:310. .387,
                     M27855.1:314. .401,M27856.1:231. .347,M27857.1:331. .387,
                     M27857.1:791. .822,M27857.1:903. .979,M27858.1:250. .446,
                     M27859.1:242. .360,M27860.1:314. .459,L35147.1:249. .394,
                     M27862.1:260. .364,M27863.1:256. .369,M27863.1:463. .626,
                     M27864.1:326. .356,M27865.1:193. .335,M27865.1:847. .896,
                     191. .2079)
                     /note="retinoblastoma susceptibility gene"
     CDS             join(M27845.1:683. .819,M27846.1:310. .436,
                     M27847.1:283. .398,M27848.1:196. .315,M27849.1:294. .332,
                     M27850.1:146. .213,M27851.1:302. .412,L35146.1:270. .412,
                     M27852.1:236. .313,M27853.1:266. .375,M27854.1:310. .387,
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                     191. .264)
                     /codon_start=1
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                     /db_xref="GI:521212"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
                     IFIAAVDLDEMSFTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDAR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
     intron          order(M27865.1:897. .>1310,<1. .190)
                     /note="1.7 kb gap; retinoblastoma susceptibility gene"
                     /number=26
     exon            191. .2079
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                     /number=27
     polyA_signal    2058. .2063
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     polyA_site      2097
                     /note="retinoblastoma susceptibility gene"
BASE COUNT      717 a    399 c    368 g    867 t      1 others
ORIGIN
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Query Match 11.5%; Score 341; DB 9; Length 2352;
Best Local Similarity 100.0%; Pred. No. 2.3e-170;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2615 CTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 2674
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Db    191 CTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 250

Qy   2675 AGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATT 2734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 AGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATT 310

Qy   2735 GTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATAT 2794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATAT 370

Qy   2795 CTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGC 2854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGC 430

Qy   2855 CACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCC 2914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 CACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCC 490

Qy   2915 ATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          |||||||||||||||||||||||||||||||||||||||||
Db    491 ATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 531
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RESULT  13
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
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  TITLE     Complete genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
FEATURES             Location/Qualifiers
     source          1. .180388
                     /organism="Homo sapiens"
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Qy    2615 CTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 2674
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Db 177005 CTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 177064

Qy    2675 AGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATT 2734
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Db 177065 AGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATT 177124

Qy    2735 GTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATAT 2794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 177125 GTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATAT 177184

Qy    2795 CTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGC 2854
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Qy    2855 CACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCC 2914
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Db 177245 CACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCC 177304

Qy    2915 ATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
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Db 177305 ATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 177345


RESULT  14
AF043224
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
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ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
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Qy     165 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 224
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Db      75 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 134

Qy     225 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 284
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Qy     285 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 344
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Db     195 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 254

Qy     345 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 404
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Db     255 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 314

Qy     405 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 464
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Db     315 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 374

Qy     465 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 502
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RESULT  15
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LOCUS       G06460       1815 bp    DNA             STS       19-OCT-1995
DEFINITION  human STS WI-7223.
ACCESSION   G06460
VERSION     G06460.1  GI:859705
KEYWORDS    STS sequence; primer; sequence tagged site.
SOURCE      human STSs derived from sequences in dbEST and the Unigene
            collection.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
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            Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1815)
  AUTHORS   Hudson,T.
  TITLE     Whitehead Institute/MIT Center for Genome Research; Physically
            Mapped ESTs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
            9 Cambridge Center, Cambridge MA 02142 USA
            Tel: 617 252 1900
            Fax: 617 252 1902
            Email: thudson@genome.wi.mit.edu

            Primer A: CAGATGCAATTGTTTGGGTG
            Primer B: TGAATGGGCAGTCAATCAAA
            STS size: 346
            PCR Profile:
                  Presoak:
                  Denaturation:
                  Annealing: 56 degrees C
                  Polymerization:
                  PCR Cycles: 35
                  Thermal Cycler:
            Protocol:
                Template: 10 ng
                Primer: each 5 pM
                dNTPs: each 4 nM
                Taq Polymerase: 0.025 units/ul
                Total Vol: 20 ul

            Buffer:
                MgCl2: 1.5 mM
                KCl: 50 mM
                Tris-HCL: 10 mM
                pH: 9.3

            Prepared with primer pairs derived from M15400 -- Unigene.
FEATURES             Location/Qualifiers
     source          1. .1815
                     /organism="Homo sapiens"
     STS             137. .482
     primer_bind     137. .156
     primer_bind     complement(463. .482)
BASE COUNT      538 a    284 c    285 g    663 t     45 others
ORIGIN


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Db      1 GGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATG 60

Qy   2749 TGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTT 2808
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Db     61 TGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTT 120

Qy   2809 GTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTA 2868
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Db    121 GTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGAGTCCTAAGCCACTTGAAATGTTA 180

Qy   2869 GTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGT 2928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGT 240

Qy   2929 AGCAGATTGTTTCCTCTTCCAAAGTAA 2955
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Db    241 AGCAGATTGTTTCCTCTTCCAAAGTAA 267
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Search completed: February 13, 2000, 11:15:20
Job time: 16216 sec

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Date: Feb 13, 2000  3:50 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -MATRIX=oligo -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US09026459 -NCPU=6
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Search information block:
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Query length: 895
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Database sequences: 214294
Database length: 59861208
Search time (sec): 316.800000

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; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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seq_documentation_block:
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; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
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US-08-959-638-7


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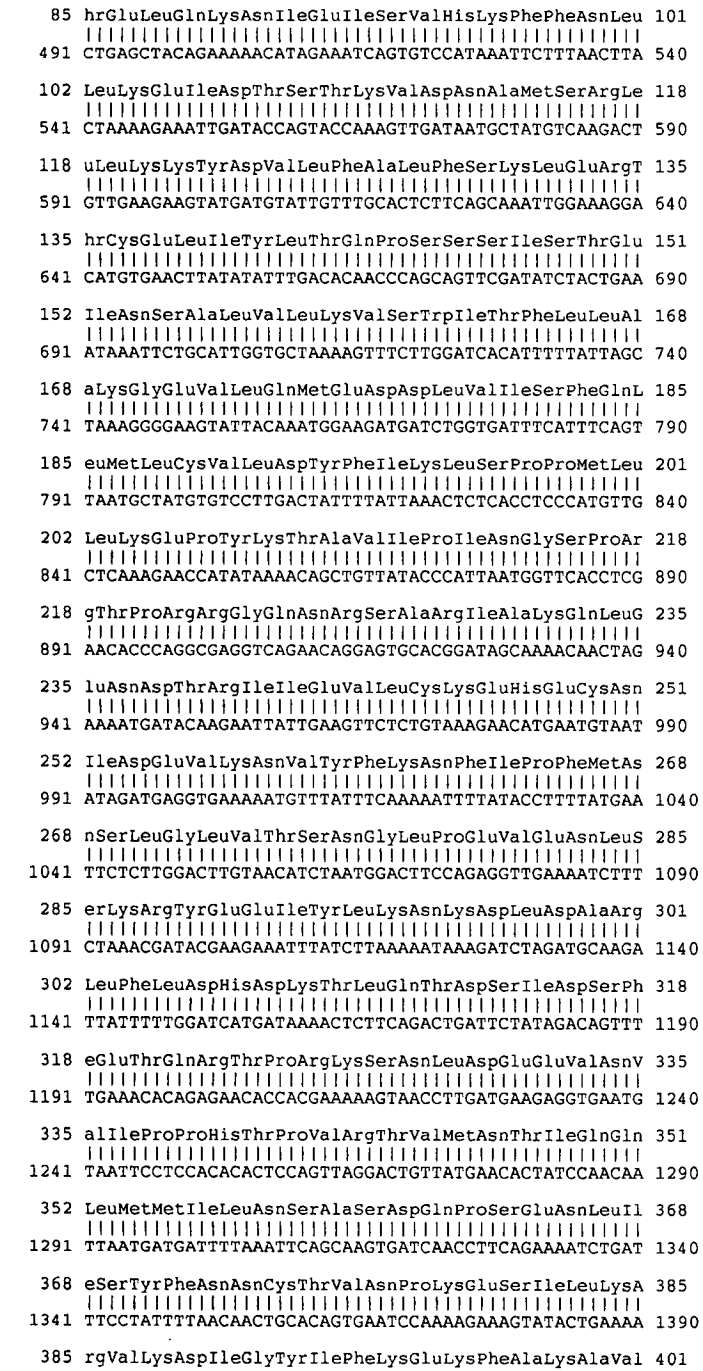
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; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


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;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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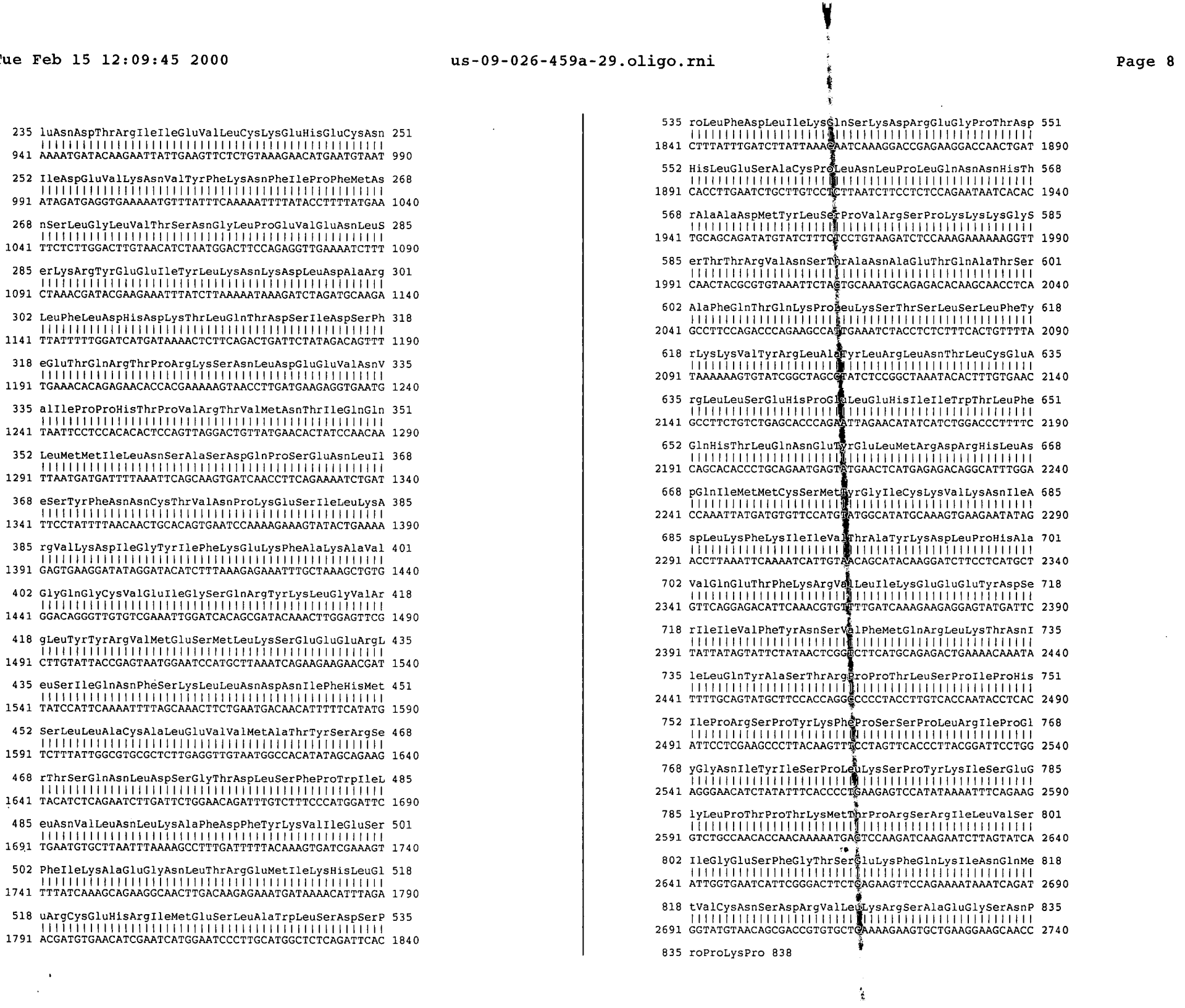
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seq_documentation_block:
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
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1857 AACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTG 1906

 709 alLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSer 725
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seq_documentation_block:
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
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;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
US-08-038-760-2


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; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
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seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
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US-08-470-091-2


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; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


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; Sequence 1, Application US/07878960
; Patent No. 5444164
;  GENERAL INFORMATION:
;    APPLICANT:  Purchio, Anthony F.
;    APPLICANT:  Skonier, John
;    APPLICANT:  Neubauer, Michael G.
;    TITLE OF INVENTION:  TGF-BETA INDUCED GENE AND PROTEIN
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/878,960
;      FILING DATE:  05-MAY-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/833,835
;      FILING DATE:  05-FEB-1992
;      NAME:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sorrentino, Joseph M.
;      REGISTRATION NUMBER:  32,598
;      REFERENCE/DOCKET NUMBER:  ON0092-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206/728-4800
;      TELEFAX:  206/727-3601
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;    SEQUENCE CHARACTERISTICS:
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;    HYPOTHETICAL:  NO
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;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  LUNG
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;      CELL LINE:  A549
US-07-878-960-1


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; Sequence 11, Application US/07891942G
; Patent No. 5679511
;  GENERAL INFORMATION:
;    APPLICANT:  Kwon, Byoung Se
;    TITLE OF INVENTION:  cDNA CLONES FOR HUMAN TYROSINASE AND FOR
;    TITLE OF INVENTION:  A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christopher A. Michaels, Barnard, Brown &
;      ADDRESSEE:  Michaels
;      STREET:  306 East State Street; Suite 220
;      CITY:  Ithaca
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  14850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/891,942G
;      FILING DATE:  01-JUN-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/915,753
;      FILING DATE:  06-OCT-1986
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/362,847
;      FILING DATE:  07-JUN-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michaels, Christopher A
;      REGISTRATION NUMBER:  34,390
;      REFERENCE/DOCKET NUMBER:  IND1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  607-273-1711
;      TELEFAX:  607-273-2609
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
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;      TOPOLOGY:  linear
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US-07-891-942G-11


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; Sequence 1, Application US/07675211
; Patent No. 5219737
;  GENERAL INFORMATION:
;    APPLICANT:  KAJIYAMA, NAOKI
;    APPLICANT:  NAKANO, EIICHI
;    TITLE OF INVENTION:  MUTANT LUCIFERASE OF A FIREFLY, MUTANT
;    TITLE OF INVENTION:  LUCIFERASE GENES, NOVEL RECOMBINANT DNAS CONTAINING THE
;    TITLE OF INVENTION:  GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  N.Y.
;      COUNTRY:  U.S.A
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/675,211
;      FILING DATE:  19910326
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MISROCK, S. LESLIE
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-026-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1644 base pairs
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US-07-675-211-1


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seq_documentation_block:
; Sequence 1, Application US/07903047
; Patent No. 5229285
;  GENERAL INFORMATION:
;    APPLICANT:  Kajiyama, Naoki
;    APPLICANT:  Nakano, Eiichi
;    TITLE OF INVENTION:  Thermostable Luciferase Of Firefly,
;    TITLE OF INVENTION:  Thermostable Luciferase Gene Of Firefly, No. 5229285el Reco
;    TITLE OF INVENTION:  DNA, And Process For The Preparation Of Thermostable
;    TITLE OF INVENTION:  Luciferase Of Firefly
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
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;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/903,047
;      FILING DATE:  19920623
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-048
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1644 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA to mRNA
US-07-903-047-1


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; Patent No. 5234811
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    APPLICANT:  Sorge, Joseph A
;    TITLE OF INVENTION:  An Assay for a New Gaucher Disease
;    TITLE OF INVENTION:  Mutation
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  3366 No. 5234811th Torrey Pines Court, Suite 240
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      APPLICATION NUMBER:  US/07/767,135
;      FILING DATE:  19910927
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0422P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7620 base pairs
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;    ANTI-SENSE:  NO
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US-07-767-135-1


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; Patent No. 5266459
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    TITLE OF INVENTION:  GAUCHER'S DISEASE: DETECTION OF A NEW
;    TITLE OF INVENTION:  MUTATION IN INTRON 2 OF THE GLUCOCEREBROSIDASE GENE
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5266459th Torrey Pines Road, TPC 8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/841,652
;      FILING DATE:  19920224
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0670P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
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GenCore version 4.5
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SUMMARIES

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c	11	24	0.8	44	2	US-08-625-209A-22	Sequence 22, Appl
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	14	22	0.7	52	1	US-07-826-928A-36	Sequence 36, Appl
c	15	22	0.7	22	1	US-08-271-946A-22	Sequence 22, Appl
c	16	22	0.7	22	1	US-08-271-946A-38	Sequence 38, Appl
c	17	22	0.7	22	1	US-08-271-942A-22	Sequence 22, Appl
c	18	22	0.7	22	1	US-08-271-942A-38	Sequence 38, Appl
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c	21	22	0.7	22	6	PCT-US95-08606-22	Sequence 22, Appl
c	22	22	0.7	22	6	PCT-US95-08606-38	Sequence 38, Appl
c	23	21	0.7	37	1	US-07-826-928A-14	Sequence 14, Appl
	24	19	0.6	1285	1	US-08-105-483-215	Sequence 215, App
c	25	19	0.6	19	1	US-08-271-942A-119	Sequence 119, App
	26	19	0.6	1285	2	US-08-709-209-215	Sequence 215, App
	27	19	0.6	1285	2	US-08-458-101-215	Sequence 215, App
c	28	19	0.6	19	6	PCT-US95-08604-119	Sequence 119, App
	29	18	0.6	3879	1	US-08-530-010-1	Sequence 1, Appli
c	30	18	0.6	1897	2	US-08-615-170-18	Sequence 18, Appl
c	31	18	0.6	1894	2	US-08-615-170-20	Sequence 20, Appl
	32	18	0.6	3879	2	US-08-484-101B-1	Sequence 1, Appli
c	33	18	0.6	18	3	US-08-511-836C-2	Sequence 2, Appli
c	34	17	0.6	2009	1	US-07-958-222A-1	Sequence 1, Appli
c	35	17	0.6	28	1	US-07-941-523-12	Sequence 12, Appl
	36	17	0.6	90	1	US-08-123-702-17	Sequence 17, Appl
c	37	17	0.6	469	1	US-08-318-905-20	Sequence 20, Appl
c	38	17	0.6	469	1	US-08-483-232-20	Sequence 20, Appl
	39	17	0.6	2628	1	US-08-143-219-1	Sequence 1, Appli
	40	17	0.6	450	2	US-08-213-452-1	Sequence 1, Appli
c	41	17	0.6	469	2	US-08-483-140-20	Sequence 20, Appl
c	42	17	0.6	8082	2	US-08-306-691B-41	Sequence 41, Appl
c	43	17	0.6	8082	2	US-08-187-785-1	Sequence 1, Appli
	44	17	0.6	4080	2	US-08-570-311-7	Sequence 7, Appli
	45	17	0.6	6241	2	US-08-570-311-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
; GENERAL INFORMATION:
; APPLICANT: SHEPARD, H. M.
; APPLICANT: WEN, SHU F.
; TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
; TITLE OF INVENTION: MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,329
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05866
; FILING DATE: 14-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RENEE A. FITTS
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16930-000400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
US-08-204-329-2

Query Match 93.2%; Score 2755; DB 2; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
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Db     240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
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Db    300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182

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Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242

Db    420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302

Db    480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

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Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022

Db   1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082

Db   1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

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Db   1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202

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Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922

Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982

Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042

Db   2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102

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Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519
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Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
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Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
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Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
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Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
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Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
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Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
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Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
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Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757
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Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994


RESULT   2
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


  Query Match             93.2%;  Score 2755;  DB 4;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2755;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
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Db    360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
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Db    420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
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Db    480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy    303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy    363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
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Db    600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy    423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
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Db    660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy    483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
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Db    720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

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Db    840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy    663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
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Db    900 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

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Db    960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

Qy    783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
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Db   1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

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Qy    903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
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Db   1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

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Qy   1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
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Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
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Db   1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
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Db   1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
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Db   1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
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Db   1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
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Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
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Db   1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
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Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
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Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
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Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

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Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
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Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
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Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
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Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
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Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
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Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994
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RESULT 3
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wills, Ken N.
; APPLICANT: Maneval, Daniel C.
; TITLE OF INVENTION: Recombinant Adenoviral Vector and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/959,638
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/328,673
;       FILING DATE:  25-OCT-1994
;       APPLICATION NUMBER:  US 08/233,777
;       FILING DATE:  19-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/142,669
;       FILING DATE:  25-OCT-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  P-CJ 1192
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2995 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2922
US-08-959-638-7
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Query Match 93.1%; Score 2752; DB 4; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
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Db    240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy     63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
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Db    480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy    303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy    363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
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Qy    423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
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Db    660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy    483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
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Db    720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy    543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
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Db    780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839

Qy    603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
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Db    840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

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Qy    723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

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Db   1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy    843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
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Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
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Db   1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
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Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
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Db   1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
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Db   1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
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Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
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Db   1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
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Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

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Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
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Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
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Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

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Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
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Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
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Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
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Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
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Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
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Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
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Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTG 2754
          ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTG 2991


RESULT   4
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


  Query Match             92.4%;  Score 2730;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2730;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

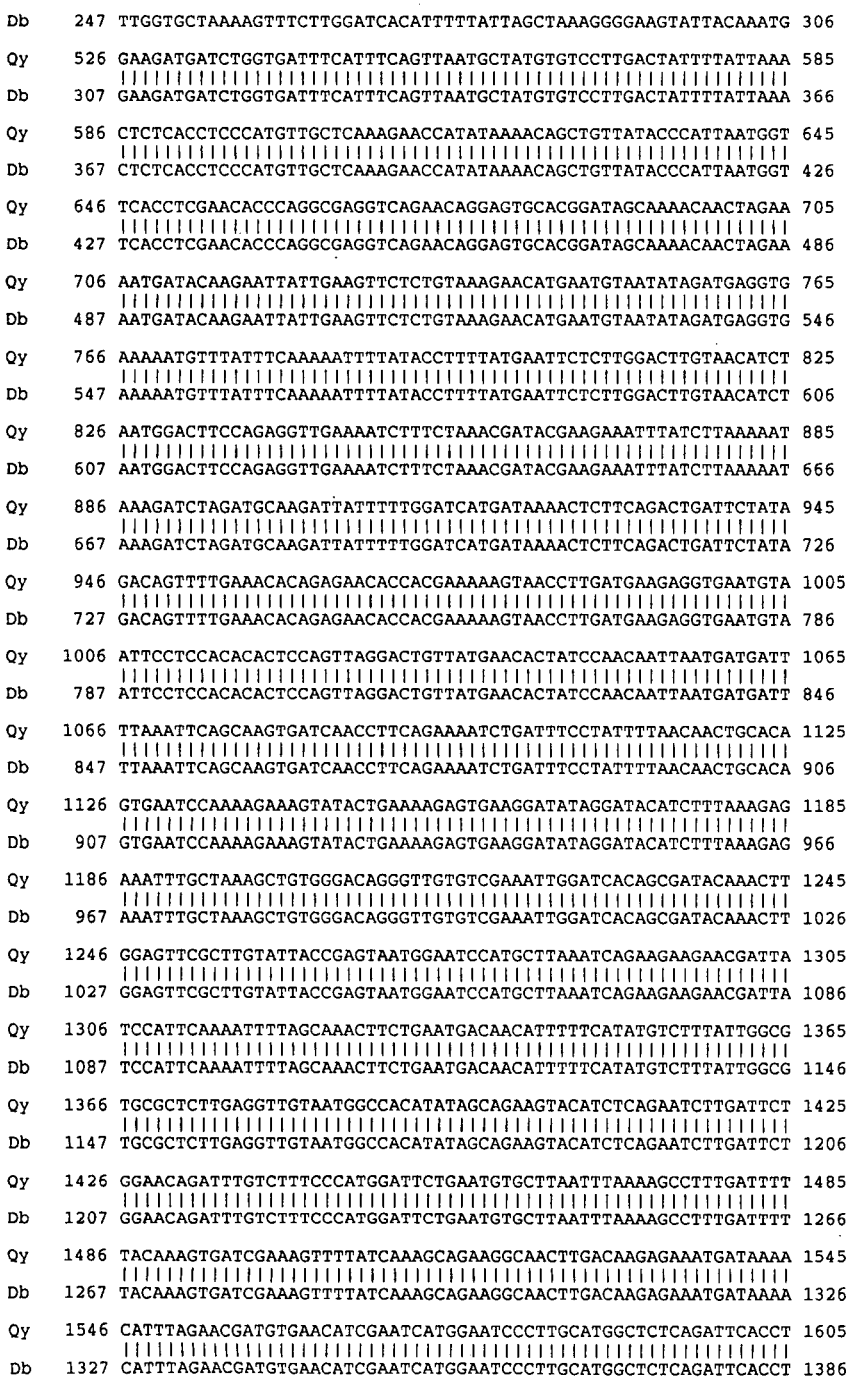
Qy    226 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy    286 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy    346 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy    406 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 465
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Db    187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy    466 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306
Qy 526 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 585
Db 307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366
Qy 586 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 645
Db 367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426
Qy 646 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 705
Db 427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486
Qy 706 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 765
Db 487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546
Qy 766 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 825
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Qy 826 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 885
Db 607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666
Qy 886 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 945
Db 667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726
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Db 727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786
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Db 787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846
Qy 1066 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1125
Db 847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906
Qy 1126 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1185
Db 907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966
Qy 1186 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1245
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Qy 1246 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1305
Db 1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086
Qy 1306 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1365
Db 1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146
Qy 1366 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1425
Db 1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206
Qy 1426 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1485
Db 1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266
Qy 1486 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1545
Db 1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326
Qy 1546 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1605
Db 1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386
Qy 1606 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1665
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Qy 1666 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1725
Db 1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506
Qy 1726 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1785
Db 1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566
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Db 1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626
Qy 1846 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1905
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Qy 1906 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1965
Db 1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746
Qy 1966 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2025
Db 1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806
Qy 2026 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2085
Db 1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866
Qy 2086 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2145
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Qy 2146 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2205
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Qy 2206 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2265
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Qy 2266 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2325
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Qy 2326 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2385
Db 2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166
Qy 2386 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2445
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Qy 2506 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2565
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Qy 2566 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2625
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Qy    2686 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2745
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Db    2467 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2526

Qy    2746 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2805
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Db    2527 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2586

Qy    2806 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2865
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Db    2587 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2646

Qy    2866 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2925
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Db    2647 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2706

Qy    2926 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
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Db    2707 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2736
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RESULT   5
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             92.4%;  Score 2730;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2730;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy     406 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 465
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Db    3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy     466 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 525
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy     526 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 585
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy     586 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 645
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Db    2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy     646 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 705
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy     706 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 765
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy     766 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 825
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Db    2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy     826 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 885
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Db    2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy     886 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 945
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Db    2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy     946 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1005
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy    1006 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1065
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Db    2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy    1066 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1125
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Db    2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy    1126 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy    1186 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1245
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Db    2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy    1246 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1305
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Db    2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy    1306 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1365
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Db    2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091
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Qy   1366 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1425
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Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy   1426 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1486 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1546 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1606 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1666 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy   1726 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy   1786 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1845
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1846 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy   1906 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1965
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1966 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2025
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Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   2086 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2145
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Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311

Qy   2146 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2206 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy   2266 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy   2326 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2386 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2446 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2506 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2566 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2626 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771

Qy   2686 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    770 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 711

Qy   2746 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    710 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 651

Qy   2806 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    650 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 591

Qy   2866 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    590 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 531

Qy   2926 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          |||||||||||||||||||||||||||||
Db    530 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 501
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RESULT   6
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
```

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;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


  Query Match             92.4%;  Score 2730;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2730;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     226 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy     286 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy     346 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 405
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy     406 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy     466 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 525
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy     526 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 585
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy     586 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 645
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy     646 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 705
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy     706 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 765
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy     766 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 825
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy     826 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 885
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy     886 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 945
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy     946 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1005
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy    1006 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1065
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy    1066 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy    1126 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy    1186 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy    1246 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1305
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy    1306 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy    1366 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy    1426 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1485
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy    1486 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1545
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy    1546 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1605
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy    1606 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1665
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy    1666 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1725
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy    1726 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1785
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy    1786 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1845
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy    1846 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1905
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy    1906 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1965
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy    1966 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2025
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy    2026 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2085
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy    2086 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926
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RESULT   8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1
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Query Match 91.5%; Score 2704; DB 6; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2754; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy     123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy     183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy     243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy     303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy     363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy     423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy     483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy     543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839

Qy     603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy     663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

Qy     723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

Qy     783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy     843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1139

Qy     903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

Qy     963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy    1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

Qy    1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy    1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy    1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy    1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy    1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy    1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
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Db   1620 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502

Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562

Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622

Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682

Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742

Db   1920 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802

Db   1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862

Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922

Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982

Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042

Db   2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102

Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162

Db   2340 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2399

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222

Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282

Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342

Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402

Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462

Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522

Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582

Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642

Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702

Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757

Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             0.9%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2602 CTGGCAGAAATGACTTCTACTCGAACAC 2629
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;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.7%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1060 ATGATTTTAAATTCAGCAAGTG 1081
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  13
US-07-826-928A-35/c
; Sequence 35, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-35


  Query Match             0.7%;  Score 22;  DB 1;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2668 TCAAACAAGGAAGAGAAATGAG 2689
          ||||||||||||||||||||||
Db     37 TCAAACAAGGAAGAGAAATGAG 16


RESULT  14
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.7%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1060 ATGATTTTAAATTCAGCAAGTG 1081
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  15
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
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                    ||||||||||||||||||||||||||||
Db       1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-08-253-155A-93/c
; Sequence 93, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-93


  Query Match             0.8%;  Score 24;  DB 2;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2666 CCTCAAACAAGGAAGAGAAATGAG 2689
           ||||||||||||||||||||||||
Db      44 CCTCAAACAAGGAAGAGAAATGAG 21


RESULT  11
US-08-625-209A-22/c
; Sequence 22, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  44 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-22


  Query Match             0.8%;  Score 24;  DB 2;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2666 CCTCAAACAAGGAAGAGAAATGAG 2689
           ||||||||||||||||||||||||
Db      44 CCTCAAACAAGGAAGAGAAATGAG 21


RESULT  12
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
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Db  2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631
Qy   826 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 885
Db  2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571
Qy   886 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 945
Db  2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511
Qy   946 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1005
Db  2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451
Qy  1006 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1065
Db  2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391
Qy  1066 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1125
Db  2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331
Qy  1126 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1185
Db  2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271
Qy  1186 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1245
Db  2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211
Qy  1246 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1305
Db  2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151
Qy  1306 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1365
Db  2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091
Qy  1366 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1425
Db  2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031
Qy  1426 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1485
Db  2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971
Qy  1486 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1545
Db  1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911
Qy  1546 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1605
Db  1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851
Qy  1606 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1665
Db  1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791
Qy  1666 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1725
Db  1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
Qy  1726 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1785
Db  1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671
Qy  1786 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1845
Db  1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611
Qy  1846 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1905
Db  1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551
Qy  1906 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1965
Db  1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491
Qy  1966 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2025
Db  1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431
Qy  2026 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2085
Db  1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371
Qy  2086 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2145
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Qy   2866 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2925
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Qy   2926 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
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Db   2707 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2736
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RESULT   7
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match             92.4%;  Score 2730;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2730;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    226 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 285
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Db   3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy    406 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 465
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Db   3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

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;       CITY:  Yorktown Heights
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10598-4412
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS 5.0
;       SOFTWARE:  Word Perfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/271,946A
;       FILING DATE:  08-JUL-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marina T. Larson
;       REGISTRATION NUMBER:  32,038
;       REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (914) 245-3252
;       TELEFAX:  (914) 962-4330
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  22
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
;     HYPOTHETICAL:  no
;     ANTI-SENSE:  no
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  human
;     FEATURE:
;       NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.7%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2360 CAACACCAACAAAAATGACTCC 2381
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Db     22 CAACACCAACAAAAATGACTCC 1


Search completed: February 13, 2000, 17:05:38
Job time: 8618 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:54:46 ; Search time 9092.07 Seconds
(without alignments)
1060.184 Million cell updates/sec

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Perfect score: 2553
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Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	c	348	13.6	411	51	AI745643	AI745643 tr24b05.x
4		257	10.1	285	33	AA382103	AA382103 EST95270
5		204	8.0	304	32	AA361277	AA361277 EST70529
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7		156	6.1	456	30	AA210875	AA210875 zr88f11.r

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	9	114	4.5	386	24	N25402 N25402 yx40c12.r1
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	12	82	3.2	525	30	AA258255 AA258255 zr59g04.r
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	26	31	1.2	174	72	AV302462 AV302462
	27	29	1.1	615	40	AA959836 AA959836 vw54h01.s
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	29	26	1.0	529	40	AA959709 AA959709 vw54a04.s
	30	25	1.0	356	41	AI020392 AI020392 ub17a05.r
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ALIGNMENTS

RESULT 1
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DEFINITION DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762D143 5', mRNA sequence.
ACCESSION AL120941
VERSION AL120941.1 GI:5926942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948410.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 180 a 128 c 98 g 166 t
ORIGIN

Query Match 18.6%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.7e-225;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1297 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1357 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1417 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1477 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1537 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1597 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1657 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT 2
AI745644/c
LOCUS AI745644 415 bp mRNA EST 21-JUN-1999
DEFINITION tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI745644
VERSION AI745644.1 GI:5113932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137189.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

```
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             13.8%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-164;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1907 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 1966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy   1967 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy   2027 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy   2087 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy   2147 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy   2207 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2258
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


  Query Match             13.6%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-162;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1911 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 1970
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy   1971 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2030
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy   2031 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2090
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy   2091 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy   2151 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy   2211 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2258
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
```

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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .285
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):107475"
                      /db_xref="taxon:9606"
                      /clone_lib="Activated T-cells II"
                      /cell_type="T-lymphocyte"
                      /dev_stage="adult"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             10.1%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-116;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1701 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATGTCCGGCTAAATAC 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATGTCCGGCTAAATAC 60

Qy   1761 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy   1821 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy   1881 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy   1941 TGTAACAGCATACAAGG 1957
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Db    241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             8.0%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 2.2e-90;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1510 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy   1570 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1630 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1689
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1690 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1750 CGGCTAAATACACTT 1764
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.3%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-69;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1305 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1364
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1365 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1425 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1465
          |||||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   7
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.1%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-66;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2398 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2458 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2518 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||||||||
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Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   8
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.2%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-54;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1100 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy    1160 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy    1220 TGTCTTTATTGG 1231
           ||||||||||||
Db      51 TGTCTTTATTGG 40


RESULT   9
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.5%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-46;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2353 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60
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Qy   2413 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  10
N41391
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


  Query Match             4.4%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-45;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2289 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2349 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329


RESULT  11
R57845
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.5%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-33;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2123 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy   2183 ATATTTCACCCCTGAAGAGTCCATATAAA 2211
          |||||||||||||||||||||||||||||
Db     61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  12
AA258255
LOCUS       AA258255      525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             3.2%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-30;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2472 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy   2532 TACCTCAAACAAGGAAGAGAAA 2553
           |||||||||||||||||||||
Db     61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  13
AA072780
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


  Query Match             1.9%;  Score 48;  DB 28;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-13;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2098 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2145
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    207 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 254


RESULT  14
AQ901300
LOCUS       AQ901300      986 bp    DNA             GSS       10-NOV-1999
DEFINITION  HS_5234_A1_B12_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=9002 Col=23 Row=C, genomic survey sequence.
ACCESSION   AQ901300
VERSION     AQ901300.1  GI:6357490
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     On Sep 10, 1998 this sequence version replaced gi:3552584.
            Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
```

```
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 9002  row: C  column: 23
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 986.
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                      /db_xref="taxon:9606"
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                      /clone_lib="RPCI-11 Human Male BAC Library"
                      /sex="male"
                      /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      252 a    205 c    176 g    353 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 3.6e-10;
  Matches   42;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    669 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 710
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Db     25 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 66


RESULT  15
AA955457
LOCUS       AA955457      472 bp    mRNA            EST       04-JUL-1999
DEFINITION  UI-R-A1-ew-g-10-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone
            UI-R-A1-ew-g-10-0-UI 3' similar to gi|603961|dbj|D25233|RATRP Rat
            mRNA for retinoblastoma protein, partial sequence, mRNA sequence.
ACCESSION   AA955457
VERSION     AA955457.1  GI:4237812
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On May 7, 1998 this sequence version replaced gi:3119031.
            Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.
            Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
            through Research Genetics This clone is also available through the
            I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
            ID=1779132 The following repetitive elements were found in this
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            Seq primer: M13 Forward
            POLYA=No.
FEATURES              Location/Qualifiers
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                      /strain="Sprague-Dawley"
                      /db_xref="taxon:10116"
                      /clone="UI-R-A1-ew-g-10-0-UI"
                      /clone_lib="UI-R-A1"
                      /dev_stage="adult"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-A1
                      library is a subtracted library derived from the UI-R-A0
                      library. The UI-R-A0 library  consisted of a mixture of
                      individually tagged normalized libraries constructed from
                      rat placenta, adult lung, brain, liver, kidney, heart,
                      spleen, ovary, and muscle. The tag is a string of 3-5
                      nucleotides present between the Not I site and the
                      oligo-dT track which allows identification of the library
                      of origin of a clone within the mixture. The subtracted
                      library (UI-R-A1) was constructed as follows: PCR
                      amplified cDNA inserts from a pool of approximately 3,840
                      UI-R-A0 clones from which 3' ESTs had been derived was
                      used as a driver in a hybridization with the UI-R-A0
                      library in the form of single-stranded circles. The
                      remaining single-stranded circles (subtracted library) was
                      purified by hydroxyapatite column chromatography,
                      converted to double-stranded circles and electroporated
                      into DH10B bacteria (Life Technologies) to generate the
                      UI-R-A1 library. This procedure has been previously
                      described (Bonaldo, Lennon and Soares, Genome Research 6:
                      791-806, 1996)"
BASE COUNT      140 a     99 c    117 g    116 t
ORIGIN


  Query Match             1.5%;  Score 38;  DB 46;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-08;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    173 TAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 210
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Db    355 TAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 392


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Job time: 15478 sec
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Date: Feb 12, 2000  7:08 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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Search information block:
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gb_pat:I09369          +  2883.00 4210.23  1.7e-226  4597  ! I09369 Sequence 1 from Patent
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gb_pat:E12560          +  2694.50 3933.14  4.7e-211  4591  ! E12560 cDNA encoding Rb (retin
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gb_ov:GDRETINB         +  2299.50 3352.58  1.0e-178  4541  ! X72218 G.domesticus retinoblas
gb_ov:U00113           +  2289.00 3339.97  5.2e-178  3456  ! U00113 Gallus gallus retinobla
gb_ov:NVRETINBP        +  1976.50 2882.72  1.5e-152  2808  ! Y09226 N.viridescens mRNA for
gb_ov:AF102861         +  1845.00 2687.47  1.1e-141  3386  ! AF102861 Oncorhynchus mykiss r
gb_ro:MMU27177         +   660.50  942.45  1.8e-44   4863  ! U27177 Mus musculus p107 (p107
gb_pr1:HUMP107A        +   658.00  944.45  1.4e-44   2808  ! M74547 H.sapiens retinoblastom
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gb_pr1:HUMRETBLAS      +   474.00  630.96  4.0e-27   180388  ! L11910 Human retinoblastoma
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gb_in1:DMRBFPRTN       +   443.00  629.21  5.0e-27   2593  ! X96975 D.melanogaster mRNA
gb_pl1:ZMU52099        +   422.00  601.89  1.7e-25   1840  ! U52099 Zea mays retinoblast
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DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
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      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
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    1208 ATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1257

      51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1258 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACA 1307

      67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
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    1308 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1357

      84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
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    1358 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1407

     101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
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     117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
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     134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
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  167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
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 1758 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1807

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  251 ThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPh 267
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 1858 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTT 1907

  267 eGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysL 284
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  284 ysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeu 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1958 AAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 2007

  301 LeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHi 317
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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  317 sThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnI 334
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  351 LysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGl 367
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 2158 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCA 2207

  367 nGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleI 384
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  384 leValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeu 400
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 2308 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCC 2357

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 2358 TCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGA 2407

  434 snIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeu 450
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  484 ysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnProPro 500
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 2558 GTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2607

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 2658 TGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAG 2707

  534 luMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSer 550
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2708 AAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2757

  551 MetAspThrSerAsnLysGluGluLys 559
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 2758 ATGGATACCTCAAACAAGGAAGAGAAA 2784

seq_name: gb_pat:I18496

seq_documentation_block:
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


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 401 GlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIlePr 417
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ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
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BASE COUNT      983 a    566 c    597 g   1086 t
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      17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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VERSION     I81465.1  GI:3209762
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            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
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  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
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  TITLE     Partial inactivation of the RB product in a family with incomplete
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  MEDLINE   94203660
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            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
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  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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BASE COUNT     1489 a    842 c    815 g   1454 t
ORIGIN

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              Ratio:  5.170                Gaps:      0
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alignment_block:
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     17 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 34
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        |||||||||||||||||||||||||||||||||||||||||||||||||||
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     51 LysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGl 67
        |||||||||||||||||||||||||||||||||||||||||||||||||||
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     67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
        |||||||||||||||||||||||||||||||||||||||||||||||||||
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        |||||||||||||||||||||||||||||||||||||||||||||||||||
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    117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
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seq_documentation_block:
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DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
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VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
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             Ratio:  5.170              Gaps:      0
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 101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
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ACCESSION   M28419
VERSION     M28419.1  GI:190962
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REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
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  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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ACCESSION   A01444
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            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
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DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
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            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
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            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
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ACCESSION   D25233
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  AUTHORS   Esumi,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-NOV-1993) to the DDBJ/EMBL/GenBank databases. Mariko
            Esumi, Nihon University School of Medicine, Department of
            Pathology; Oyaguchikami-machi, Itabashi-ku, Tokyo 173-8610, Japan
            (E-mail:mesumi@med.nihon-u.ac.jp, Tel:81-3-3972-8111(ex.2250),
            Fax:81-3-3972-8830)
REFERENCE   2  (sites)
  AUTHORS   Roy,N.K., Ballesteros,A. and Garte,S.J.
  TITLE     Cloning and sequence of the rat retinoblastoma (Rb) gene cDNA
  JOURNAL   Nucleic Acids Res. 21 (1), 170 (1993)
  MEDLINE   93181172
REFERENCE   3  (bases 1 to 4432)
  AUTHORS   Esumi,M.
  JOURNAL   Unpublished (1995)
REFERENCE   4  (sites)
  AUTHORS   Esumi,M., Idutsu,T., Kinugasa,S., Ohno,M., Nakabayashi,H., Ikeda,T.
            and Shikata,T.
  TITLE     Isolation and sequence polymorphism of a rat retinoblastoma (RB)
            cDNA
  JOURNAL   Gene 161 (2), 231-235 (1995)
  MEDLINE   95394362
COMMENT     On Dec 23, 1994 this sequence version replaced gi:516833.
            Submitted (10-Nov-1993) to DDBJ by:
            Mariko Esumi
            First Department of Pathology
            Nihon University School of Medicine
            30-1 Ooyaguchikami-machi
            Itabashi-ku, Tokyo 173
            Japan
            Phone: 03-3972-8111 x2250
            Fax:   03-3972-8830
            Sequence updated(12-Dec-1994) by:
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      18 tIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrP 35
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      35 heAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLys 51
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      52 AspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGl 68
         |||:::|||:::|||||||||||||||||||||::|||||||||||||||
    1177 GATGTTGGACACATCTTTAAAGAGAAGTTTGCTAGCGCTGTGGGGCAGGG 1226

      68 yCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrT 85
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      85 yrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIle 101
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     118 uAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerG 135
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     468 uSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysA 485
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DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
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COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
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REFERENCE   1  (bases 1 to 4541)
  AUTHORS   Boehmelt,G., Ulrich,E., Kurzbauer,R., Mellitzer,G., Bird,A. and
            Zenke,M.
  TITLE     Structure and expression of the chicken retinoblastoma gene
  JOURNAL   Cell Growth Differ. 5 (2), 221-230 (1994)
  MEDLINE   94235568
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  AUTHORS   Zenke,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-1993) M. Zenke, Institute of Molecular Pathologie
            (IMP), Dr. Bohrgasse 7, 1030 Wien, AUSTRIA
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  AUTHORS   Feinstein,R., Bolton,W.K., Quinones,J.N., Mosialos,G., Sif,S.,
            Huff,J.L., Capobianco,A.J. and Gilmore,T.D.
  TITLE     Characterization of a chicken cDNA encoding the retinoblastoma gene
            product
  JOURNAL   Biochim. Biophys. Acta 1218 (1), 82-86 (1994)
  MEDLINE   94250698
REFERENCE   2  (bases 1 to 3456)
  AUTHORS   Gilmore,T.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-1993) Thomas D. Gilmore, Biology Department,
            Boston University, 5 Cummington Street, Boston, MA, 02215, USA
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/08204329
; Patent No. 5710255
; GENERAL INFORMATION:
; APPLICANT: SHEPARD, H. M.
; APPLICANT: WEN, SHU F.
; TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
; TITLE OF INVENTION: MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,329
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05866
; FILING DATE: 14-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RENEE A. FITTS
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16930-000400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
US-08-204-329-2

Query Match 99.9%; Score 2551; DB 2; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
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Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
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Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422

Db    732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

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Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651
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Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

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Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   2
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
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US-08-959-638-7

Query Match 99.9%; Score 2551; DB 4; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
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Db    852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

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Db    972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

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Db   1152 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

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Db   1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

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Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
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Db   1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

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Qy   2103 CTTGTCACCAATACCTGACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
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Db   2472 CTTGTCACCAATACCTGACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2771

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
```

RESULT 3
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
; GENERAL INFORMATION:
; APPLICANT: Lee, Wen-Hwa
; APPLICANT: Lee, Eva Y-H.P
; TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
; TITLE OF INVENTION: and Regulator
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,627
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,947
; FILING DATE: 28-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs

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;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2924
US-08-482-627-4

  Query Match             99.9%;  Score 2551;  DB 4;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 431

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     432 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 491

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy     183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     552 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 611

Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy     363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     792 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 851

Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy     543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 971

Qy     603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

Qy     663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 1091

Qy     723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1092 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1151

Qy     783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1152 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

Qy     843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1271

Qy     903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1272 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

Qy     963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

Qy    1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1392 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1451

Qy    1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1452 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

Qy    1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy    1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy    1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy    1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy    1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

Qy    1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1871

Qy    1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1872 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

Qy    1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy    1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy    1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2052 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

Qy    1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2171

Qy    1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2172 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

Qy    1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2232 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2291

Qy    1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2292 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2351

Qy    1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2352 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

Qy    2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2471

Qy    2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2472 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

Qy    2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy    2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy    2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy    2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2771

Qy    2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy    2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy    2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||||
Db    2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   4
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


  Query Match          97.9%;  Score 2500;  DB 6;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2550;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 431

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     432 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 491

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy     183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     552 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 611

Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy     363 TTTATTAGCTAAAGGGCAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     732 TTTATTAGCTAAAGGGCAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     792 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 851

Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy     543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 971

Qy     603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

Qy     663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 1091

Qy     723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1092 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1151

Qy     783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1152 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211
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Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1271

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1451

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1871

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1872 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2052 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2171

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2291

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2292 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2351

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2471

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2472 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAAACTACGCTTTGA 2771

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 5
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE: 19930325
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

```
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1
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Query Match 96.4%; Score 2460; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy    1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy    1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy    1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy    1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy    1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
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Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466


RESULT   6
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             96.4%;  Score 2460;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311
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Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2074 TTGCAGTATGCTTCCAGCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TTGCAGTATGCTTCCAGCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   7
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  19..2469
US-08-470-091-1


  Query Match             96.4%;  Score 2460;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
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Db     427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
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Db    1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
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Db    1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
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Db    1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy    1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy    1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy    1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy    1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy    1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy    1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy    2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy    2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy    2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy    2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy    2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy    2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy    2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy    2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy    2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT   8
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match             96.4%;  Score 2460;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391
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Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311
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Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
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Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
```

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;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.1%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00037;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2470 CTGGCAGAAATGACTTCTACTCGAACAC 2497
           ||||||||||||||||||||||||||||
Db       1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     928 ATGATTTTAAATTCAGCAAGTG 949
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Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  11
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     928 ATGATTTTAAATTCAGCAAGTG 949
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Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  12
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      22 CAACACCAACAAAAATGACTCC 1


RESULT  13
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2228 CAACACCAACAAAAATGACTCC 2249
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Db      22 CAACACCAACAAAAATGACTCC 1


RESULT  14
PCT-US95-08604-22/c
; Sequence 22, Application PC/TUS9508604
;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  HSC Reasearch and Development Limitied Partnership
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  125
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08604
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US 08/271,942
;      FILING DATE:  08-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
PCT-US95-08604-22


  Query Match             0.9%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2228 CAACACCAACAAAAATGACTCC 2249
          ||||||||||||||||||||||
Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  15
PCT-US95-08606-22/c
; Sequence 22, Application PC/TUS9508606
;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Capatos, Denis
;    APPLICANT:  Matthews, David E.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08606
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:  US 08/271,946
;      APPLICATION NUMBER:  08-JUL-1994
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
PCT-US95-08606-22


  Query Match             0.9%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2228 CAACACCAACAAAAATGACTCC 2249
          ||||||||||||||||||||||
Db     22 CAACACCAACAAAAATGACTCC 1


Search completed: February 13, 2000, 17:08:13
Job time: 8773 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:29:20 ; Search time 683.56 Seconds
(without alignments)
913.569 Million cell updates/sec

Title: US-09-026-459A-34_COPY_7_2502
Perfect score: 2496
Sequence: 1 ATGCTGTGGGGAATCTGTAT.....CCTCAAACAAGGAAGAGAAA 2496

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2496	100.0	3266	1	V58444	Modified retinobla
	2	2493	99.9	2994	1	Q04713	Cancer supressing
	3	2493	99.9	2994	1	Q41545	Retinoblastoma gen
	4	2493	99.9	3555	1	V58440	Modified retinobla
	5	2493	99.9	3455	1	V58441	Modified retinobla
	6	2493	99.9	3392	1	V58442	Modified retinobla
	7	2493	99.9	3323	1	V58443	Modified retinobla
	8	2493	99.9	3555	1	V54990	DNA sequence of th
	9	2493	99.9	2994	1	V40004	Retinoblastoma pro
	10	2493	99.9	2995	1	X00737	cDNA encoding a re
	11	2460	98.6	3233	1	Q72690	Retinoblastoma 94k
	12	2460	98.6	3461	1	V58447	Modified retinobla
	13	2460	98.6	3323	1	V58446	Modified retinobla
	14	2448	98.1	3554	1	V58452	Modified retinobla
	15	2448	98.1	3218	1	V54991	DNA sequence of th
	16	2442	97.8	4597	1	N81369	Human retinoblasto
	17	2442	97.8	4597	1	Q70536	Human retinoblasto
	18	2442	97.8	2995	1	Q90059	Retinoblastoma tum
	19	2442	97.8	4597	1	X04501	Human retinoblasto
	20	2343	93.9	3113	1	V58445	Modified retinobla
	21	2289	91.7	2995	1	Q86398	Human Rb110 cDNA.
	22	2242	89.8	3347	1	V58448	Modified retinobla
	23	2062	82.6	3161	1	V58449	Modified retinobla
	24	2061	82.6	3377	1	V58450	Modified retinobla
	25	1885	75.5	3383	1	V58451	Modified retinobla
	26	1548	62.0	5056	1	N90489	cDNA of human reti
	27	1410	56.5	4579	1	N81261	Probe for retinobl
	28	198	7.9	18303	1	X04502	Human retinoblasto
	29	165	6.6	18177	1	N90490	DNA of human retin
c	30	26	1.0	26	1	V49234	rb gene antisense
c	31	26	1.0	26	1	V49235	rb gene antisense
	32	24	1.0	24	1	V01247	Retinoblastoma 1 P
	33	24	1.0	39	1	V58457	Primer OMRbSd2-97
	34	24	1.0	39	1	V59925	Sense primer OMRbS
c	35	23	0.9	32	1	V58466	Primer for Modifie
c	36	23	0.9	32	1	V59932	PCR primer used to
	37	22	0.9	52	1	Q27110	PCR primer for the
	38	22	0.9	50	1	Q27131	5' PCR primer for
	39	22	0.9	50	1	Q99012	Chelating peptide-
c	40	22	0.9	22	1	T11461	Retinoblastoma gen
c	41	22	0.9	22	1	T12860	PCR 3' primer for
c	42	22	0.9	22	1	V58453	Primer OMRbAS300 f
	43	22	0.9	31	1	V58460	Primer for Modifie
	44	22	0.9	31	1	V58464	Primer for Modifie
c	45	22	0.9	31	1	V58465	Primer for Modifie

ALIGNMENTS

RESULT 1
V58444
ID V58444 standard; DNA; 3266 BP.
AC V58444;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2505
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69368.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 166-170; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T;

Query Match 100.0%; Score 2496; DB 1; Length 3266;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       7 ATGCTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACT 66

Qy      61 TTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAA 120
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Db      67 TTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAA 126

Qy     121 GAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGAT 180
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Qy     181 GTATTGTTTGCACTCTTCAGGAAATTGGAAAGGACATGTGAACTTATATATTTGACACAA 240
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Db     187 GTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAA 246

Qy     241 CCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATC 300
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Db     247 CCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATC 306

Qy     301 ACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTT 360
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Db     307 ACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTT 366

Qy     361 CAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAA 420
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Db    367 CAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAA 426

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Db    427 GAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGT 486

Qy    481 CAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTT 540

Db    487 CAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTT 546

Qy    541 CTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTT 600

Db    547 CTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTT 606

Qy    601 ATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAAT 660

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Qy    661 CTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTT 720

Db    667 CTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTT 726

Qy    721 TTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACA 780

Db    727 TTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACA 786

Qy    781 CCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGG 840

Db    787 CCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGG 846

Qy    841 ACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCT 900

Db    847 ACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCT 906

Qy    901 TCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTG 960

Db    907 TCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTG 966

Qy    961 AAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAG 1020

Db    967 AAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAG 1026

Qy   1021 GGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTA 1080

Db   1027 GGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTA 1086

Qy   1081 ATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTT 1140

Db   1087 ATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTT 1146

Qy   1141 CTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCC 1200

Db   1147 CTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCC 1206

Qy   1201 ACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGG 1260

Db   1207 ACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGG 1266

Qy   1261 ATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATC 1320

Db   1267 ATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATC 1326

Qy   1321 AAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGA 1380

Db   1327 AAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGA 1386

Qy   1381 ATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCA 1440

Db   1387 ATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCA 1446

Qy   1441 AAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTC 1500

Db   1447 AAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTC 1506

Qy   1501 CAGAATAATCACACTGGAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAA 1560

Db   1507 CAGAATAATCACACTGGAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAA 1566

Qy   1561 GGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTC 1620

Db   1567 GGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTC 1626

Qy   1621 CAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGG 1680

Db   1627 CAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGG 1686

Qy   1681 CTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTA 1740

Db   1687 CTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTA 1746

Qy   1741 GAACATATCATCTGGAGCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGA 1800

Db   1747 GAACATATCATCTGGAGCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGA 1806

Qy   1801 GACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAAT 1860

Db   1807 GACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAAT 1866

Qy   1861 ATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAG 1920

Db   1867 ATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAG 1926

Qy   1921 GAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTAT 1980

Db   1927 GAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTAT 1986

Qy   1981 AACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCC 2040

Db   1987 AACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCC 2046

Qy   2041 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCC 2100

Db   2047 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCC 2106

Qy   2101 TTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCA 2160

Db   2107 TTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCA 2166

Qy   2161 GAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGT 2220

Db   2167 GAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGT 2226

Qy   2221 GAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGAC 2280

Db   2227 GAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGAC 2286

Qy   2281 CGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGC 2340

Db   2287 CGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGC 2346

Qy   2341 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2400

Db   2347 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2406

Qy   2401 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2460

Db   2407 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2466

Qy   2461 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496

Db   2467 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2502


RESULT   2
Q04713
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ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of California.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;
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Query Match 99.9%; Score 2493; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
Db     430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
Db     490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549

Qy     124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
Db     550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

Qy     184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
Db     610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy     244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
Db     670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy     304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
Db     730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy     364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
Db     790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy     424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
Db     850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

Qy     484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
Db     910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969

Qy     544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
Db     970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

Qy     604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
Db    1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089

Qy     664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
Db    1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149

Qy     724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
Db    1150 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

Qy     784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
Db    1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269

Qy     844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
Db    1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

Qy     904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
Db    1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389

Qy     964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
Db    1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449

Qy    1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
Db    1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

Qy    1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
Db    1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569

Qy    1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
Db    1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy    1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
Db    1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689

Qy    1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
Db    1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

Qy    1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
Db    1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

Qy    1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
Db    1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869

Qy    1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
Db    1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929

Qy    1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
Db    1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989

Qy    1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
Db    1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049

Qy    1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
Db    2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

Qy    1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
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Db   2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2769

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   3
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;   974 A;   618 C;   594 G;   808 T;


  Query Match             99.9%;  Score 2493;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549

Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
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Db   1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783

Db   1150 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843

Db   1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903

Db   1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963

Db   1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023

Db   1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083

Db   1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143

Db   1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569

Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203

Db   1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263

Db   1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689

Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323

Db   1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383

Db   1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443

Db   1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869

Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503

Db   1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563

Db   1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623

Db   1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683

Db   2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743

Db   2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803

Db   2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863

Db   2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923

Db   2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983

Db   2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043

Db   2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103

Db   2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163

Db   2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223

Db   2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283

Db   2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343

Db   2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2769

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403

Db   2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463

Db   2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496

Db   2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 4
V58440
ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69364.
PT Retinoblastoma suppressor protein with N-terminal modification -

PT inhibiting cellular proliferation, particularly cancer
PS Disclosure; Page 121-126; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 99.9%; Score 2493; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 357

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 417

Qy     124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 477

Qy     184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 537

Qy     244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 597

Qy     304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 657

Qy     364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     658 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 717

Qy     424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     718 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 777

Qy     484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     778 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 837

Qy     544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 897

Qy     604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     898 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 957

Qy     664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     958 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1017

Qy     724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1018 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1077

Qy     784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1078 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1137

Qy     844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1197

Qy     904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1198 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1257

Qy     964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1317

Qy    1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1377

Qy    1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1437

Qy    1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1497

Qy    1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1557

Qy    1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1617

Qy    1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1618 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1677

Qy    1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1678 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1737

Qy    1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1738 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1797

Qy    1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1798 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1857

Qy    1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1858 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1917

Qy    1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1918 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1977

Qy    1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1978 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2037

Qy    1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2038 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2097

Qy    1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2098 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2157

Qy    1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2158 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2217

Qy    1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2218 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2277
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Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2278 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2337

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2338 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2397

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2398 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2457

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2458 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2517

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2518 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2577

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2578 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2637

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2638 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2697

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2698 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2757

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
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Db   2758 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT 5
V58441
ID V58441 standard; DNA; 3455 BP.
AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2694
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 T;

Query Match 99.9%; Score 2493; DB 1; Length 3455;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 258

Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 318

Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 378

Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 438

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 498

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 558

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 618

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 678

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 738

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 798

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 858

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 918

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 978

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1038

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1098

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1158

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1218

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1278
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Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1338

Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1398

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1458

Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1518

Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1578

Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1638

Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1698

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1758

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1818

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1878

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1938

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1998

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2058

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2118

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2178

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2238

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2298

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2358
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Qy   2164 GGTCTGCCAACACCAAGAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2359 GGTCTGCCAACACCAAGAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2418

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2478

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 GTGCTCAAAAGAAGTGGTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2538

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2598

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2599 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2658

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2659 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
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RESULT 6
V58442
ID V58442 standard; DNA; 3392 BP.
AC V58442;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2641
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69366.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 150-155; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3392 BP; 1137 A; 614 C; 607 G; 1034 T;

Query Match 99.9%; Score 2493; DB 1; Length 3392;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    136 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 195

Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    196 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 255

Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    256 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 315
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Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    316 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 375

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 435

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 495

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 555

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 615

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 675

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 735

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 795

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    796 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 855

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    856 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 915

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    916 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 975

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    976 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1035

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1095

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1155

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1215

Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1275

Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1335

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1395
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Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1455

Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1515

Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1516 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1575

Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1576 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1635

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1695

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1755

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1815

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1875

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1935

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1995

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2055

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2115

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2116 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2175

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2235

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2295

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2355

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2356 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2415

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2475

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2476 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2535

Qy    2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2536 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2595

Qy    2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          |||||||||||||||||||||||||||||||||
Db    2596 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628


RESULT   7
V58443
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;


  Query Match             99.9%;  Score 2493;  DB 1;  Length 3323;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 126

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 186

Qy     124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 246

Qy     184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 306

Qy     244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 366

Qy     304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 426

Qy     364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 486

Qy     424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 546

Qy     484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 606

Qy     544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 666

Qy     604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 726

Qy     664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 786

Qy     724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 846

Qy     784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 906

Qy     844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 966

Qy     904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1026

Qy     964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1027 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1086

Qy    1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1146

Qy    1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1147 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1206

Qy    1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1207 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1266

Qy    1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1267 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1326

Qy    1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1327 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1386

Qy    1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1387 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1446

Qy    1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1447 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1506

Qy    1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
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Db   1507 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1566

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1626

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1686

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1746

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1806

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1866

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1926

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1986

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2046

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2106

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2166

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2226

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2286

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2346

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2406

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2466

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2467 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2526

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2527 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559

RESULT   8
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V54990
ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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  Query Match             99.9%;  Score 2493;  DB 1;  Length 3555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 357

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 417

Qy     124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 477

Qy     184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 537

Qy     244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 597

Qy     304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 657

Qy     364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     658 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 717
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Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 777

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 837

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 897

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 957

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1017

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1077

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1137

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1197

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1257

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1317

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1377

Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1437

Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1497

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1557

Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1617

Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1618 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1677

Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1678 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1737

Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1738 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1797

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1798 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1857

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1858 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1917

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1918 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1977

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1978 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2037

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2038 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2097

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2098 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2157

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2158 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2217

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2218 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2277

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2278 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2337

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2338 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2397

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2398 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2457

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2458 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2517

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2518 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2577

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2578 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2637

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2638 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2697

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2698 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2757

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2758 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790


RESULT   9
V40004
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
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DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465). A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain. Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease. Tissue-specific expression of E2F-RB fusions is
CC   provided. The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;

  Query Match            99.9%;  Score 2493;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549

Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569

Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689

Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869

Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929
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Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2769

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 10
X00737
ID X00737 standard; cDNA; 2995 BP.
AC X00737;
DT 13-APR-1999 (first entry)
DE cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 139. .2925
FT /*tag= a
FT /product= RB_protein
FT /transl_except= (pos: 226. .228, aa: Glu)
PN US5851991-A.
PD 22-DEC-1998.
PF 13-SEP-1994; 306513.
PR 13-SEP-1994; US-306513.
PR 31-AUG-1987; US-091547.
PR 17-SEP-1987; US-098612.
PR 15-OCT-1987; US-108748.
PR 31-OCT-1988; US-265829.
PR 11-JUL-1990; US-550877.
PR 16-JUL-1990; US-553892.
PR 16-JUL-1990; US-553905.
PR 17-OCT-1991; US-778510.
PR 14-JUL-1992; US-914039.
PR 02-OCT-1992; US-956472.
PR 17-JUN-1993; US-079207.
PR 13-SEP-1993; US-121108.
PR 24-SEP-1993; US-126810.
PA (CANJ-) CANJI INC.
PA (REGC) UNIV CALIFORNIA.
PI Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI Wang NP;
DR WPI; 99-080477/07.
DR P-PSDB; W67801.
PT Inhibition of cancer cell proliferation - with retinoblastoma
PT protein or polypeptide
PS Example 1; Fig 2A-K; 72pp; English.
CC The present sequence encodes a human retinoblastoma (RB) protein
CC designated ppRB-110 or p110-RB. The protein is used in a method
CC for inhibiting proliferation of pathologically proliferating cells
CC lacking endogenous functional retinoblastoma protein. The method
CC comprises contacting the cells with a polypeptide comprising a 56 kD
CC C-terminal fragment of retinoblastoma protein. The method is useful
CC for treating cancers, especially retinoblastoma or secondary
CC osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T;

Query Match 99.9%; Score 2493; DB 1; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549

Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
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Db    730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423

Db    790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483

Db    850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543

Db    910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603

Db    970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663

Db   1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723

Db   1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783

Db   1150 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843

Db   1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903

Db   1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963

Db   1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023

Db   1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083

Db   1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143

Db   1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569

Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203

Db   1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263

Db   1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689

Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323

Db   1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383

Db   1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443

Db   1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869

Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503

Db   1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563

Db   1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623

Db   1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683

Db   2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743

Db   2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803

Db   2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863

Db   2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923

Db   2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983

Db   2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043

Db   2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103

Db   2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163

Db   2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223

Db   2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649

Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283

Db   2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343

Db   2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2769

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403

Db   2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463

Db   2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496

Db   2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT  11
Q72690
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;

  Query Match             98.6%;  Score 2460;  DB 1;  Length 3233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy      97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy     157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy     217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy     277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy     337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy     397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy     457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy     517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy     577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy     637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy     697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy     757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy     817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy     877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy     937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy     997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy    1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy    1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy    1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy    1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy    1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy    1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy    1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy    1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy    1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy    1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626
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Qy   1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy   1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2017 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT  12
V58447
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;
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  Query Match             98.6%;  Score 2460;  DB 1;  Length 3461;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 297

Qy     97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 357

Qy    157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 417

Qy    217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 477

Qy    277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 537

Qy    337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 597

Qy    397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 657

Qy    457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    658 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 717

Qy    517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 777

Qy    577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 837

Qy    637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 897

Qy    697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 957

Qy    757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1017
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Qy    817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1077

Qy    877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1137

Qy    937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1197

Qy    997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1257

Qy   1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1317

Qy   1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1377

Qy   1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1437

Qy   1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1497

Qy   1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1557

Qy   1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1617

Qy   1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1618 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1677

Qy   1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1678 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1737

Qy   1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1738 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1797

Qy   1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1798 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1857

Qy   1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1858 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1917

Qy   1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1918 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1977

Qy   1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1978 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2037

Qy   1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2038 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2097

Qy   1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2098 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2157

Qy   1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2158 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2217

Qy   2017 TTGCAGTATGCTTCCAGCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2218 TTGCAGTATGCTTCCAGCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2277

Qy   2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2278 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2337

Qy   2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2338 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2397

Qy   2197 TCAAGAATCTTAGTATGAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2398 TCAAGAATCTTAGTATGAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2457

Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2458 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2517

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2518 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2577

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2578 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2637

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2638 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2697
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RESULT 13
V58446
ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

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  Query Match             98.6%;  Score 2460;  DB 1;  Length 3323;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC  96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 159

Qy      97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     160 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 219

Qy     157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 279

Qy     217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     280 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 339

Qy     277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     340 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 399

Qy     337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 459

Qy     397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     460 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 519

Qy     457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     520 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 579

Qy     517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 639

Qy     577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 699

Qy     637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 759

Qy     697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 819

Qy     757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 879

Qy     817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 939

Qy     877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 999

Qy     937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1059

Qy     997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1119

Qy    1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1179

Qy    1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1239

Qy    1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1299

Qy    1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1359

Qy    1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1419

Qy    1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1479

Qy    1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1539

Qy    1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1599

Qy    1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1659

Qy    1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1719

Qy    1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1779

Qy    1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1839

Qy    1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1899

Qy    1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1959

Qy    1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2019

Qy    1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2079

Qy    2017 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2139

Qy    2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2199

Qy    2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
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Db   2200 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2259

Qy   2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
Db   2260 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2319

Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
Db   2320 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2379

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
Db   2380 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2439

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
Db   2440 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2499

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
Db   2500 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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RESULT 14
V58452
ID V58452 standard; DNA; 3554 BP.
AC V58452;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69376.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 226-230; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3554 BP; 1170 A; 683 C; 653 G; 1048 T;

Query Match 98.1%; Score 2448; DB 1; Length 3554;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     49 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 108
Db    343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 402

Qy    109 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 168
Db    403 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 462

Qy    169 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 228
Db    463 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 522

Qy    229 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 288
Db    523 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 582

Qy    289 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 348
Db    583 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

Qy    349 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 408
Db    643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 702

Qy    409 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 468
Db    703 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 762

Qy    469 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 528
Db    763 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 822

Qy    529 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 588
Db    823 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 882

Qy    589 TTCAAAAATTTTATACGTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 648
Db    883 TTCAAAAATTTTATACGTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 942

Qy    649 GAGGTTGAAAATCTTTGTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 708
Db    943 GAGGTTGAAAATCTTTGTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 1002

Qy    709 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 768
Db   1003 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1062

Qy    769 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 828
Db   1063 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1122

Qy    829 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 888
Db   1123 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1182

Qy    889 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 948
Db   1183 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242

Qy    949 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1008
Db   1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1302

Qy   1009 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1068
Db   1303 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1362

Qy   1069 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1128
Db   1363 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1422

Qy   1129 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1188
Db   1423 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1482

Qy   1189 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1248
Db   1483 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1542

Qy   1249 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1308
Db   1543 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1602

Qy   1309 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1368
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Db   1663 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1722

Qy   1429 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1488

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Db   1783 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1842

Qy   1549 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1608

Db   1843 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1902

Qy   1609 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1668

Db   1903 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1962

Qy   1669 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1728

Db   1963 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2022

Qy   1729 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1788

Db   2023 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2082

Qy   1789 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1848

Db   2083 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2142

Qy   1849 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1908

Db   2143 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2202

Qy   1909 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1968

Db   2203 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2262

Qy   1969 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2028

Db   2263 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2322

Qy   2029 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2088

Db   2323 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2382

Qy   2089 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2148

Db   2383 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2442

Qy   2149 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2208

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Qy   2209 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2268

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Qy   2269 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2328

Db   2563 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2622

Qy   2329 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2388

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Qy   2389 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2448

Db   2683 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2742

Qy   2449 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496

Db   2743 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT 15
V54991
ID V54991 standard; DNA; 3218 BP.
AC V54991;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2457
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71355.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 153-157; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T;

Query Match 98.1%; Score 2448; DB 1; Length 3218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     49 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 108

Db      7 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 66

Qy    109 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 168

Db     67 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 126

Qy    169 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 228

Db    127 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 186

Qy    229 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 288

Db    187 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 246

Qy    289 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 348

Db    247 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 306
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Qy    349 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 408
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Db    307 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 366

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Qy    469 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    529 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 588
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Qy    589 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 648
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Qy    649 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 708
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Qy    829 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 888
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Qy    949 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1008
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Qy   1009 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1068
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Qy   1369 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1428
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Qy   1549 CCAAAGAAAAAAGGTTGAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1608
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Qy   1789 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1848
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Qy   1849 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1908
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Qy   1909 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1968
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Db   1867 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1926

Qy   1969 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2028
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Qy   2089 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2148
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Qy   2149 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2208
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Qy   2329 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2388
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Db   2407 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2454
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Search completed: February 13, 2000, 20:31:39
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:54:56 ; Search time 9092.07 Seconds
(without alignments)
1036.514 Million cell updates/sec

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Perfect score: 2496
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Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

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Word size : 0

Number of hits that pass the threshold : 9077268

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75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	476	19.1	572	64	AL120941	AL120941 DKFZp762D
c	2	352	14.1	415	51	AI745644	AI745644 tr24b06.x
c	3	348	13.9	411	51	AI745643	AI745643 tr24b05.x
	4	257	10.3	285	33	AA382103	AA382103 EST95270
	5	204	8.2	304	32	AA361277	AA361277 EST70529
c	6	161	6.5	329	36	AA664676	AA664676 nu64f09.s
	7	156	6.2	456	30	AA210875	AA210875 zr88f11.r

c	8	132	5.3	171	38	AA765882 AA765882 oa14a06.s
	9	114	4.6	386	24	N25402 N25402 yx40c12.r1
	10	113	4.5	457	24	N41391 N41391 yw70g06.r1
	11	89	3.6	152	22	R57845 R57845 F6142 Fetal
	12	82	3.3	525	30	AA258255 AA258255 zr59g04.r
	13	48	1.9	522	28	AA072780 AA072780 mm76a05.r
	14	42	1.7	986	89	AQ901300 AQ901300 HS_5234_A
	15	38	1.5	472	46	AA955457 AA955457 UI-R-A1-e
c	16	35	1.4	914	38	AA763411 AA763411 vw54a04.r
c	17	35	1.4	871	38	AA763485 AA763485 vw54h01.r
	18	34	1.4	427	37	AA709628 AA709628 vv41c11.r
c	19	33	1.3	462	48	AI606529 AI606529 vb27g08.y
	20	33	1.3	832	49	AI646038 AI646038 vw54a10.x
	21	33	1.3	709	49	AI646097 AI646097 vw54h07.x
	22	33	1.3	575	49	AI662832 AI662832 vb27g08.x
	23	31	1.2	284	59	AV111279 AV111279 AV111279
	24	31	1.2	174	72	AV302462 AV302462 AV302462
	25	29	1.2	615	40	AA959836 AA959836 vw54h01.s
c	26	26	1.0	405	39	AA861150 AA861150 ak36a12.s
	27	26	1.0	529	40	AA959709 AA959709 vw54a04.s
	28	25	1.0	356	41	AI020392 AI020392 ub17a05.r
c	29	24	1.0	492	33	AA396353 AA396353 vb27g08.r
c	30	20	0.8	439	21	R12275 R12275 yf40f10.r1
c	31	20	0.8	424	21	R21339 R21339 yg50d05.r1
c	32	20	0.8	372	21	R21352 R21352 yg50f05.r1
c	33	20	0.8	351	21	T78368 T78368 yc99g02.r1
c	34	20	0.8	478	22	H06003 H06003 yl76c05.r1
c	35	20	0.8	299	36	AA618388 AA618388 nq18h09.s
	36	20	0.8	405	38	AA774885 AA774885 ae83f10.s
	37	20	0.8	175	39	AA825220 AA825220 oc66f12.s
	38	20	0.8	446	40	AA926650 AA926650 om28c01.s
	39	20	0.8	453	44	AI309208 AI309208 qo70d01.x
c	40	20	0.8	188	71	AV320612 AV320612 AV320612
	41	20	0.8	548	81	B72527 B72527 RPCI11-9E12
	42	20	0.8	353	99	AQ217005 AQ217005 HS_2262_B
	43	20	0.8	574	103	AQ498524 AQ498524 HS_5120_B
c	44	19	0.8	305	20	T54299 T54299 ya91a05.s3
c	45	19	0.8	612	105	AQ624615 AQ624615 HS_2110_B

ALIGNMENTS

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RESULT   1
AL120941
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


  Query Match           19.1%;  Score 476;  DB 64;  Length 572;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-227;
  Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1180 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1240 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1300 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1360 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1420 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1480 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1540 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1600 ACACAAGCAACCTCAGCGTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1655
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCGTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476


RESULT   2
AI745644/c
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
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            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             14.1%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-165;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1850 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 1909
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy    1910 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 1969
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy    1970 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2029
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy    2030 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2089
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy    2090 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2149
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy    2150 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2201
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


  Query Match             13.9%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-163;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1854 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 1913
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy    1914 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 1973
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy    1974 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2033
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy    2034 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2093
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy    2094 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy    2154 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2201
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .285
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):107475"
                      /db_xref="taxon:9606"
                      /clone_lib="Activated T-cells II"
                      /cell_type="T-lymphocyte"
                      /dev_stage="adult"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match           10.3%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-117;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1644 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1703
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy   1704 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1763
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy   1764 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy   1824 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1883
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy   1884 TGTAACAGCATACAAGG 1900
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Db    241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match           8.2%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity  99.6%;  Pred. No. 5.8e-91;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1453 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy   1513 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1573 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1632
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1633 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1693 CGGCTAAATACACTT 1707
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES              Location/Qualifiers
     source           1. .329
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1215497"
                      /clone_lib="NCI_CGAP_Alv1"
                      /tissue_type="alveolar rhabdomyosarcoma"
                      /lab_host="DH10B"
                      /note="Vector: pAMP10; mRNA made from alveolar
                      rhabdomyosarcoma, cDNA made by oligo-dT priming.
                      Non-directionally cloned. Size-selected on agarose gel,
                      average insert  size 600 bp. Reference:  Krizman et al.
                      (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.5%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-69;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1248 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1308 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1367
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1368 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1408
          |||||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   7
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES              Location/Qualifiers
     source           1. .456
                      /organism="Homo sapiens"
                      /db_xref="GDB:5586117"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:682797"
                      /clone_lib="NCI_CGAP_GCB1"
                      /tissue_type="germinal center B cell"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was prepared from human tonsillar cells enriched for
                      germinal center B cells by flow sorting (CD20+, IgD-),
                      provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                      (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                      primed with a Not I - oligo(dT) primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                      3']. Double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization, and was
                      constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.2%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-67;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2341 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2401 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2461 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          |||||||||||||||||||||||||||||||||||
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Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   8
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.3%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-55;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1043 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy    1103 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy    1163 TGTCTTTATTGG 1174
           ||||||||||||
Db      51 TGTCTTTATTGG 40


RESULT   9
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.6%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-46;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2296 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60
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Qy   2356 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  10
N41391
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


  Query Match             4.5%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-45;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2232 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2292 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2344
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329


RESULT  11
R57845
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.6%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 2e-33;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2066 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy   2126 ATATTTCACCCCTGAAGAGTCCATATAAA 2154
          |||||||||||||||||||||||||||||
Db     61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  12
AA258255
LOCUS       AA258255      525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             3.3%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-30;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2415 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2474
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2475 TACCTCAAACAAGGAAGAGAAA 2496
           |||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  13
AA072780
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


  Query Match             1.9%;  Score 48;  DB 28;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-13;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2041 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2088
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     207 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 254


RESULT  14
AQ901300
LOCUS       AQ901300      986 bp    DNA             GSS       10-NOV-1999
DEFINITION  HS_5234_A1_B12_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=9002 Col=23 Row=C, genomic survey sequence.
ACCESSION   AQ901300
VERSION     AQ901300.1  GI:6357490
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     On Sep 10, 1998 this sequence version replaced gi:3552584.
            Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
```

```
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 9002  row: C  column: 23
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 986.
FEATURES              Location/Qualifiers
     source           1. .986
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="Plate=9002 Col=23 Row=C"
                      /clone_lib="RPCI-11 Human Male BAC Library"
                      /sex="male"
                      /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      252 a    205 c    176 g    353 t
ORIGIN


  Query Match             1.7%;  Score 42;  DB 89;  Length 986;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-10;
  Matches   42;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    612 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 653
          |||||||||||||||||||||||||||||||||||||||||||
Db     25 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 66


RESULT  15
AA955457
LOCUS       AA955457      472 bp    mRNA            EST       04-JUL-1999
DEFINITION  UI-R-A1-ew-g-10-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone
            UI-R-A1-ew-g-10-0-UI 3' similar to gi|603961|dbj|D25233|RATRP Rat
            mRNA for retinoblastoma protein, partial sequence, mRNA sequence.
ACCESSION   AA955457
VERSION     AA955457.1  GI:4237812
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On May 7, 1998 this sequence version replaced gi:3119031.
            Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.
            Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
            through Research Genetics This clone is also available through the
            I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
            ID=1779132 The following repetitive elements were found in this
            cDNA sequence: 3-38, >(CGG)n#Simple_repeat
            Seq primer: M13 Forward
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .472
                      /organism="Rattus norvegicus"
                      /strain="Sprague-Dawley"
                      /db_xref="taxon:10116"
                      /clone="UI-R-A1-ew-g-10-0-UI"
                      /clone_lib="UI-R-A1"
                      /dev_stage="adult"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-A1
                      library is a subtracted library derived from the UI-R-A0
                      library. The UI-R-A0 library  consisted of a mixture of
                      individually tagged normalized libraries constructed from
                      rat placenta, adult lung, brain, liver, kidney, heart,
                      spleen, ovary, and muscle. The tag is a string of 3-5
                      nucleotides present between the Not I site and the
                      oligo-dT track which allows identification of the library
                      of origin of a clone within the mixture. The subtracted
                      library (UI-R-A1) was constructed as follows: PCR
                      amplified cDNA inserts from a pool of approximately 3,840
                      UI-R-A0 clones from which 3' ESTs had been derived was
                      used as a driver in a hybridization with the UI-R-A0
                      library in the form of single-stranded circles. The
                      remaining single-stranded circles (subtracted library) was
                      purified by hydroxyapatite column chromatography,
                      converted to double-stranded circles and electroporated
                      into DH10B bacteria (Life Technologies) to generate the
                      UI-R-A1 library. This procedure has been previously
                      described (Bonaldo, Lennon and Soares, Genome Research 6:
                      791-806, 1996)"
BASE COUNT      140 a     99 c    117 g    116 t
ORIGIN


  Query Match             1.5%;  Score 38;  DB 46;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-08;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    116 TAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 153
          |||||||||||||||||||||||||||||||||||||
Db    355 TAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 392


Search completed: February 13, 2000, 16:55:04
Job time: 15486 sec
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:55:04 ; Search time 9092.07 Seconds
(without alignments)
972.978 Million cell updates/sec

Title: US-09-026-459A-36_COPY_7_2349
Perfect score: 2343
Sequence: 1 ATGTCAAGACTGTTGAAGAA.....CCTCAAACAAGGAAGAGAAA 2343

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
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26: gb_est7:*
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59: gb_est33:*
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83: em_gss1:*
84: em_gss2:*
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100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		476	20.3	572	64	AL120941	AL120941 DKFZp762D
2	c	352	15.0	415	51	AI745644	AI745644 tr24b06.x
3	c	348	14.9	411	51	AI745643	AI745643 tr24b05.x
4		257	11.0	285	33	AA382103	AA382103 EST95270
5		204	8.7	304	32	AA361277	AA361277 EST70529
6	c	161	6.9	329	36	AA664676	AA664676 nu64f09.s
7		156	6.7	456	30	AA210875	AA210875 zr88f11.r

c	8	132	5.6	171	38	AA765882 AA765882 oa14a06.s
	9	114	4.9	386	24	N25402 N25402 yx40c12.r1
	10	113	4.8	457	24	N41391 N41391 yw70g06.r1
	11	89	3.8	152	22	R57845 R57845 F6142 Fetal
	12	82	3.5	525	30	AA258255 AA258255 zr59g04.r
	13	48	2.0	522	28	AA072780 mm76a05.r
	14	42	1.8	986	89	AQ901300 AQ901300 HS_5234_A
c	15	35	1.5	914	38	AA763411 AA763411 vw54a04.r
c	16	35	1.5	871	38	AA763485 AA763485 vw54h01.r
	17	34	1.5	427	37	AA709628 AA709628 vv41c11.r
c	18	33	1.4	462	48	AI606529 AI606529 vb27g08.y
	19	33	1.4	832	49	AI646038 AI646038 vw54a10.x
	20	33	1.4	709	49	AI646097 AI646097 vw54h07.x
	21	33	1.4	575	49	AI662832 AI662832 vb27g08.x
	22	31	1.3	284	59	AV111279 AV111279
	23	31	1.3	174	72	AV302462 AV302462 AV302462
	24	29	1.2	615	40	AA959836 AA959836 vw54h01.s
c	25	26	1.1	405	39	AA861150 AA861150 ak36a12.s
	26	26	1.1	529	40	AA959709 AA959709 vw54a04.s
	27	25	1.1	356	41	AI020392 AI020392 ub17a05.r
c	28	24	1.0	492	33	AA396353 AA396353 vb27g08.r
c	29	20	0.9	439	21	R12275 R12275 yf40f10.r1
c	30	20	0.9	424	21	R21339 R21339 yg50d05.r1
c	31	20	0.9	372	21	R21352 R21352 yg50f05.r1
c	32	20	0.9	351	21	T78368 T78368 yc99g02.r1
c	33	20	0.9	478	22	H06003 H06003 yl76c05.r1
c	34	20	0.9	299	36	AA618388 AA618388 nq18h09.s
	35	20	0.9	175	39	AA825220 AA825220 oc66f12.s
	36	20	0.9	446	40	AA926650 AA926650 om28c01.s
	37	20	0.9	453	44	AI309208 AI309208 qo70d01.x
c	38	20	0.9	188	71	AV320612 AV320612 AV320612
	39	20	0.9	548	81	B72527 B72527 RPCI11-9E12
	40	20	0.9	353	99	AQ217005 AQ217005 HS_2262_B
c	41	19	0.8	305	20	T54299 T54299 ya91a05.s3
c	42	19	0.8	396	21	R13142 R13142 yf72f11.r1
c	43	19	0.8	356	21	T71292 T71292 yc61b02.s1
c	44	19	0.8	365	22	R64348 R64348 yi18h10.s1
c	45	19	0.8	612	105	AQ624615 AQ624615 HS_2110_B

ALIGNMENTS

```
RESULT   1
AL120941
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN
```

Query Match 20.3%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 6.7e-228;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1027 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1087 ACAGATTTGTCTTTCCGATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCGATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1147 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1207 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1267 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1327 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1387 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1447 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT   2
AI745644/c
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
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            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


  Query Match             15.0%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-165;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1697 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 1756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy   1757 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 1816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy   1817 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 1876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy   1877 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 1936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy   1937 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 1996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy   1997 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .411
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219217"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


  Query Match             14.9%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-163;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1701 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 1760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy   1761 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 1820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy   1821 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 1880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy   1881 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 1940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy   1941 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy   2001 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2048
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .285
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):107475"
                      /db_xref="taxon:9606"
                      /clone_lib="Activated T-cells II"
                      /cell_type="T-lymphocyte"
                      /dev_stage="adult"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             11.0%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-118;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1491 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy   1551 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy   1611 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy   1671 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy   1731 TGTAACAGCATACAAGG 1747
          ||||||||||||||||
Db    241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277       304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             8.7%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 2.1e-91;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1300 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy   1360 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1420 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1479
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1480 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1540 CGGCTAAATACACTT 1554
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.9%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-70;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1095 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1154
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1155 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1215 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1255
          |||||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   7
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.7%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-67;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2188 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2248 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2308 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2343
          |||||||||||||||||||||||||||||||||||
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Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   8
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.6%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-55;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    890 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy    950 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1010 TGTCTTTATTGG 1021
          ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT   9
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.9%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-46;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2143 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60
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Qy   2203 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  10
N41391
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT     159 a     77 c     93 g    128 t
ORIGIN


  Query Match             4.8%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-46;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2079 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2139 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329


RESULT  11
R57845
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT      43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.8%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-33;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1913 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 1972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy   1973 ATATTTCACCCCTGAAGAGTCCATATAAA 2001
          |||||||||||||||||||||||||||||
Db     61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  12
AA258255
LOCUS       AA258255      525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             3.5%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-30;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2262 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2322 TACCTCAAACAAGGAAGAGAAA 2343
           |||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  13
AA072780
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


  Query Match             2.0%;  Score 48;  DB 28;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-13;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1888 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 1935
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     207 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 254


RESULT  14
AQ901300
LOCUS       AQ901300      986 bp    DNA             GSS       10-NOV-1999
DEFINITION  HS_5234_A1_B12_SP6E_RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=9002 Col=23 Row=C, genomic survey sequence.
ACCESSION   AQ901300
VERSION     AQ901300.1  GI:6357490
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     On Sep 10, 1998 this sequence version replaced gi:3552584.
            Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
```

```
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 9002  row: C  column: 23
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 986.
FEATURES              Location/Qualifiers
     source           1. .986
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="Plate=9002 Col=23 Row=C"
                      /clone_lib="RPCI-11 Human Male BAC Library"
                      /sex="male"
                      /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      252 a    205 c    176 g    353 t
ORIGIN


  Query Match             1.8%;  Score 42;  DB 89;  Length 986;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-10;
  Matches   42;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    459 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 500
          |||||||||||||||||||||||||||||||||||||||||||
Db     25 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 66


RESULT  15
AA763411/c
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:10090"
                      /clone="IMAGE:1247598"
                      /clone_lib="Soares mouse mammary gland NMLMG"
                      /sex="female (lactating)"
                      /tissue_type="mammary gland"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; 1st strand cDNA was prepared from mammary
                      gland tissue from a lactating female, and was then primed
                      with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                      ligated to Eco RI adaptors (Pharmacia), digested with Not
                      I  and cloned into the Not I and Eco RI sites of the
                      modified pT7T3 vector.  Library is normalized.  Library
                      was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


  Query Match             1.5%;  Score 35;  DB 38;  Length 914;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1120 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1154
           |||||||||||||||||||||||||||||||||||
Db    367 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 333


Search completed: February 13, 2000, 16:55:11
Job time: 15493 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:31:39 ; Search time 683.56 Seconds
(without alignments)
857.569 Million cell updates/sec

Title: US-09-026-459A-36_COPY_7_2349
Perfect score: 2343
Sequence: 1 ATGTCAAGACTGTTGAAGAA.....CCTCAAACAAGGAAGAGAAA 2343

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2343	100.0	2994	1	Q04713	Cancer supressing
2	2343	100.0	2994	1	Q41545	Retinoblastoma gen
3	2343	100.0	3233	1	Q72690	Retinoblastoma 94k
4	2343	100.0	3461	1	V58447	Modified retinobla
5	2343	100.0	3554	1	V58452	Modified retinobla
6	2343	100.0	3555	1	V58440	Modified retinobla
7	2343	100.0	3455	1	V58441	Modified retinobla
8	2343	100.0	3392	1	V58442	Modified retinobla
9	2343	100.0	3323	1	V58443	Modified retinobla
10	2343	100.0	3266	1	V58444	Modified retinobla
11	2343	100.0	3113	1	V58445	Modified retinobla
12	2343	100.0	3323	1	V58446	Modified retinobla
13	2343	100.0	3555	1	V54990	DNA sequence of th
14	2343	100.0	3218	1	V54991	DNA sequence of th
15	2343	100.0	2994	1	V40004	Retinoblastoma pro
16	2343	100.0	2995	1	X00737	cDNA encoding a re
17	2292	97.8	4597	1	N81369	Human retinoblasto
18	2292	97.8	4597	1	Q70536	Human retinoblasto
19	2292	97.8	2995	1	Q90059	Retinoblastoma tum
20	2292	97.8	4597	1	X04501	Human retinoblasto
21	2242	95.7	3347	1	V58448	Modified retinobla
22	2139	91.3	2995	1	Q86398	Human Rb110 cDNA.
23	2062	88.0	3161	1	V58449	Modified retinobla
24	2061	88.0	3377	1	V58450	Modified retinobla
25	1885	80.5	3383	1	V58451	Modified retinobla
26	1548	66.1	5056	1	N90489	cDNA of human reti
27	1410	60.2	4579	1	N81261	Probe for retinobl
28	198	8.5	18303	1	X04502	Human retinoblasto
29	165	7.0	18177	1	N90490	DNA of human retin
c 30	26	1.1	26	1	V49234	rb gene antisense
c 31	26	1.1	26	1	V49235	rb gene antisense
32	24	1.0	24	1	V01247	Retinoblastoma 1 P
c 33	23	1.0	32	1	V58466	Primer for Modifie
c 34	23	1.0	32	1	V59932	PCR primer used to
35	22	0.9	52	1	Q27110	PCR primer for the
36	22	0.9	50	1	Q27131	5' PCR primer for
37	22	0.9	50	1	Q99012	Chelating peptide-
c 38	22	0.9	22	1	T11461	Retinoblastoma gen
c 39	22	0.9	22	1	T12860	PCR 3' primer for
c 40	22	0.9	22	1	V58453	Primer OMRbAS300 f
41	22	0.9	31	1	V58464	Primer for Modifie
c 42	22	0.9	31	1	V58465	Primer for Modifie
c 43	22	0.9	22	1	V55002	Antisense PCR prim
44	22	0.9	31	1	V59929	Sense primer used
c 45	22	0.9	31	1	V59931	PCR primer used to

ALIGNMENTS

RESULT 1
Q04713
ID Q04713 standard; cDNA; 2994 BP.
AC Q04713;
DT 11-OCT-1990 (first entry)
DE Cancer supressing gene (CSG).
KW Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW RB; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 139. .2922
FT /*tag= a
PN WO9005180-A.
PD 17-MAY-1990.
PF 30-OCT-1989; 004808.
PR 31-OCT-1988; US-265829.
PA (REGC) Univ of Califonia.
PI Lee WH, Huang HJS;
DR WPI; 90-178822/23.
DR P-PSDB; R05305.
PT Controlling cancer -
PT by replacing ineffective cancer suppressing gene with cloned,
PT active gene.
PS Claim 35; Page 86; 105pp; English.
CC Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC By installing a working CSG, safe and specific treatment and
CC prophylaxis can be given to cancer patients.
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

Query Match 100.0%; Score 2343; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
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Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
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Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
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Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
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Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
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Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
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Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999
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Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
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Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
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Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
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Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
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Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
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Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
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Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
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Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
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Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
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Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
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Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
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Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
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Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
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Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

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Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
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Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
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Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
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Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
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Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
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Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
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Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
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Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
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Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
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Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
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Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
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Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
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Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
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Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy   2341 AAA 2343
          |||
Db   2920 AAA 2922
```

RESULT 2
Q41545
ID Q41545 standard; DNA; 2994 BP.
AC Q41545;
DT 24-AUG-1993 (first entry)
DE Retinoblastoma gene.
KW RB gene product; p56RB portion; cell cycle progression control;
KW combination; therapeutic methods; arrest; tumourigenesis;
KW regulation; physiological processes; blood cell prodn.;
KW gamete prodn.; ss.
OS Homo sapiens SR-40 cell line.
FH Key Location/Qualifiers
FT cds 139. .2925

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FT                  /*tag= a
FT                  /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;
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Query Match 100.0%; Score 2343; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
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Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    2341 AAA 2343
Db    2920 AAA 2922
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RESULT   3
Q72690
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;
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  Query Match           100.0%;  Score 2343;  DB 1;  Length 3233;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
Db    124 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 183

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
Db    184 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 243

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
Db    244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
Db    304 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 363

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
Db    364 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 423

Qy    301 GGTTCACCTCGAACACCGAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
Db    424 GGTTCACCTCGAACACCGAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 483

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
Db    484 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 543

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
Db    544 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 603

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
Db    604 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 663

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
Db    664 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 723

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
Db    724 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 783

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
Db    784 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 843

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
Db    844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
Db    904 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 963

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
Db    964 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1023

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
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Db   1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1083

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020

Db   1084 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1143

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080

Db   1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140

Db   1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200

Db   1264 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260

Db   1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1383

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320

Db   1384 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1443

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380

Db   1444 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1503

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440

Db   1504 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1563

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500

Db   1564 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560

Db   1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1683

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620

Db   1684 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1743

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680

Db   1744 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1803

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740

Db   1804 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1863

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800

Db   1864 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1923

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860

Db   1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1983

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920

Db   1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980

Db   2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040

Db   2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100

Db   2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160

Db   2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220

Db   2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280

Db   2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340

Db   2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463

Qy   2341 AAA 2343

Db   2464 AAA 2466
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RESULT 4
V58447
ID V58447 standard; DNA; 3461 BP.
AC V58447;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2700
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69371.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 188-192; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3461 BP; 1141 A; 675 C; 627 G; 1018 T;

Query Match 100.0%; Score 2343; DB 1; Length 3461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60

Db    355 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 414

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120

Db    415 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 474

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
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Db    475 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 534
Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
Db    535 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 594
Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
Db    595 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 654
Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
Db    655 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 714
Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
Db    715 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 774
Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
Db    775 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 834
Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
Db    835 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 894
Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
Db    895 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 954
Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
Db    955 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1014
Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
Db   1015 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1074
Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
Db   1075 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1134
Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
Db   1135 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1194
Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
Db   1195 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1254
Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
Db   1255 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1314
Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
Db   1315 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1374
Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
Db   1375 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1434
Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
Db   1435 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1494
Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
Db   1495 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1554
Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
Db   1555 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1614
Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
Db   1615 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1674
Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
Db   1675 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734
Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
Db   1735 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1794
Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
Db   1795 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1854
Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
Db   1855 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1914
Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
Db   1915 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1974
Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
Db   1975 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2034
Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
Db   2035 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2094
Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
Db   2095 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2154
Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
Db   2155 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2214
Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
Db   2215 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2274
Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
Db   2275 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2334
Qy   1981 CCCCTGAAGAGTCCATATAAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
Db   2335 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2394
Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
Db   2395 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2454
Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
Db   2455 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2514
Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
Db   2515 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2574
Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
Db   2575 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2634
Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
Db   2635 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2694
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Qy   2341 AAA 2343
          |||
Db   2695 AAA 2697


RESULT   5
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;

  Query Match             100.0%;  Score 2343;  DB 1;  Length 3554;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 507

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 567

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 627

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 687

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 807

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 867

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 927

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    928 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 987

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    988 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1047

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1048 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1107

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1108 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1167

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1168 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1227

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1228 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1287

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1288 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1347

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1348 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1407

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1467

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1527

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1528 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1587

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1588 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1647

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1648 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1707

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1708 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1767

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1768 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1827

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1828 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1887

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1888 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1947

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1948 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2007
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Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2008 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2067

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2127

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2187

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2247

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2307

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2367

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2427

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2487

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2547

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2607

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2667

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2727

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2787

Qy   2341 AAA 2343
          |||
Db   2788 AAA 2790
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RESULT   6
V58440
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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  Query Match           100.0%;  Score 2343;  DB 1;  Length 3555;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 507

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 567

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 627

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 687

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 807

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 867

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 927

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    928 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 987

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    988 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1047

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1048 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1107

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1108 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1167

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1168 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1227
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Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1228 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1287

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1288 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1347

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1348 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1407

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1467

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1527

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1528 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1587

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1588 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1647

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1648 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1707

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1708 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1767

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1768 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1827

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1828 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1887

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1888 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1947

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1948 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2007

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2008 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2067

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2127

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2187

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2247

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2307

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2367

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2427

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2487

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2547

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2607

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2667

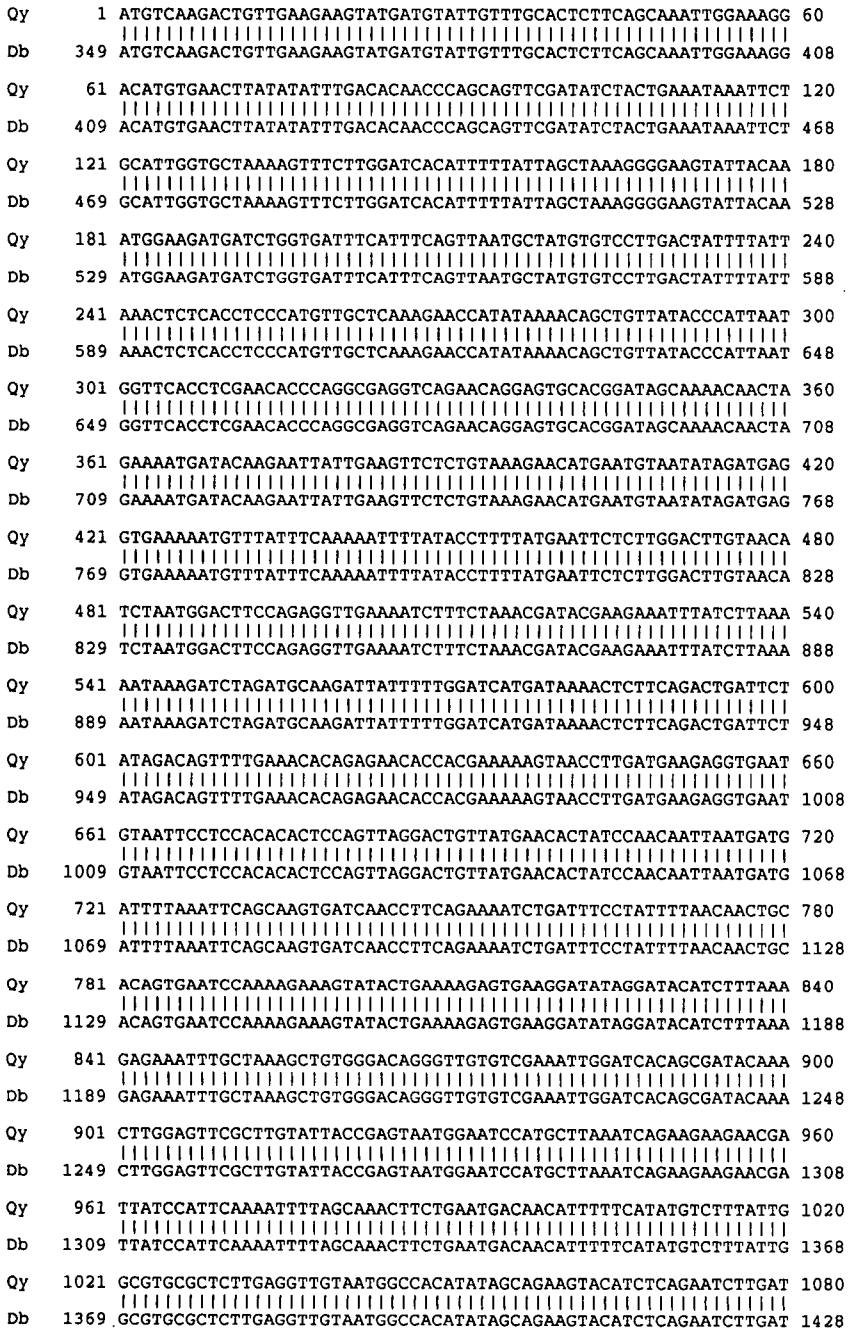
Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2727

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2787

Qy   2341 AAA 2343
          |||
Db   2788 AAA 2790
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RESULT 7
V58441
ID V58441 standard; DNA; 3455 BP.
AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2694
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 T;

Query Match 100.0%; Score 2343; DB 1; Length 3455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


Qy 1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
Db 349 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 408
Qy 61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
Db 409 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 468
Qy 121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
Db 469 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 528
Qy 181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
Db 529 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 588
Qy 241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
Db 589 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 648
Qy 301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
Db 649 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 708
Qy 361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
Db 709 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 768
Qy 421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
Db 769 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 828
Qy 481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
Db 829 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 888
Qy 541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
Db 889 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 948
Qy 601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
Db 949 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1008
Qy 661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
Db 1009 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1068
Qy 721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
Db 1069 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1128
Qy 781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
Db 1129 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1188
Qy 841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
Db 1189 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1248
Qy 901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
Db 1249 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1308
Qy 961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
Db 1309 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1368
Qy 1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
Db 1369 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1428
Qy 1081 TCTGGAACAGATTTGTGTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
Db 1429 TCTGGAACAGATTTGTGTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1488
Qy 1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
Db 1489 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1548
Qy 1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
Db 1549 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1608
Qy 1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
Db 1609 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1668
Qy 1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
Db 1669 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1728
Qy 1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
Db 1729 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1788
Qy 1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
Db 1789 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1848
Qy 1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
Db 1849 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1908
Qy 1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
Db 1909 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1968
Qy 1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
Db 1969 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2028
Qy 1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
Db 2029 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2088
Qy 1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
Db 2089 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2148
Qy 1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
Db 2149 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2208
Qy 1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
Db 2209 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2268
Qy 1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
Db 2269 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2328
Qy 1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
Db 2329 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2388
Qy 2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
Db 2389 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2448
Qy 2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
Db 2449 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2508
Qy 2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2568

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2628

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2688

Qy   2341 AAA 2343
          |||
Db   2689 AAA 2691


RESULT   8
V58442
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


  Query Match             100.0%;  Score 2343;  DB 1;  Length 3392;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 345

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 405

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 465

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 525

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 585

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 645

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 705

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 765

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 825

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 885

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 945

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1005

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1065

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1125

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1185

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1245

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1305

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1365

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1425

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1485

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1545

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1605

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1665

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
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Db   1666 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1725

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500

Db   1726 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1785

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560

Db   1786 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1845

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620

Db   1846 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1905

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680

Db   1906 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1965

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740

Db   1966 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2025

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800

Db   2026 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2085

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860

Db   2086 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2145

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920

Db   2146 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2205

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980

Db   2206 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2265

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040

Db   2266 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2325

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100

Db   2326 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2385

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160

Db   2386 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2445

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220

Db   2446 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2505

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280

Db   2506 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2565

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340

Db   2566 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2625

Qy   2341 AAA 2343

Db   2626 AAA 2628


RESULT   9
V58443
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;


  Query Match           100.0%;  Score 2343;  DB 1;  Length 3323;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60

Db    217 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 276

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120

Db    277 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 336

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180

Db    337 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 396

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240

Db    397 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 456

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300

Db    457 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 516

Qy    301 GGTTCACCTCGAACACGCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360

Db    517 GGTTCACCTCGAACACGCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 576

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420

Db    577 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 636

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480

Db    637 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 696

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540

Db    697 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 756

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600

Db    757 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 816

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
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Db    817 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 876

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720

Db    877 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 936

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780

Db    937 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 996

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840

Db    997 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1056

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900

Db   1057 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1116

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960

Db   1117 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1176

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020

Db   1177 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1236

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080

Db   1237 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1296

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140

Db   1297 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1356

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200

Db   1357 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1416

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260

Db   1417 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1476

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320

Db   1477 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1536

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380

Db   1537 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1596

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440

Db   1597 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1656

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500

Db   1657 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1716

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560

Db   1717 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1776

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620

Db   1777 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1836

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680

Db   1837 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1896

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740

Db   1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1956

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800

Db   1957 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2016

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860

Db   2017 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2076

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920

Db   2077 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2136

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980

Db   2137 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2196

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040

Db   2197 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2256

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100

Db   2257 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2316

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160

Db   2317 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2376

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220

Db   2377 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2436

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280

Db   2437 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2496

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340

Db   2497 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2556

Qy   2341 AAA 2343

Db   2557 AAA 2559
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RESULT  10
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
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CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;

  Query Match            100.0%;  Score 2343;  DB 1;  Length 3266;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     160 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 219

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 279

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     280 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 339

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     340 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 399

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 459

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     460 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 519

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     520 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 579

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 639

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 699

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 759

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 819

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 879

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 939

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 999

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1059

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1060 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1179

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1239

Qy    1081 TCTGGAACAGATTTGTGTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 TCTGGAACAGATTTGTGTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1299

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1359

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1419

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1479

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1539

Qy    1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1599

Qy    1441 GCAGAGACACAAGCAAGCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCAGAGACACAAGCAAGCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1659

Qy    1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1719

Qy    1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1779

Qy    1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1839

Qy    1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1899

Qy    1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1959

Qy    1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2019

Qy    1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2079

Qy    1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2139

Qy    1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2199
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Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2259

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2319

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2379

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2439

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2499

Qy   2341 AAA 2343
          |||
Db   2500 AAA 2502
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RESULT  11
V58445
ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;
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  Query Match             100.0%;  Score 2343;  DB 1;  Length 3113;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 66

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 126

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 186

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 246

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 366

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 426

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 486

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 546

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 666

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 726

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 786

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 846

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 966

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1026

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1086

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1146

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1206

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1266
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Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1326

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1386

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1446

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1506

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1566

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1626

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1686

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1746

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1806

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1866

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1926

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1986

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2046

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2106

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2166

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2226

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2286

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2346
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Qy   2341 AAA 2343
          |||
Db   2347 AAA 2349
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RESULT 12
V58446
ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

Query Match 100.0%; Score 2343; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 276

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 336

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 396

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 456

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 516

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 576

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 636

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 696
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Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    697 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 756

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 816

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 876

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 936

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 996

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1056

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1116

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1176

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1236

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1296

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1356

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1416

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1476

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1536

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1537 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1596

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1597 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1656

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1657 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1716

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1717 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1776

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1777 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1836

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1837 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1896

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1956

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1957 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2016

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2017 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2076

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2077 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2136

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2137 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2196

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2197 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2256

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2257 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2316

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2317 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2376

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2377 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2436

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2437 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2496

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2497 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2556

Qy   2341 AAA 2343
          |||
Db   2557 AAA 2559
```

RESULT 13
V54990
ID V54990 standard; DNA; 3555 BP.
AC V54990;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837185-A2.

PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 100.0%; Score 2343; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 507

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 567

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 627

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 687

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 807

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 867

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 927

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     928 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 987

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     988 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1047

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1048 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1107

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1108 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1167

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1168 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1227

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1228 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1287

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1288 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1347

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1348 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1407

Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1408 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1467

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1468 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1527

Qy    1081 TCTGGAACAGATTTGTGTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1528 TCTGGAACAGATTTGTGTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1587

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1588 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1647

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1648 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1707

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1708 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1767

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1768 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1827

Qy    1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1828 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1887

Qy    1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1888 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1947

Qy    1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1948 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2007

Qy    1561 CGCCTTCTGTCTGAGCAGCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2008 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2067

Qy    1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2068 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2127

Qy    1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2128 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2187
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Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2247

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2307

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2367

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2427

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2487

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2547

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2607

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2667

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2727

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2787

Qy   2341 AAA 2343
          |||
Db   2788 AAA 2790
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RESULT 14
V54991
ID V54991 standard; DNA; 3218 BP.
AC V54991;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2457
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71355.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 153-157; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T;

Query Match 100.0%; Score 2343; DB 1; Length 3218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    112 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 171

Qy     61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    172 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 231

Qy    121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    232 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 291

Qy    181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    292 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 351

Qy    241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    352 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 411

Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 471

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    472 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 531

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    532 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 591

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    592 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 651

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    652 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 711

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    712 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 771

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    772 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 831

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    832 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 891

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    892 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 951
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Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    952 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1011

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1012 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1071

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1072 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1131

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1132 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1191

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1192 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1251

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1252 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1311

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1312 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1371

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1372 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1431

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1432 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1491

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1492 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1551

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1552 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1611

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1612 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1671

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1672 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1731

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1732 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1791

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1792 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1851

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1852 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1911

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1912 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1971

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1972 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2031

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2032 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2091

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2092 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2151

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2152 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2211

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2212 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2271

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2272 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2331

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2332 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2391

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2392 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2451

Qy   2341 AAA 2343
          |||
Db   2452 AAA 2454
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RESULT 15
V40004
ID V40004 standard; DNA; 2994 BP.
AC V40004;
DT 15-FEB-1999 (first entry)
DE Retinoblastoma protein RB.
KW Retinoblastoma protein RB; E2F; transcription factor; human;
KW bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW thyroid hyperplasia; Grave's disease; psoriasis;
KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW peripheral vascular disease; therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 139. .2925
FT /*tag= a
PN WO9821228-A1.
PD 22-MAY-1998.
PF 13-NOV-1997; U21821.
PR 14-FEB-1997; US-801092.
PR 15-NOV-1996; US-751517.
PA (CANJ-) CANJI INC.
PI Antelman D, Gregory RJ, Wills KN;
DR WPI; 98-297858/26.
DR P-PSDB; W62465.
PT New fusion polypeptide of, e.g. transcription factor - used to
PT treat, e.g. hyper-proliferative disease such as cancer and
PT restenosis
PS Example 1; Fig 2A; 91pp; English.
CC This nucleotide sequence includes a coding region for retinoblastoma
CC protein RB (see W62465). A new claimed polypeptide is a fusion of:
CC (i) a transcription factor (TF) comprising a DNA binding domain,
CC and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC suppression domain. Also new are: (1) a nucleic acid encoding the
CC fusion protein, and (2) expression vectors containing such DNA.
CC The fusion protein, particularly expressed from gene therapy
CC vectors (especially adenovirus vectors), is used to treat
CC hyperproliferative conditions, specifically cancer (particularly of
CC the bladder) or restenosis (after angioplasty), but also diabetic
CC retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral

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CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;

  Query Match           100.0%;  Score 2343;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     961 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619
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Qy    2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
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Qy    2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
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Qy    2341 AAA 2343
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Db    2920 AAA 2922
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Search completed: February 13, 2000, 20:34:00
Job time: 11719 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 11:36:02 ; Search time 14294.3 Seconds
(without alignments)
-542.305 Million cell updates/sec

Title: US-09-026-459A-38_COPY_7_2559
Perfect score: 2553
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2553

Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
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48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2461	96.4	3232	5	I18496	I18496 Sequence 1
c 2	2461	96.4	3232	5	I18497	I18497 Sequence 2
3	2460	96.4	4597	5	I05311	I05311 Sequence 1
4	2460	96.4	2994	5	I81465	I81465 Sequence 2
5	2460	96.4	4839	10	HUMRB1MRNA	L41870 Homo sapien
6	2460	96.4	4600	10	HUMRBA1RA	M33647 Human retin
7	2460	96.4	2994	10	HUMRBSA	M28419 Human retin
8	2409	94.4	4597	5	I09369	I09369 Sequence 1
9	2208	86.5	4740	10	HUMRBS	M15400 Human retin
10	1420	55.6	4580	5	A01444	A01444 H.sapiens D
11	277	10.8	426	11	AF043224	AF043224 Homo sapi
12	207	8.1	480	9	HUMRBSY79	M19701 Human mutat
13	198	7.8	693	5	I09384	I09384 Sequence 17
14	198	7.8	693	9	HUMRBS15	M27858 Human retin
15	198	7.8	180388	9	HUMRETBLAS	L11910 Human retin
16	196	7.7	340	10	HUMRB1501V	L49220 Homo sapien
17	167	6.5	555	10	HUMRB4MU2	L41904 Homo sapien
18	165	6.5	935	5	I09389	I09389 Sequence 22
19	165	6.5	935	9	HUMRBS20	M27863 Human retin
20	165	6.5	420	10	HUMRB23EX	L41910 Homo sapien
21	163	6.4	252	10	HUMRB1777L	L49230 Homo sapien
22	155	6.1	555	10	HUMRB17MU2	L41924 Homo sapien
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24	148	5.8	717	9	HUMRBS18	L35147 Human retin
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26	147	5.8	224	10	HUMRB1SDDL	L49225 Homo sapien
27	146	5.7	650	5	I09386	I09386 Sequence 19
28	146	5.7	650	9	HUMRBS17	M27860 Human retin
29	145	5.7	609	5	I09377	I09377 Sequence 10
30	145	5.7	609	9	HUMRBS08	L35146 Human retin
31	145	5.7	316	10	HUMRB08EX	L41896 Homo sapien
32	144	5.6	1310	9	HUMRBS22	M27865 Human retin
33	144	5.6	625	10	HUMRB25EX	L41912 Homo sapien
34	132	5.2	224	10	HUMRB1610K	L49223 Homo sapien
35	131	5.1	317	10	HUMRB17MUT	L41999 Homo sapien
36	125	4.9	350	10	HUMRB20MUU	L41996 Homo sapien
37	124	4.9	444	10	HUMRB04MUT	L41892 Homo sapien
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39	123	4.8	570	5	I09373	I09373 Sequence 6
40	123	4.8	570	9	HUMRBS04	M27848 Human retin
41	122	4.8	589	5	I09385	I09385 Sequence 18
42	122	4.8	589	9	HUMRBS16	M27859 Human retin
43	122	4.8	224	10	HUMRB1646F	L49224 Homo sapien
44	122	4.8	222	10	HUMRB18EX	L41905 Homo sapien
45	119	4.7	323	10	HUMRB1D18	L49221 Homo sapien

ALIGNMENTS

RESULT 1
I18496
LOCUS I18496 3232 bp DNA PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5496731.
ACCESSION I18496
VERSION I18496.1 GI:1598851
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3232)
AUTHORS Xu,H., Hu,S. and Benedict,W.F.

```
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN
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Query Match 96.4%; Score 2461; DB 5; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      93 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 152
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Qy     153 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 212
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Db      66 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 125

Qy     213 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 272
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Db     126 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 185

Qy     273 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 332
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Db     186 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 245

Qy     333 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 392
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Qy     393 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 452
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Db     306 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 365

Qy     453 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 512
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Db     366 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 425

Qy     513 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 572
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Qy     573 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 632
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Qy     633 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 692
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Qy     693 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 752
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Qy     753 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 812
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Db     666 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 725

Qy     813 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 872
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Qy     873 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 932
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Db     786 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 845

Qy     933 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 992
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Qy     993 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1052
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Db     906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 965

Qy    1053 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1112
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Qy    1113 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1172
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Db    1026 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1085

Qy    1173 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1232
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Qy    1953 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2012
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Qy    2013 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2072
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Qy   2133 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2192
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Qy   2253 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2312
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Db   2466 A 2466


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DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


  Query Match             96.4%;  Score 2461;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    153 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 212
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Qy    213 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 272
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Qy    273 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 332
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Qy    333 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 392
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Qy    393 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 452
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Qy    453 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 512
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Qy    633 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 692
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Db   2691 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 2632

Qy    693 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2631 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 2572

Qy    753 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 812
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Db   2571 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 2512

Qy    813 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2511 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 2452

Qy    873 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 932
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Db   2451 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 2392

Qy    933 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 992
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Db   2391 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 2332

Qy    993 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1052
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Db   2331 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 2272

Qy   1053 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1112
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Qy   1113 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1172
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Qy   1173 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1232
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Db   2151 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 2092

Qy   1233 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1292
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Qy   1293 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1352
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Qy   1353 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1412
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Db   1911 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1852

Qy   1473 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1532
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Db   1851 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1792

Qy   1533 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1592
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Qy   1653 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712
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Qy   1713 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1772
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Qy   1773 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1832
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Qy   1833 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1892
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Qy   1893 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1952
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Db   1431 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1372

Qy   1953 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2012
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Db   1311 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1252

Qy   2073 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2133 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2192
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Db   1191 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 1132

Qy   2193 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2252
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Qy   2253 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2312
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Db   1071 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 1012

Qy   2313 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2372
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Db   1011 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 952

Qy   2373 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2432
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Db    951 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 892
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Qy   2433 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2492
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Db    891 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 832

Qy   2493 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2552
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DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN
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Query Match 96.4%; Score 2460; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
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Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 444

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
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Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 564

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
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Db    565 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 624

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
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Db    625 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 684

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
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Db    685 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 744

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
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Db    745 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 804

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
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Db    805 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 864
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Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
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Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
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Db    925 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 984

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
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Db    985 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1044

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
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Db   1045 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1104

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
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Db   1105 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1164

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
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Db   1165 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1224

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
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Db   1225 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1284

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
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Db   1285 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1344

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
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Db   1345 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1404

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
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Db   1405 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1464

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
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Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
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Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
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Db   1645 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1704

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
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Db   1705 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1764

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
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Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
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Db   1825 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1884

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
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Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
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Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
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Db   2005 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2064

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
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Db   2125 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2184

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
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Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
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Db   2245 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2304

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
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Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
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Db   2425 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2484

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Db   2485 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2544

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
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Db   2545 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2604

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
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Db   2605 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2664

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
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Db   2665 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2724

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
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REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
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ORIGIN

Query Match 96.4%; Score 2460; DB 5; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
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HUMRB1MRNA
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
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ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     462 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 521

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
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Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
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Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
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Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
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RESULT   6
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
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BASE COUNT 1489 a 842 c 815 g 1454 t

ORIGIN

Query Match 96.4%; Score 2460; DB 10; Length 4600;
Best Local Similarity 100.0%; Pred. No. 0;
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Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
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Db    2308 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2367

Qy    2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
Db    2368 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2427

Qy    2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
Db    2428 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2487

Qy    2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
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Qy    2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
Db    2548 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2607

Qy    2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
Db    2608 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2667

Qy    2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
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Qy    2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
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RESULT   7
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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                     /tissue_type="retinoblastoma"
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                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
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Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
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Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
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Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
Db     883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
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Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
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Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
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Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

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Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
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Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
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Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
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Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
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Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
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Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
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Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
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Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
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Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
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Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
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Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
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Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
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Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
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Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
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Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
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Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
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Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
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Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
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Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
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Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
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RESULT   8
I09369
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DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


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Matches 2459; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db     325 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 384

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
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Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
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Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
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Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
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Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
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Db    1525 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1584

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1585 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1644

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1645 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1704

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1705 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1764

Qy    1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1765 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1824

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1825 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1884

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1885 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1944

Qy    1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1945 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2004

Qy    1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2005 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2064

Qy    1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2065 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2124

Qy    1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2125 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2184

Qy    1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2185 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2244

Qy    2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2245 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2304

Qy    2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2305 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2364

Qy    2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2365 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2424

Qy    2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2425 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2484
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Qy    2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2485 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2544

Qy    2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
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Db    2545 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2604

Qy    2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    2605 CCTAAACCACTGAAAAAACTACGCTTTCATATTGAAGGATCAGATGAAGCAGATGGAAGT 2664

Qy    2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2665 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2724

Qy    2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2725 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
     source          1. .4740
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                     /db_xref="taxon:9606"
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                     /tissue_type="retina"
                     /map="13q14.2"
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                     /note="rbs mRNA"
     gene            139. .2925
                     /gene="RB1"
     CDS             139. .2925
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                     /note="retinoblastoma susceptibility protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA69807.1"
                     /db_xref="GI:190959"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPEEDPEQDSGPEDLPL
                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
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                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.
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  Query Match           86.5%;  Score 2208;  DB 10;  Length 4740;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 2408;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     142 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 570

Qy     202 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     571 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 630

Qy     262 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     631 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690

Qy     322 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 750

Qy     382 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 810

Qy     442 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 870

Qy     502 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 930

Qy     562 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990

Qy     622 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 1050

Qy     682 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 1110

Qy     742 TATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAG 801
           |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db    1111 TATCTTAAAAATAAAGATCTAGATCGAAGATTATTTTTGGATCATGATAAAACTCTTCAG 1170

Qy     802 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 861
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1171 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 1230

Qy     862 GAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 921
           ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1231 GAGGTGAATATAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1290

Qy     922 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 981
           ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db    1291 TTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1350
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Qy    982 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1410

Qy   1042 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1470

Qy   1102 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1530

Qy   1162 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1590

Qy   1222 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1650

Qy   1282 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1341
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1710

Qy   1342 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1401
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Db   1711 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1770

Qy   1402 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1461
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Db   1771 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1830

Qy   1462 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1521
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Db   1831 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1890

Qy   1522 CACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1581
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Db   1891 CACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1950

Qy   1582 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 1641
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Db   1951 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 2010

Qy   1642 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 1701
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Db   2011 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 2070

Qy   1702 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 1761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 2130

Qy   1762 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 1821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 2190

Qy   1822 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 1881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2250

Qy   1882 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 1941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2310

Qy   1942 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2370

Qy   2002 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2430
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Qy   2062 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2121
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Db   2431 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2490

Qy   2122 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2181
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Db   2491 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2550

Qy   2182 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2241
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Db   2551 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2610

Qy   2242 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2301
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Db   2611 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2670

Qy   2302 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2361
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Db   2671 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2730

Qy   2362 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2421
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Db   2731 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2790

Qy   2422 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2481
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Db   2791 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2850

Qy   2482 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2910

Qy   2542 AAGGAAGAGAAA 2553
          ||||||||||||
Db   2911 AAGGAAGAGAAA 2922
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RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN
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  Query Match             55.6%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy    535 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 594
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    595 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    655 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 714
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    715 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy    775 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 834
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy    835 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 894
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy    895 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy    955 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1014
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy   1015 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1074
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy   1075 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy   1135 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy   1195 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1255 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1314
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy   1315 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy   1375 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy   1435 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1494
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy   1495 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy   1555 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1614
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Db   1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy   1615 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1674
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Db   1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy   1675 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950
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Qy   1735 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1794
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Db   1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy   1795 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy   1855 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy   1915 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 1974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy   1975 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy   2035 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2094
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy   2095 CCCCCTACCTTGTCAGCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2154
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy   2155 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy   2215 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2275 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2335 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2394
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2395 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2455 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2515 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
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Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
AF043224
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
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  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
     exon            <1. .7
                     /gene="RB1"
                     /number=5
     CDS             <1. .137
                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
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     exon            8. .76
                     /gene="RB1"
                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
                     /gene="RB1"
                     /number=5
     exon            351. .418
                     /gene="RB1"
                     /number=6
     exon            419. .>426
                     /gene="RB1"
                     /number=7
BASE COUNT      145 a     61 c     82 g    138 t
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  Query Match             10.8%;  Score 277;  DB 11;  Length 426;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-137;
  Matches  277;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     136 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 195

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 255

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 315

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 375

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 370
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Db     376 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 412
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RESULT  12
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
                     /note="mutated retinoblastoma protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.
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  Best Local Similarity   100.0%;  Pred. No. 6.2e-100;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     375 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy     435 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 393

Qy     495 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 453

Qy     555 GATAGCAAAACAACTAGAAAATGATAC 581
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Db     454 GATAGCAAAACAACTAGAAAATGATAC 480
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RESULT  13
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.8%;  Score 198;  DB 5;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1268 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1327
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1328 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1388 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1447
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1448 CCCTTGCATGGCTCTCAG 1465
           ||||||||||||||||||
Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  14
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
                     /number=16
     exon            250. .446
                     /note="retinoblastoma susceptibility gene"
                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.8%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1268 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1327
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1328 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1388 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1447
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1448 CCCTTGCATGGCTCTCAG 1465
           ||||||||||||||||||
Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  15
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
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          Yandell,D.W. and Dryja,T.P.
  TITLE   Complete genomic sequence of the human retinoblastoma
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  JOURNAL Genomics 17 (3), 535-543 (1993)
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GenCore version 4.5
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Searched: 821193 seqs, -1518192014 residues

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Word size : 0

Number of hits that pass the threshold : 1642386

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3232)
AUTHORS Xu,H., Hu,S. and Benedict,W.F.

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  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
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Qy   1791 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850
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Db    1566 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

Qy   1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1626 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1685

Qy   1911 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1686 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1745

Qy   1971 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1746 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1805

Qy   2031 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 2090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1806 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1865

Qy   2091 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1866 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1925

Qy   2151 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1985
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Qy   2211 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2045

Qy   2271 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2046 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2105

Qy   2331 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2106 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2165

Qy   2391 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2166 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

Qy   2451 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2285

Qy   2511 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2286 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2345

Qy   2571 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2346 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2405

Qy   2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2406 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2465

Qy   2691 A 2691
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Db   2466 A 2466
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RESULT   2
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN
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  Query Match             91.5%;  Score 2461;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 3172

Qy    291 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3171 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 3112

Qy    351 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3111 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 3052

Qy    411 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3051 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 2992

Qy    471 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2991 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 2932

Qy    531 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2931 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 2872

Qy    591 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2871 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 2812

Qy    651 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2811 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 2752

Qy    711 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2751 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 2692

Qy    771 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2691 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 2632

Qy    831 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2631 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 2572

Qy    891 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2571 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 2512

Qy    951 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 1010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2511 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 2452

Qy   1011 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 1070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2451 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 2392

Qy   1071 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2391 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 2332

Qy   1131 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2331 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 2272

Qy   1191 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2271 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 2212

Qy   1251 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2211 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 2152

Qy   1311 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2151 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 2092

Qy   1371 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2091 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 2032

Qy   1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2031 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1972
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Qy   1491 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1550
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Db   1971 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1912

Qy   1551 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1911 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1852

Qy   1611 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1851 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1792

Qy   1671 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1791 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1732

Qy   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1672

Qy   1791 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1671 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1612

Qy   1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1611 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1552

Qy   1911 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1551 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1492

Qy   1971 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1491 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1432

Qy   2031 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 2090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1431 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1372

Qy   2091 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1371 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1312

Qy   2151 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1311 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1252

Qy   2211 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1251 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 1192

Qy   2271 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1191 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 1132

Qy   2331 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1131 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 1072

Qy   2391 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1071 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 1012

Qy   2451 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1011 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 952

Qy   2511 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    951 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 892
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Qy   2571 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630
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Db    891 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 832

Qy   2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2690
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Db    831 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 772

Qy   2691 A 2691
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Db    771 A 771
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RESULT   3
I05311
LOCUS       I05311       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN
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Query Match 91.4%; Score 2460; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 384

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 444

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 504

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 564

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 624

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 684

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 744

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 804

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 864
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Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    865 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 924

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 984

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    985 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1044

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1104

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1105 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1164

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1224

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1284

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1344

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1404

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1405 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1464

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
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Db   1465 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1524

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
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Db   1525 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1584

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
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Db   1585 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1644

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
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Db   1645 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1704

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
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Db   1705 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1764

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1765 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1824

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
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Db   1825 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1884

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1885 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1944
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Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
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Db   1945 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2004

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2005 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2064

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2065 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2124

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
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Db   2125 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2184

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
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Db   2185 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2244

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
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Db   2245 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2304

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
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Db   2305 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2364

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
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Db   2365 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2424

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
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Db   2425 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2484

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2485 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2544

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2545 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2604

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
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Db   2605 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2664

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
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Db   2665 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2724

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2725 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT   4
I81465
LOCUS       I81465      2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
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/organism="unknown"
BASE COUNT 974 a 618 c 593 g 809 t
ORIGIN

Query Match 91.4%; Score 2460; DB 5; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
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Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
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Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
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Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
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Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1792 GAGACACAAGCAACCTGAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
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Db   2023 GAGACACAAGCAACCTGAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1912 CTTCTGTCTGAGCACCGAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCGAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
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Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
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Qy   2092 AAGGATCTTCCTCATGGTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
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Db   2323 AAGGATCTTCCTCATGGTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
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Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy    2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
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Db    2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy    2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy    2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy    2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
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Qy    2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
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RESULT   5
HUMRB1MRNA
LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
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BASE COUNT     1489 a    842 c    815 g   1454 t
ORIGIN
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Query Match 91.4%; Score 2460; DB 10; Length 4600;
Best Local Similarity 100.0%; Pred. No. 0;
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Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
Db    748 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 807

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
Db    808 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 867

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
Db    868 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 927

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
Db    928 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 987

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
Db    988 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1047

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
Db   1048 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1107

Qy   1012 ATTCCTCCACACACTCGAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
Db   1108 ATTCCTCCACACACTCGAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1167

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Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
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Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
Db   1288 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1347

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
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Db   1408 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1467

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Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
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Db   2068 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2127

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
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Db   2248 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2307

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271

Db   2308 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2367

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Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391

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Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451

Db   2488 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2547

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511

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Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631

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RESULT   7
HUMRBSA
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DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


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  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411

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Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471

Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531

Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591

Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651

Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711

Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771

Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831

Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
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Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
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Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
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Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
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Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
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Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
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Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
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Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
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Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
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Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
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Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
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Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
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Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
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Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202
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Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
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Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
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Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
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REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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ORIGIN


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Db    325 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 384

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
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Db    385 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 444

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 504

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 564

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 624

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 684

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
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Db    685 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 744

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
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Db    745 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 804

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
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Db    805 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 864

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
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Db    865 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 924

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
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Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
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Db    985 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1044

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1104

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
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Db   1105 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1164

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1224

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1284

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1344

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
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Db   1345 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1404
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Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
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Db   1405 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1464

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
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Db   1465 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1524

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
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Db   1525 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1584

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
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Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
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Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
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Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
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Db   1825 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1884

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
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Db   1885 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1944

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
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Db   1945 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2004

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
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Db   2005 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2064

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
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Db   2065 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2124

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
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Db   2125 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2184

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
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Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
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Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
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Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
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Db   2365 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2424

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2425 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2484
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Qy    2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2485 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2544

Qy    2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2545 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2604

Qy    2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
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Qy    2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
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Qy    2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
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Db    2725 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
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                     /gene="RB1"
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                     /db_xref="GI:190959"
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                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
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                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.
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  Query Match             82.1%;  Score 2208;  DB 10;  Length 4740;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2408;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     280 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 570

Qy     340 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 399
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Qy     400 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 459
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Db     631 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690

Qy     460 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 519
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 750

Qy     520 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 579
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 810

Qy     580 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 639
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811 TATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATA 870

Qy     640 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 699
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 930

Qy     700 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 759
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Db     931 AAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990

Qy     760 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 819
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Db     991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 1050

Qy     820 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATT 1110

Qy     880 TATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAG 939
           ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
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Qy     940 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 999
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Db    1171 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 1230

Qy    1000 GAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1059
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1231 GAGGTGAATATAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1290

Qy    1060 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1119
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Db    1291 TTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1350
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Qy   1120 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1179
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Db   1351 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATAC 1410

Qy   1180 ATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAG 1239
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Qy   1240 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1299
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Db   1471 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAA 1530

Qy   1300 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1359
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Db   1531 GAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1590

Qy   1360 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1419
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Db   1591 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1650

Qy   1420 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1479
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Db   1651 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAA 1710

Qy   1480 GCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGA 1539
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Qy   1540 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1599
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Db   1771 GAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC 1830

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Db   1951 ATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCT 2010

Qy   1780 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 1839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCT 2070

Qy   1840 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 1899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 2130

Qy   1900 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 1959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 CTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 2190

Qy   1960 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 2250

Qy   2020 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATT 2310

Qy   2080 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 GTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATC 2370

Qy   2140 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 AAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 2430
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Qy   2200 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2490

Qy   2260 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2550

Qy   2320 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAA 2610

Qy   2380 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 ATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAG 2670

Qy   2440 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 TTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAA 2730

Qy   2500 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2790

Qy   2560 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2850

Qy   2620 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2910

Qy   2680 AAGGAAGAGAAA 2691
          ||||||||||||
Db   2911 AAGGAAGAGAAA 2922
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RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match             52.8%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy    673 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    733 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    793 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    853 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy    913 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 972
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy    973 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy   1033 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy   1093 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy   1153 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1212
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy   1213 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy   1273 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy   1333 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1393 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1452
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy   1453 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy   1513 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy   1573 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1632
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy   1633 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy   1693 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy   1753 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy   1813 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950
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Qy   1873 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy   1933 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy   1993 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy   2053 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy   2113 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2172
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy   2173 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy   2233 CCCCCTACCTTGTCACGAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2292
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 CCCCCTACCTTG-CACGAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy   2293 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy   2353 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2413 GGTGAATCATTCGGGAGTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 GGTGAATCATTCGGGAGTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2473 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2532
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2533 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2593 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2653 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          |||||||||||||||||||||||||||||||||||||||
Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
AF043224
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
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  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
     exon            <1. .7
                     /gene="RB1"
                     /number=5
     CDS             <1. .137
                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
                     "
     exon            8. .76
                     /gene="RB1"
                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
                     /gene="RB1"
                     /number=5
     exon            351. .418
                     /gene="RB1"
                     /number=6
     exon            419. .>426
                     /gene="RB1"
                     /number=7
BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN
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  Query Match             10.3%;  Score 277;  DB 11;  Length 426;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-137;
  Matches  277;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     136 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 195

Qy     292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 255

Qy     352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 315

Qy     412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 375

Qy     472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 508
           |||||||||||||||||||||||||||||||||||||
Db     376 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 412
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RESULT  12
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
                     /note="mutated retinoblastoma protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.
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  Query Match             7.7%;  Score 207;  DB 9;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-99;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     513 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy     573 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 393

Qy     633 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 453

Qy     693 GATAGCAAAACAACTAGAAAATGATAC 719
           |||||||||||||||||||||||||||
Db     454 GATAGCAAAACAACTAGAAAATGATAC 480
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RESULT  13
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
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ORIGIN


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Qy   1526 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1585
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Qy   1586 CCCTTGCATGGCTCTCAG 1603
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  14
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LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
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ORIGIN


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Qy   1586 CCCTTGCATGGCTCTCAG 1603
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RESULT  15
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LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
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ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
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  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
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          Yandell,D.W. and Dryja,T.P.
  TITLE   Complete genomic sequence of the human retinoblastoma
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  JOURNAL Genomics 17 (3), 535-543 (1993)
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

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SUMMARIES

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ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN
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Query Match 18.6%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.4e-203;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1237 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1297 ACAGATTTGTCTTTCCGATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCGATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1357 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1417 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1477 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1537 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1597 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1657 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT   2
AI745644/c
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
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            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             13.8%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-148;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1907 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 1966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy   1967 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy   2027 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy   2087 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy   2147 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy   2207 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .411
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219217"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


  Query Match             13.6%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-146;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1911 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 1970
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy   1971 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2030
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy   2031 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2090
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy   2091 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy   2151 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy   2211 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             10.1%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-105;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1701 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy    1761 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy    1821 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy    1881 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy    1941 TGTAACAGCATACAAGG 1957
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Db     241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277       304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             8.0%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 3.4e-81;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1510 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy    1570 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1630 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1689
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1690 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1750 CGGCTAAATACACTT 1764
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.3%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-62;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1305 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1364
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1365 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1425 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1465
          |||||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   7
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.1%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-59;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2398 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2458 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2518 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||||||||
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Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   8
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.2%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-49;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1100 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy   1160 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1220 TGTCTTTATTGG 1231
           ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT   9
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.5%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2353 AGTGCTGAAGGAAGCAAGCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAAGCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60
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Qy   2413 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  10
N41391
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


  Query Match             4.4%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-40;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2289 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2349 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329


RESULT  11
R57845
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.5%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-29;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2123 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy   2183 ATATTTCACCCCTGAAGAGTCCATATAAA 2211
          |||||||||||||||||||||||||||||
Db     61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  12
AA258255
LOCUS       AA258255      525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             3.2%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 2e-26;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2472 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2532 TACCTCAAACAAGGAAGAGAAA 2553
           |||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  13
AA072780
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


  Query Match             1.9%;  Score 48;  DB 28;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-11;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2098 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2145
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     207 CCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 254


RESULT  14
AQ901300
LOCUS       AQ901300      986 bp    DNA             GSS       10-NOV-1999
DEFINITION  HS_5234_A1_B12_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=9002 Col=23 Row=C, genomic survey sequence.
ACCESSION   AQ901300
VERSION     AQ901300.1  GI:6357490
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     On Sep 10, 1998 this sequence version replaced gi:3552584.
            Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
```

```
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 9002  row: C  column: 23
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 986.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
                      /clone="Plate=9002 Col=23 Row=C"
                      /clone_lib="RPCI-11 Human Male BAC Library"
                      /sex="male"
                      /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      252 a    205 c    176 g    353 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 1.6e-08;
  Matches   42;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    669 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 710
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Db     25 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 66


RESULT  15
AA955457
LOCUS       AA955457      472 bp    mRNA            EST       04-JUL-1999
DEFINITION  UI-R-A1-ew-g-10-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone
            UI-R-A1-ew-g-10-0-UI 3' similar to gi|603961|dbj|D25233|RATRP Rat
            mRNA for retinoblastoma protein, partial sequence, mRNA sequence.
ACCESSION   AA955457
VERSION     AA955457.1  GI:4237812
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On May 7, 1998 this sequence version replaced gi:3119031.
            Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.
            Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
            through Research Genetics This clone is also available through the
            I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
            ID=1779132 The following repetitive elements were found in this
            cDNA sequence: 3-38, >(CGG)n#Simple_repeat
            Seq primer: M13 Forward
            POLYA=No.
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                      /strain="Sprague-Dawley"
                      /db_xref="taxon:10116"
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                      /dev_stage="adult"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-A1
                      library is a subtracted library derived from the UI-R-A0
                      library. The UI-R-A0 library  consisted of a mixture of
                      individually tagged normalized libraries constructed from
                      rat placenta, adult lung, brain, liver, kidney, heart,
                      spleen, ovary, and muscle. The tag is a string of 3-5
                      nucleotides present between the Not I site and the
                      oligo-dT track which allows identification of the library
                      of origin of a clone within the mixture. The subtracted
                      library (UI-R-A1) was constructed as follows: PCR
                      amplified cDNA inserts from a pool of approximately 3,840
                      UI-R-A0 clones from which 3' ESTs had been derived was
                      used as a driver in a hybridization with the UI-R-A0
                      library in the form of single-stranded circles. The
                      remaining single-stranded circles (subtracted library) was
                      purified by hydroxyapatite column chromatography,
                      converted to double-stranded circles and electroporated
                      into DH10B bacteria (Life Technologies) to generate the
                      UI-R-A1 library. This procedure has been previously
                      described (Bonaldo, Lennon and Soares, Genome Research 6:
                      791-806, 1996)"
BASE COUNT      140 a     99 c    117 g    116 t
ORIGIN


  Query Match             1.5%;  Score 38;  DB 46;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-06;
  Matches   38;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    355 TAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 392


Search completed: February 13, 2000, 16:55:19
Job time: 15501 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 17:10:30 ; Search time 404.96 Seconds
(without alignments)
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Title: US-09-026-459A-38_COPY_7_2559
Perfect score: 2553
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Scoring table: OLIGO_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2461	96.4	3232	1	US-08-038-760-1	Sequence 1, Appli
c	2	2461	96.4	3232	1	US-08-038-760-2	Sequence 2, Appli
	3	2461	96.4	3232	4	US-08-470-091-1	Sequence 1, Appli
c	4	2461	96.4	3232	4	US-08-470-091-2	Sequence 2, Appli
	5	2460	96.4	2994	2	US-08-204-329-2	Sequence 2, Appli
	6	2460	96.4	2995	4	US-08-959-638-7	Sequence 7, Appli
	7	2460	96.4	2994	4	US-08-482-627-4	Sequence 4, Appli
	8	2409	94.4	2994	6	PCT-US94-10357-1	Sequence 1, Appli
	9	28	1.1	28	4	US-08-859-998-1097	Sequence 1097, Ap
	10	25	1.0	40	2	US-08-253-155A-92	Sequence 92, Appl
	11	25	1.0	40	2	US-08-625-209A-21	Sequence 21, Appl
	12	22	0.9	52	1	US-07-826-928A-15	Sequence 15, Appl
	13	22	0.9	52	1	US-07-826-928A-36	Sequence 36, Appl
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c	44	17	0.7	28	1	US-07-941-523-12	Sequence 12, Appl
	45	17	0.7	90	1	US-08-123-702-17	Sequence 17, Appl

ALIGNMENTS

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RESULT 1
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


  Query Match             96.4%;  Score 2461;  DB 1;  Length 3232;
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Qy    453 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 512
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Qy    873 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 932
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Db    786 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 845

Qy    933 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 992
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Qy    993 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1052
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Qy   1053 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1112
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Qy   1113 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1172
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Db   1386 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1445

Qy   1533 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1505

Qy   1593 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1652
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Db   1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1565

Qy   1653 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712
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Db   1566 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

Qy   1713 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1772
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Db   1626 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1685

Qy   1773 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1832
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Qy   1893 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1952
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Db   1806 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1865

Qy   1953 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2012
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Qy   2013 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2072
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Db   1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1985

Qy   2073 TTTGCAGTATGCTTCCACGAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 TTTGCAGTATGCTTCCACGAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2045

Qy   2133 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2046 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2105

Qy   2193 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2106 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2165

Qy   2253 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2166 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

Qy   2313 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2372
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Db    2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2285

Qy    2373 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2286 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2345

Qy    2433 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2346 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2405

Qy    2493 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2406 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2465

Qy    2553 A 2553
          |
Db    2466 A 2466


RESULT   2
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             96.4%;  Score 2461;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      93 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 3172

Qy     153 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3171 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 3112

Qy     213 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3111 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 3052

Qy     273 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3051 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 2992

Qy     333 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2991 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 2932

Qy     393 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2931 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 2872

Qy     453 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2871 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 2812

Qy     513 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2811 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 2752

Qy     573 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2751 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 2692

Qy     633 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2691 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 2632

Qy     693 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2631 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 2572

Qy     753 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2571 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 2512

Qy     813 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2511 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 2452

Qy     873 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2451 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 2392

Qy     933 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2391 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 2332

Qy     993 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2331 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 2272

Qy    1053 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2271 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 2212

Qy    1113 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2211 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 2152

Qy    1173 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2151 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 2092

Qy    1233 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1292
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Db   2091 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 2032

Qy   1293 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1352

Db   2031 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1972

Qy   1353 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1412

Db   1971 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1912

Qy   1413 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1472

Db   1911 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1852

Qy   1473 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1532

Db   1851 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1792

Qy   1533 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1592

Db   1791 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1732

Qy   1593 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1652

Db   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1672

Qy   1653 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712

Db   1671 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1612

Qy   1713 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1772

Db   1611 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1552

Qy   1773 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1832

Db   1551 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1492

Qy   1833 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1892

Db   1491 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1432

Qy   1893 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1952

Db   1431 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1372

Qy   1953 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2012

Db   1371 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1312

Qy   2013 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2072

Db   1311 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1252

Qy   2073 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2132

Db   1251 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 1192

Qy   2133 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2192

Db   1191 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 1132

Qy   2193 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2252

Db   1131 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 1072

Qy   2253 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2312

Db   1071 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 1012

Qy   2313 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2372
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Db   1011 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 952

Qy   2373 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2432

Db    951 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 892

Qy   2433 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2492

Db    891 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 832

Qy   2493 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2552

Db    831 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 772

Qy   2553 A 2553

Db    771 A 771
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RESULT 3
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,091
; FILING DATE: JUN-16-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..2469
US-08-470-091-1

Query Match 96.4%; Score 2461; DB 4; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      93 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 65

Qy     153 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      66 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 125

Qy     213 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 185

Qy     273 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 245

Qy     333 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 305

Qy     393 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     306 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 365

Qy     453 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     366 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 425

Qy     513 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     426 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 485

Qy     573 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 545

Qy     633 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     546 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 605

Qy     693 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     606 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 665

Qy     753 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 812
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     666 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 725

Qy     813 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 872
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     726 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 785

Qy     873 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 932
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     786 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 845

Qy     933 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 992
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     846 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 905

Qy     993 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1052
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 965

Qy    1053 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     966 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1025

Qy    1113 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1172
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1026 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1085

Qy    1173 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1086 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1145

Qy    1233 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1146 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1205

Qy    1293 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1206 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1265

Qy    1353 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1266 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1325

Qy    1413 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1326 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1385

Qy    1473 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1532
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1386 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1445

Qy    1533 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1446 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1505

Qy    1593 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1565

Qy    1653 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712
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Db    1566 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

Qy    1713 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1772
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1626 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1685

Qy    1773 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1832
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1686 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1745

Qy    1833 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1892
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1746 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1805

Qy    1893 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1952
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1806 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1865

Qy    1953 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2012
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1866 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1925

Qy    2013 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2072
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1985

Qy    2073 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1986 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2045

Qy    2133 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2046 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2105

Qy    2193 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2106 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2165

Qy    2253 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2312
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Db    2166 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

Qy    2313 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2285

Qy    2373 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2286 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2345

Qy    2433 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2346 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2405

Qy    2493 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2406 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2465

Qy    2553 A 2553
           |
Db    2466 A 2466


RESULT   4
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2

  Query Match           96.4%;  Score 2461;  DB 4;  Length 3232;

  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      93 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 3172

Qy     153 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3171 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 3112

Qy     213 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3111 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 3052

Qy     273 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3051 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 2992

Qy     333 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2991 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 2932

Qy     393 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2931 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 2872

Qy     453 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2871 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 2812

Qy     513 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2811 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 2752

Qy     573 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2751 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 2692

Qy     633 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2691 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 2632

Qy     693 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2631 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 2572

Qy     753 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 812
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2571 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 2512

Qy     813 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 872
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2511 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 2452

Qy     873 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 932
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2451 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 2392

Qy     933 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 992
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2391 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 2332

Qy     993 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1052
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2331 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 2272

Qy    1053 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2271 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 2212

Qy    1113 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1172
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2211 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 2152

Qy   1173 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2151 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 2092

Qy   1233 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2091 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 2032

Qy   1293 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2031 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1972

Qy   1353 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1971 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1912

Qy   1413 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1911 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1852

Qy   1473 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1851 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1792

Qy   1533 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1791 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1732

Qy   1593 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1672

Qy   1653 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1671 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1612

Qy   1713 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1611 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1552

Qy   1773 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1551 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1492

Qy   1833 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1491 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1432

Qy   1893 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1952
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1431 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1372

Qy   1953 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1371 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1312

Qy   2013 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2072
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1311 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1252

Qy   2073 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1251 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 1192

Qy   2133 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1191 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 1132

Qy   2193 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1131 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 1072

Qy   2253 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1071 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 1012

Qy   2313 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1011 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 952

Qy   2373 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    951 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 892

Qy   2433 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    891 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 832

Qy   2493 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    831 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 772

Qy   2553 A 2553
          |
Db    771 A 771
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RESULT   5
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match             96.4%;  Score 2460;  DB 2;  Length 2994;
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
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Db    1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
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Db    1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
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Db    1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
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Db    1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
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Db    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
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Db    1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
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Db    1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
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Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
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Db    1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

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Db    1543 TCCATTCAAAATTTTAGGAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
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Db    1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
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Db    1663 GGAACAGATTTGTCTTTGCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
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Db    1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
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Db    1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
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Db    1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
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Db    1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
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Db    2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy    1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
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Db    2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy    1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
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Db    2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy    1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
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Db    2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy    1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
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Qy    2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
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Db    2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy    2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
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Db    2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy    2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
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Db    2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy    2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
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Db    2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622
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Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
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Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
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Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
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Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
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Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   6
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
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US-08-959-638-7

Query Match 96.4%; Score 2460; DB 4; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
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Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

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Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
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Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

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Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
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Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

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Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
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Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
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Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
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Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
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Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

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Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
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Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
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Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

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Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
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Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

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Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
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Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
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Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
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Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562
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Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   7
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4
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Query Match 96.4%; Score 2460; DB 4; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy    1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy    1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy    1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy    1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy    1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy    1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy    2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy    2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy    2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy    2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
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Db    2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy    2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
Db    2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy    2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
Db    2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy    2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
Db    2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy    2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
Db    2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy    2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
Db    2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1
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  Query Match           94.4%;  Score 2409;  DB 6;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2459;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
Db     643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
Db     763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
Db     883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
Db    1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
Db    1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
Db    1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
Db    1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
Db    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
Db    1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
Db    1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
Db    1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542
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Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622
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Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097
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  Query Match             1.1%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00029;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    2470 CTGGCAGAAATGACTTCTACTCGAACAC 2497
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Db       1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-08-253-155A-92
; Sequence 92, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-92


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.0082;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  11
US-08-625-209A-21
; Sequence 21, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-21


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.0082;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  12
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
```

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;       TELEPHONE:  317-276-3589
;       TELEFAX:  317-276-1294
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  52 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  13
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, Leslie D.
;     APPLICANT:  Cook, James A.
;     APPLICANT:  David, Gary S.
;     APPLICANT:  Hochschwender, Susan M.
;     APPLICANT:  Kasher, Mary S.
;     APPLICANT:  Smith, Michele C.
;     APPLICANT:  Stemmer, Willem P.
;     TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;     TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;     NUMBER OF SEQUENCES:  38
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Eli Lilly and Company
;       STREET:  Lilly Corporate Center
;       CITY:  Indianapolis
;       STATE:  IN
;       COUNTRY:  USA
;       ZIP:  46285
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/826,928A
;       FILING DATE:  19920124
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murphy, Richard B.
;       REGISTRATION NUMBER:  35,296
;       REFERENCE/DOCKET NUMBER:  X8180A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  317-276-3589
;       TELEFAX:  317-276-1294
;   INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  52 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     928 ATGATTTTAAATTCAGCAAGTG 949
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Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  14
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;     APPLICANT:  Stevens, John K.
;     APPLICANT:  Dunn, James M.
;     TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;     TITLE OF INVENTION:  from a Patient Sample
;     NUMBER OF SEQUENCES:  60
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Oppedahl & Larson
;       STREET:  1992 Commerce Street, Suite 309
;       CITY:  Yorktown Heights
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10598-4412
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS 5.0
;       SOFTWARE:  Word Perfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/271,946A
;       FILING DATE:  08-JUL-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marina T. Larson
;       REGISTRATION NUMBER:  32,038
;       REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (914) 245-3252
;       TELEFAX:  (914) 962-4330
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  22
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
;     HYPOTHETICAL:  no
;     ANTI-SENSE:  no
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  human
;     FEATURE:
;       NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2228 CAACACCAACAAAAATGACTCC 2249
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Db      22 CAACACCAACAAAAATGACTCC 1


RESULT  15
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
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; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,942A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 23 of human RB1 gene
US-08-271-942A-22

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2228 CAACACCAACAAAAATGACTCC 2249
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Db 22 CAACACCAACAAAAATGACTCC 1

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Job time: 8983 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 17:11:43 ; Search time 404.96 Seconds
(without alignments)
795.568 Million cell updates/sec

Title: US-09-026-459A-40_COPY_7_2697
Perfect score: 2691
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Scoring table: OLIGO_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2461	91.5	3232	1	US-08-038-760-1	Sequence 1, Appli
c	2	2461	91.5	3232	1	US-08-038-760-2	Sequence 2, Appli
	3	2461	91.5	3232	4	US-08-470-091-1	Sequence 1, Appli
c	4	2461	91.5	3232	4	US-08-470-091-2	Sequence 2, Appli
	5	2460	91.4	2994	2	US-08-204-329-2	Sequence 2, Appli
	6	2460	91.4	2995	4	US-08-959-638-7	Sequence 7, Appli
	7	2460	91.4	2994	4	US-08-482-627-4	Sequence 4, Appli
	8	2409	89.5	2994	6	PCT-US94-10357-1	Sequence 1, Appli
	9	28	1.0	28	4	US-08-859-998-1097	Sequence 1097, Ap
	10	25	0.9	40	2	US-08-253-155A-92	Sequence 92, Appl
	11	25	0.9	40	2	US-08-625-209A-21	Sequence 21, Appl
	12	22	0.8	52	1	US-07-826-928A-15	Sequence 15, Appl
	13	22	0.8	52	1	US-07-826-928A-36	Sequence 36, Appl
c	14	22	0.8	22	1	US-08-271-946A-22	Sequence 22, Appl
c	15	22	0.8	22	1	US-08-271-942A-22	Sequence 22, Appl
c	16	22	0.8	22	6	PCT-US95-08604-22	Sequence 22, Appl
c	17	22	0.8	22	6	PCT-US95-08606-22	Sequence 22, Appl
	18	20	0.7	48	1	US-07-826-928A-13	Sequence 13, Appl
	19	20	0.7	633	1	US-08-234-783-1	Sequence 1, Appli
	20	20	0.7	633	1	US-08-456-907-1	Sequence 1, Appli
c	21	20	0.7	44	2	US-08-253-155A-93	Sequence 93, Appl
c	22	20	0.7	44	2	US-08-625-209A-22	Sequence 22, Appl
	23	20	0.7	633	6	PCT-US95-05523-1	Sequence 1, Appli
	24	19	0.7	2095	2	US-08-336-408B-3	Sequence 3, Appli
c	25	19	0.7	2952	2	US-08-306-691B-54	Sequence 54, Appl
c	26	19	0.7	276	3	US-08-712-948-3	Sequence 3, Appli
c	27	19	0.7	3509	3	US-08-817-436A-1	Sequence 1, Appli
c	28	19	0.7	6530	4	US-08-146-930-1	Sequence 1, Appli
	29	19	0.7	2095	6	PCT-US91-00399-3	Sequence 3, Appli
c	30	19	0.7	6530	6	PCT-US93-03993-1	Sequence 1, Appli
c	31	19	0.7	4008	6	PCT-US95-11808-5	Sequence 5, Appli
c	32	18	0.7	37	1	US-07-826-928A-14	Sequence 14, Appl
c	33	18	0.7	37	1	US-07-826-928A-35	Sequence 35, Appl
	34	18	0.7	3879	1	US-08-530-010-1	Sequence 1, Appli
	35	18	0.7	3879	2	US-08-484-101B-1	Sequence 1, Appli
c	36	18	0.7	18	3	US-08-511-836C-2	Sequence 2, Appli
c	37	18	0.7	2850	3	US-08-224-482-7	Sequence 7, Appli
c	38	18	0.7	747	3	US-08-679-765-2	Sequence 2, Appli
	39	18	0.7	4534	4	US-08-935-450-1	Sequence 1, Appli
c	40	18	0.7	747	4	US-09-196-525-2	Sequence 2, Appli
c	41	18	0.7	3760	4	US-08-724-354D-1	Sequence 1, Appli
c	42	17	0.6	2009	1	US-07-958-222A-1	Sequence 1, Appli
c	43	17	0.6	1037	1	US-08-240-124-1	Sequence 1, Appli
c	44	17	0.6	28	1	US-07-941-523-12	Sequence 12, Appl
	45	17	0.6	90	1	US-08-123-702-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE: 19930325
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..2469
US-08-038-760-1

Query Match 91.5%; Score 2461; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 290
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Db 6 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 65

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Qy    291 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 125

Qy    351 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 185

Qy    411 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 245

Qy    471 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 305

Qy    531 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 365

Qy    591 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 425

Qy    651 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 710
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Db    426 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 485

Qy    711 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 545

Qy    771 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 830
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Db    546 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 605

Qy    831 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 890
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Db    606 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 665

Qy    891 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 725

Qy    951 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 1010
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Db    726 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 785

Qy   1011 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 1070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 845

Qy   1071 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 905

Qy   1131 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 965

Qy   1191 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1025

Qy   1251 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1085

Qy   1311 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1145

Qy   1371 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1205

Qy   1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1265

Qy   1491 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1325

Qy   1551 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1326 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1385

Qy   1611 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1445

Qy   1671 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1730
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Db   1446 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1505

Qy   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1565

Qy   1791 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

Qy   1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1685

Qy   1911 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1745

Qy   1971 GCAGAATGAGTATGAACTGATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 GCAGAATGAGTATGAACTGATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1805

Qy   2031 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 2090
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Db   1806 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1865

Qy   2091 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1866 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1925

Qy   2151 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2210
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Db   1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1985

Qy   2211 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2045

Qy   2271 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2330
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Db   2046 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2105

Qy   2331 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2390
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Db   2106 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2165

Qy   2391 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2166 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

Qy   2451 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2510
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Db   2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2285

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Db   2286 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2345

Qy   2571 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630
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Db   2346 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2405

Qy   2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2690
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Db   2406 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2465

Qy   2691 A 2691
          |
Db   2466 A 2466


RESULT   2
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             91.5%;  Score 2461;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 290
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Db   3231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 3172

Qy    291 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3171 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 3112

Qy    351 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3111 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 3052

Qy    411 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 470
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Db   3051 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 2992

Qy    471 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 530
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Db   2991 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 2932

Qy    531 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 590
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Db   2931 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 2872

Qy    591 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 650
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Db   2871 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 2812

Qy    651 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 710
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Db   2811 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 2752

Qy    711 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2751 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 2692

Qy    771 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 830
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Db   2691 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 2632

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Db   2631 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 2572

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Db   2571 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 2512

Qy    951 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 1010
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Db   2511 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 2452

Qy   1011 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 1070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2451 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 2392

Qy   1071 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1130
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Db   2391 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 2332

Qy   1131 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1190
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Db   2331 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 2272

Qy   1191 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1250
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Db   2271 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 2212

Qy   1251 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2211 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 2152

Qy   1311 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2151 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 2092

Qy   1371 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430
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Db   2091 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 2032

Qy   1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1490

Db   2031 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1972

Qy   1491 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1550

Db   1971 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1912

Qy   1551 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1610

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Db   1851 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1792

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Db   1671 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1612

Qy   1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1910

Db   1611 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1552

Qy   1911 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1970

Db   1551 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1492

Qy   1971 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030

Db   1491 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1432

Qy   2031 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 2090

Db   1431 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1372

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Db   1371 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1312

Qy   2151 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2210

Db   1311 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1252

Qy   2211 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2270

Db   1251 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 1192

Qy   2271 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2330

Db   1191 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 1132

Qy   2331 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2390

Db   1131 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 1072

Qy   2391 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2450

Db   1071 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 1012

Qy   2451 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2510
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Db   1011 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 952

Qy   2511 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2570

Db    951 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 892

Qy   2571 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630

Db    891 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 832

Qy   2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2690

Db    831 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 772

Qy   2691 A 2691

Db    771 A 771
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RESULT   3
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


  Query Match             91.5%;  Score 2461;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 65

Qy    291 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 125

Qy    351 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 185

Qy    411 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 245

Qy    471 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 305

Qy    531 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 365

Qy    591 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 650
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Db    366 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 425

Qy    651 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 710
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Db    426 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 485

Qy    711 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 770
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Db    486 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 545

Qy    771 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 830
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Db    546 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 605

Qy    831 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 665

Qy    891 TAAAGATCTAGATGCAAGATTATTTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 TAAAGATCTAGATGCAAGATTATTTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 725

Qy    951 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 1010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 785

Qy   1011 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 1070
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Db    786 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 845

Qy   1071 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1130
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Db    846 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 905

Qy   1131 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1190
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Db    906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 965

Qy   1191 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1250
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Db    966 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1025

Qy   1251 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1085

Qy   1311 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1145

Qy   1371 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1205

Qy   1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1265

Qy   1491 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1325

Qy   1551 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1610
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Db   1326 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1385

Qy   1611 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1445

Qy   1671 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1505

Qy   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1790
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Db   1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1565

Qy   1791 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

Qy   1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1685

Qy   1911 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1745

Qy   1971 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1805

Qy   2031 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 2090
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Qy   2091 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1866 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1925

Qy   2151 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2210
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Db   1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1985

Qy   2211 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2270
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Db   1986 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2045

Qy   2271 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2330
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Db   2046 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2105

Qy   2331 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2106 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2165

Qy   2391 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2450
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Db    2166 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

Qy    2451 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2510
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Db    2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2285

Qy    2511 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2570
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Db    2286 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2345

Qy    2571 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630
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Db    2346 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2405

Qy    2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2690
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Db    2406 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2465

Qy    2691 A 2691
           |
Db    2466 A 2466


RESULT   4
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2

  Query Match             91.5%;  Score 2461;  DB 4;  Length 3232;

  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 290
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Db    3231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 3172

Qy     291 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3171 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 3112

Qy     351 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3111 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 3052

Qy     411 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 470
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3051 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 2992

Qy     471 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 530
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2991 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 2932

Qy     531 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 590
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2931 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 2872

Qy     591 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 650
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2871 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 2812

Qy     651 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 710
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2811 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 2752

Qy     711 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2751 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 2692

Qy     771 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 830
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2691 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 2632

Qy     831 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 890
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Db    2631 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 2572

Qy     891 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 950
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Db    2571 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 2512

Qy     951 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 1010
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2511 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 2452

Qy    1011 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 1070
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2451 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 2392

Qy    1071 TTTAAATTCAGCAAGTGATGAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2391 TTTAAATTCAGCAAGTGATGAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 2332

Qy    1131 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2331 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 2272

Qy    1191 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1250
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Db    2271 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 2212

Qy    1251 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1310
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Db   2211 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 2152

Qy   1311 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2151 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 2092

Qy   1371 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2091 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 2032

Qy   1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2031 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1972

Qy   1491 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1971 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1912

Qy   1551 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1911 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1852

Qy   1611 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1851 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1792

Qy   1671 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1791 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1732

Qy   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1672

Qy   1791 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850
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Db   1671 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1612

Qy   1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1611 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1552

Qy   1911 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1551 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1492

Qy   1971 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1491 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1432

Qy   2031 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 2090
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Db   1431 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1372

Qy   2091 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2150
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Db   1371 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1312

Qy   2151 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1311 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1252

Qy   2211 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1251 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 1192

Qy   2271 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1191 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 1132

Qy   2331 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1131 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 1072

Qy   2391 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1071 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 1012

Qy   2451 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1011 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 952

Qy   2511 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2570
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Db    951 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 892

Qy   2571 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630
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Db    891 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 832

Qy   2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2690
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Db    831 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 772

Qy   2691 A 2691
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Db    771 A 771
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RESULT   5
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match          91.4%;  Score 2460;  DB 2;  Length 2994;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
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Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
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Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
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Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
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Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
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Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
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Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
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Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
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Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
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Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
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Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
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Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
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Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
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Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
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Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
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Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
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Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622
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Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   6
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
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US-08-959-638-7

Query Match 91.4%; Score 2460; DB 4; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
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Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
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Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
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Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
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Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy    1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
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Db    1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy    1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy    1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy    1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
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Db    1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy    1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
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Db    1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy    1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy    1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
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Db    1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy    1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
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Db    1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy    1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
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Db    2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy    1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy    1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
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Db    2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy    1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
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Db    2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy    2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
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Db    2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy    2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
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Db    2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy    2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy    2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
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Db    2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy    2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562
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Qy    2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy    2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy    2452 AATCAGATGGTATGTAAGAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2683 AATCAGATGGTATGTAAGAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy    2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
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Db    2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy    2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
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Db    2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy    2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
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Db    2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   7
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4
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Query Match             91.4%;  Score 2460;  DB 4;  Length 2994;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy     412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
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Db     643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy     472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy     592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
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Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
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Db    1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy     832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
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Db    1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy     892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
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Db    1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy     952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy    1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy    1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
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Db    1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy    1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
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Db    1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy    1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy    1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy    1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy    1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy    1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy    1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy    1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy    1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy    1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy    1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy    1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy    1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy    1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy    2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy    2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy    2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy    2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy    2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy    2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
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Db    2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy    2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451

Db    2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy    2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511

Db    2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy    2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571

Db    2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy    2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631

Db    2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy    2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691

Db    2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
```

RESULT 8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: and Canji, Inc.
; TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
; TITLE OF INVENTION: Susceptibility Gene Product
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10357
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,108
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: FP-UC 1117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..2923
PCT-US94-10357-1

Query Match 89.5%; Score 2409; DB 6; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2459; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291

Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351

Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411

Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy     412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471

Db     643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy     472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531

Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591

Db     763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy     592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651

Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     652 TCACCTCGAACACCCAGGGGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711

Db     883 TCACCTCGAACACCCAGGGGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771

Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831

Db    1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy     832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891

Db    1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy     892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951

Db    1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy     952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011

Db    1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy    1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071

Db    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy    1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131

Db    1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy    1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191

Db    1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy    1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251

Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311

Db    1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542
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Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622
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Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
```

RESULT 9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1097:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1097

Query Match 1.0%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2608 CTGGCAGAAATGACTTCTACTCGAACAC 2635
          ||||||||||||||||||||||||||||
Db      1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT 10
US-08-253-155A-92
; Sequence 92, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-92


  Query Match             0.9%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.0085;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCCGCCCAAAACCCCCCGAAAAACG 27
           |||||||||||||||||||||||||
Db      16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT 11
US-08-625-209A-21
; Sequence 21, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-21


  Query Match             0.9%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.0085;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCCGCCCAAAACCCCCCGAAAAACG 27
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Db      16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT 12
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  317-276-3589
;       TELEFAX:  317-276-1294
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  52 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1066 ATGATTTTAAATTCAGCAAGTG 1087
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Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  13
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, Leslie D.
;     APPLICANT:  Cook, James A.
;     APPLICANT:  David, Gary S.
;     APPLICANT:  Hochschwender, Susan M.
;     APPLICANT:  Kasher, Mary S.
;     APPLICANT:  Smith, Michele C.
;     APPLICANT:  Stemmer, Willem P.
;     TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;     TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;     NUMBER OF SEQUENCES:  38
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Eli Lilly and Company
;       STREET:  Lilly Corporate Center
;       CITY:  Indianapolis
;       STATE:  IN
;       COUNTRY:  USA
;       ZIP:  46285
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/826,928A
;       FILING DATE:  19920124
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murphy, Richard B.
;       REGISTRATION NUMBER:  35,296
;       REFERENCE/DOCKET NUMBER:  X8180A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  317-276-3589
;       TELEFAX:  317-276-1294
;   INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  52 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1066 ATGATTTTAAATTCAGCAAGTG 1087
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  14
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;     APPLICANT:  Stevens, John K.
;     APPLICANT:  Dunn, James M.
;     TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;     TITLE OF INVENTION:  from a Patient Sample
;     NUMBER OF SEQUENCES:  60
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Oppedahl & Larson
;       STREET:  1992 Commerce Street, Suite 309
;       CITY:  Yorktown Heights
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10598-4412
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS 5.0
;       SOFTWARE:  Word Perfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/271,946A
;       FILING DATE:  08-JUL-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marina T. Larson
;       REGISTRATION NUMBER:  32,038
;       REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (914) 245-3252
;       TELEFAX:  (914) 962-4330
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  22
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
;     HYPOTHETICAL:  no
;     ANTI-SENSE:  no
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  human
;     FEATURE:
;       NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2366 CAACACCAACAAAAATGACTCC 2387
          ||||||||||||||||||||||
Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  15
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
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;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2366 CAACACCAACAAAAATGACTCC 2387
          ||||||||||||||||||||||
Db     22 CAACACCAACAAAAATGACTCC 1



Search completed: February 13, 2000, 17:12:58
Job time: 9058 sec
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:55:19 ; Search time 9092.07 Seconds
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Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

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103: gb_gss13:*
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105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		476	17.7	572	64	AL120941	AL120941 DKFZp762D
2	c	352	13.1	415	51	AI745644	AI745644 tr24b06.x
3	c	348	12.9	411	51	AI745643	AI745643 tr24b05.x
4		257	9.6	285	33	AA382103	AA382103 EST95270
5		204	7.6	304	32	AA361277	AA361277 EST70529
6	c	161	6.0	329	36	AA664676	AA664676 nu64f09.s
7		156	5.8	456	30	AA210875	AA210875 zr88f11.r

c	8	143	5.3	571	41	AI074792 AI074792 oy03a06.s
c	9	132	4.9	171	38	AA765882 AA765882 oa14a06.s
	10	114	4.2	386	24	N25402 N25402 yx40c12.r1
	11	113	4.2	457	24	N41391 N41391 yw70g06.r1
	12	89	3.3	152	22	R57845 R57845 F6142 Fetal
	13	82	3.0	525	30	AA258255 AA258255 zr59g04.r
	14	48	1.8	397	22	R70325 R70325 yj81b10.r1
	15	48	1.8	522	28	AA072780 AA072780 mm76a05.r
	16	42	1.6	986	89	AQ901300 AQ901300 HS_5234_A
	17	38	1.4	472	46	AA955457 AA955457 UI-R-A1-e
c	18	35	1.3	914	38	AA763411 AA763411 vw54a04.r
c	19	35	1.3	871	38	AA763485 AA763485 vw54h01.r
	20	34	1.3	427	37	AA709628 AA709628 vv41c11.r
c	21	33	1.2	462	48	AI606529 AI606529 vb27g08.y
	22	33	1.2	832	49	AI646038 AI646038 vw54a10.x
	23	33	1.2	709	49	AI646097 AI646097 vw54h07.x
	24	33	1.2	575	49	AI662832 AI662832 vb27g08.x
	25	31	1.2	284	59	AV111279 AV111279
	26	31	1.2	174	72	AV302462 AV302462
	27	29	1.1	615	40	AA959836 AA959836 vw54h01.s
c	28	26	1.0	405	39	AA861150 ak36a12.s
	29	26	1.0	529	40	AA959709 AA959709 vw54a04.s
	30	25	0.9	356	41	AI020392 AI020392 ub17a05.r
c	31	24	0.9	492	33	AA396353 AA396353 vb27g08.r
c	32	22	0.8	440	33	AA440741 AA440741 LD15614.5
c	33	22	0.8	332	44	AI259982 AI259982 LP03562.5
	34	22	0.8	586	59	AI770926 AI770926 606063D04
c	35	21	0.8	640	38	AA752076 AA752076 96AS1023
	36	21	0.8	219	38	AA752355 AA752355 96GS0852
c	37	21	0.8	501	74	AV391000 AV391000
c	38	20	0.7	439	21	R12275 R12275 yf40f10.r1
c	39	20	0.7	424	21	R21339 R21339 yg50d05.r1
c	40	20	0.7	372	21	R21352 R21352 yg50f05.r1
c	41	20	0.7	351	21	T78368 T78368 yc99g02.r1
c	42	20	0.7	478	22	H06003 H06003 yl76c05.r1
c	43	20	0.7	299	36	AA618388 AA618388 nq18h09.s
	44	20	0.7	712	38	AA392812 AA392812 LD11946.5
	45	20	0.7	574	103	AQ498524 AQ498524 HS_5120_B

ALIGNMENTS

RESULT 1
AL120941
LOCUS AL120941 572 bp mRNA EST 27-SEP-1999
DEFINITION DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762D143 5', mRNA sequence.
ACCESSION AL120941
VERSION AL120941.1 GI:5926942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948410.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.
No sl sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES Location/Qualifiers
source 1..572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762D143"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 180 a 128 c 98 g 166 t
ORIGIN

Query Match 17.7%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 3.4e-204;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1375 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1434
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Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1435 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1495 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1555 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1615 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1675 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1735 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1795 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT 2
AI745644/c
LOCUS AI745644 415 bp mRNA EST 21-JUN-1999
DEFINITION tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI745644
VERSION AI745644.1 GI:5113932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137189.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

```
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             13.1%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-148;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2045 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 2104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy    2105 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2164
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy    2165 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy    2225 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2284
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy    2285 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2344
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy    2345 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .411
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219217"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


  Query Match             12.9%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 2e-146;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2049 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy    2109 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy    2169 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy    2229 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy    2289 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2348
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy    2349 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2396
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
```

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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             9.6%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-105;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1839 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1898
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy    1899 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1958
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy    1959 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 2018
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy    2019 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2078
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy    2079 TGTAACAGCATACAAGG 2095
           ||||||||||||||||
Db     241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277       304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             7.6%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-81;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1648 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1707
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy    1708 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1767
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1768 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1827
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1828 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1887
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1888 CGGCTAAATACACTT 1902
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.0%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-62;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1443 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1503 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1563 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1603
          |||||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   7
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             5.8%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-60;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2536 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2596 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2656 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          |||||||||||||||||||||||||||||||||||
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Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   8
AI074792/c
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


  Query Match             5.3%;  Score 143;  DB 41;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-54;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      85 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 309

Qy     145 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 249

Qy     205 CATGTCAGAGAGAGAGCTTGGTT 227
           |||||||||||||||||||||||
Db     248 CATGTCAGAGAGAGAGCTTGGTT 226


RESULT   9
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             4.9%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-49;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1238 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy    1298 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy    1358 TGTCTTTATTGG 1369
           ||||||||||||
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```
Db     51 TGTCTTTATTGG 40


RESULT  10
N25402
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.2%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2491 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60

Qy    2551 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2604
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  11
N41391
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


  Query Match             4.2%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-40;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2427 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy    2487 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2539
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329


RESULT  12
R57845
```

```
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898    Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.3%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-29;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2261 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy    2321 ATATTTCACCCCTGAAGAGTCCATATAAA 2349
           |||||||||||||||||||||||||||||
Db      61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  13
AA258255
LOCUS       AA258255       525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662    Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c     107 g     179 t
ORIGIN


  Query Match             3.0%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-26;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2610 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2669
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2670 TACCTCAAACAAGGAAGAGAAA 2691
           ||||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  14
R70325
LOCUS       R70325        397 bp    mRNA            EST       01-JUN-1995
DEFINITION  yj81b10.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:155131 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   R70325
VERSION     R70325.1  GI:843842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
```

```
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 803
            High quality sequence stops: 324
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 803    Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1. .397
                     /organism="Homo sapiens"
                     /db_xref="GDB:569832"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155131"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot -
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      130 a     47 c     71 g    147 t      2 others
ORIGIN


  Query Match             1.8%;  Score 48;  DB 22;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 4e-11;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    136 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 334


RESULT  15
AA072780
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
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                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
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BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


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  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Search completed: February 13, 2000, 16:55:27
Job time: 15509 sec
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 11:46:35 ; Search time 14294.3 Seconds
(without alignments)
-547.403 Million cell updates/sec

Title: US-09-026-459A-42_COPY_7_2583
Perfect score: 2577
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Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

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50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2242	87.0	4597	5	I05311	I05311 Sequence 1
2	2242	87.0	3232	5	I18496	I18496 Sequence 1
c 3	2242	87.0	3232	5	I18497	I18497 Sequence 2
4	2242	87.0	2994	5	I81465	I81465 Sequence 2
5	2242	87.0	4839	10	HUMRB1MRNA	L41870 Homo sapien
6	2242	87.0	4600	10	HUMRBA1RA	M33647 Human retin
7	2242	87.0	2994	10	HUMRBSA	M28419 Human retin
8	2191	85.0	4597	5	I09369	I09369 Sequence 1
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent EP 0259031.
ACCESSION I05311
VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
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BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN
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Query Match 87.0%; Score 2242; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
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Db     825 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 884

Qy     996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     885 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 944

Qy    1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
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Db     945 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1004

Qy    1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1005 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1064

Qy    1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1065 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1124

Qy    1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1125 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1184

Qy    1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1185 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1244

Qy    1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1245 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1304

Qy    1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
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Db    1305 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1364

Qy    1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1365 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1424

Qy    1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
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Db    1425 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1484

Qy    1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
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Db    1485 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1544

Qy    1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
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Db    1545 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1604

Qy    1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1605 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1664

Qy    1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1665 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1724
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Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1725 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1784

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1844

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
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Db   1845 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1904

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
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Db   1905 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1964

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2024

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2084

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2144

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2204

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2264

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2324

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2325 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2384

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2385 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2444

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
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Db   2445 TACCTCAAACAAGGAAGAGAAA 2466
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RESULT   3
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
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  Query Match             87.0%;  Score 2242;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3012 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 2953

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2952 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 2893

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2892 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 2833

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2832 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 2773

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2772 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 2713

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2712 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 2653

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 2593

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2592 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 2533

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 2473

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2472 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 2413

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2412 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 2353

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 2293

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2292 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 2233

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 2173

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 2113

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2112 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 2053

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
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Db   2052 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1993
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Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1992 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1933

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1932 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1873

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1872 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1813

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1812 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1753

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1693

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1633

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
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Db   1632 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1573

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
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Db   1572 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1513

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1453

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1393

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1333

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1273

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1213

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1153

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 1093

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 1033

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
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Db   1032 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 973

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
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Db    972 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 913
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Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
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Db    912 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 853

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 793

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
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Db    792 TACCTCAAACAAGGAAGAGAAA 771
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RESULT   4
I81465
LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
                     /organism="unknown"
BASE COUNT      974 a    618 c    593 g    809 t
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  Query Match            87.0%;  Score 2242;  DB 5;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGA▲AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
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Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
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Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
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Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
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Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
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Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
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Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
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Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
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Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
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Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
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Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
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Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
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Db   2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT   5
HUMRB1MRNA
LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
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            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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Db   1760 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1819

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
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Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
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Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
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Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
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Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
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Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
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Qy    2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
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Qy    2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
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Qy    2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
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Qy    2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
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Db    2840 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2899

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RESULT   6
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
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BASE COUNT     1489 a    842 c    815 g    1454 t
ORIGIN


  Query Match           87.0%;  Score 2242;  DB 10;  Length 4600;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
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Qy     456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
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Qy     516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
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Qy     576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
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Qy     636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
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Qy     816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
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Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
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Db   1446 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1505

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Db   2766 TACCTCAAACAAGGAAGAGAAA 2787
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RESULT   7
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
            phosphoprotein associated with DNA binding activity
  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


  Query Match             87.0%;  Score 2242;  DB 10;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
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Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
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Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT   8
I09369
LOCUS       I09369       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


  Query Match             85.0%;  Score 2191;  DB 5;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2241;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 602

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 662

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 722

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    723 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 782

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    783 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 842

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    843 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 902

Qy    696 TTCTCTTGGACTTGTAAGATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    903 TTCTCTTGGACTTGTAAGATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 962

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    963 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1022

Qy    816 AACTCTTCAGACTGATTGTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1023 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1082

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
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Db   1083 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1142

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1143 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1202

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1203 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1262

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
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Db   1263 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1322

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1323 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1382

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
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Db   1383 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1442

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
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Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
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Db   1503 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1562

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1563 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1622

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1623 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1682

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1683 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1742

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1743 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1802

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1803 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1862

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
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Db   1863 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1922

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1923 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1982

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
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Db   1983 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2042

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2043 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2102

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
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Db   2103 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2162

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2163 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2222

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
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Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
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Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
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Db   2403 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2462

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2463 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2522

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2523 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2582

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2583 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGAAGG 2642

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2643 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2702

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2703 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2762

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2763 TACCTCAAACAAGGAAGAGAAA 2784


RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
     source          1. .4740
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RB-[1,5]"
                     /dev_stage="foetus"
                     /tissue_type="retina"
                     /map="13q14.2"
     mRNA            <1. .4740
                     /note="rbs mRNA"
     gene            139. .2925
                     /gene="RB1"
     CDS             139. .2925
                     /gene="RB1"
                     /note="retinoblastoma susceptibility protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA69807.1"
                     /db_xref="GI:190959"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPEEDPEQDSGPEDLPL
                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
                     IFIARVDLDEMSFTLLSYRKTYEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


  Query Match           79.1%;  Score 2038;  DB 10;  Length 4740;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 2238;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
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Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635

Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695

Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755

Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815

Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATCGAAGATTATTTTTGGATCATGATAA 1160

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875

Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935

Db   1221 CCTTGATGAAGAGGTGAATATAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995

Db   1281 TATCCAACAATTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055

Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115

Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175

Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235

Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295

Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355

Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415

Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475

Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535

Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595

Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655

Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715

Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775

Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835

Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895

Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955

Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015

Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075

Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135

Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195

Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255

Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315

Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375

Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435

Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495

Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2496 GGCAGAAATGACTTCTACTGGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555

Db   2841 GGCAGAAATGACTTCTACTGGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577

Db   2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
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KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match             55.1%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy     559 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy     619 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy     679 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 738
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy     739 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy     799 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 858
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy     859 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 918
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy     919 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 978
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy     979 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1038
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy    1039 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1098
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy    1099 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy    1159 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1218
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy    1219 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy    1279 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1338
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy    1339 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1398
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy    1399 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1458
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy    1459 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1518
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy    1519 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1578
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy    1579 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy    1639 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1698
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy    1699 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy    1759 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy    1819 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy    1879 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1938
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy    1939 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 1998
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy    1999 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2058
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy    2059 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy    2119 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2178
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy    2179 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2238
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy    2239 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2298
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Db    2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy    2299 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2358
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Db    2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy    2359 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2418
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Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2419 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2478
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Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2479 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2538
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Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2539 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2577
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Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768


RESULT  11
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
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     gene            139. .300
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BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


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Qy    399 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 458
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Db    274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy    459 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 518
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Qy    519 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 578
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Db    394 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 453

Qy    579 GATAGCAAAACAACTAGAAAATGATAC 605
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Db    454 GATAGCAAAACAACTAGAAAATGATAC 480


RESULT  12
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
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BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


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Qy   1292 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1351
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Qy   1352 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1411
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Qy   1412 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1471
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1472 CCCTTGCATGGCTCTCAG 1489
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  13
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
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BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


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Qy   1292 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1351
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Qy   1352 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1411
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Qy   1472 CCCTTGCATGGCTCTCAG 1489
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  14
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
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  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
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Qy   1352 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1411
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Db  78203 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 78262

Qy   1472 CCCTTGCATGGCTCTCAG 1489
          ||||||||||||||||||
Db  78263 CCCTTGCATGGCTCTCAG 78280


RESULT  15
HUMRB1501V
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
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Qy   1354 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1413
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Db    126 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 185

Qy   1414 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1473
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Db    186 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 245

Qy   1474 CTTGCATGGCTCTCAG 1489
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Db    246 CTTGCATGGCTCTCAG 261


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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

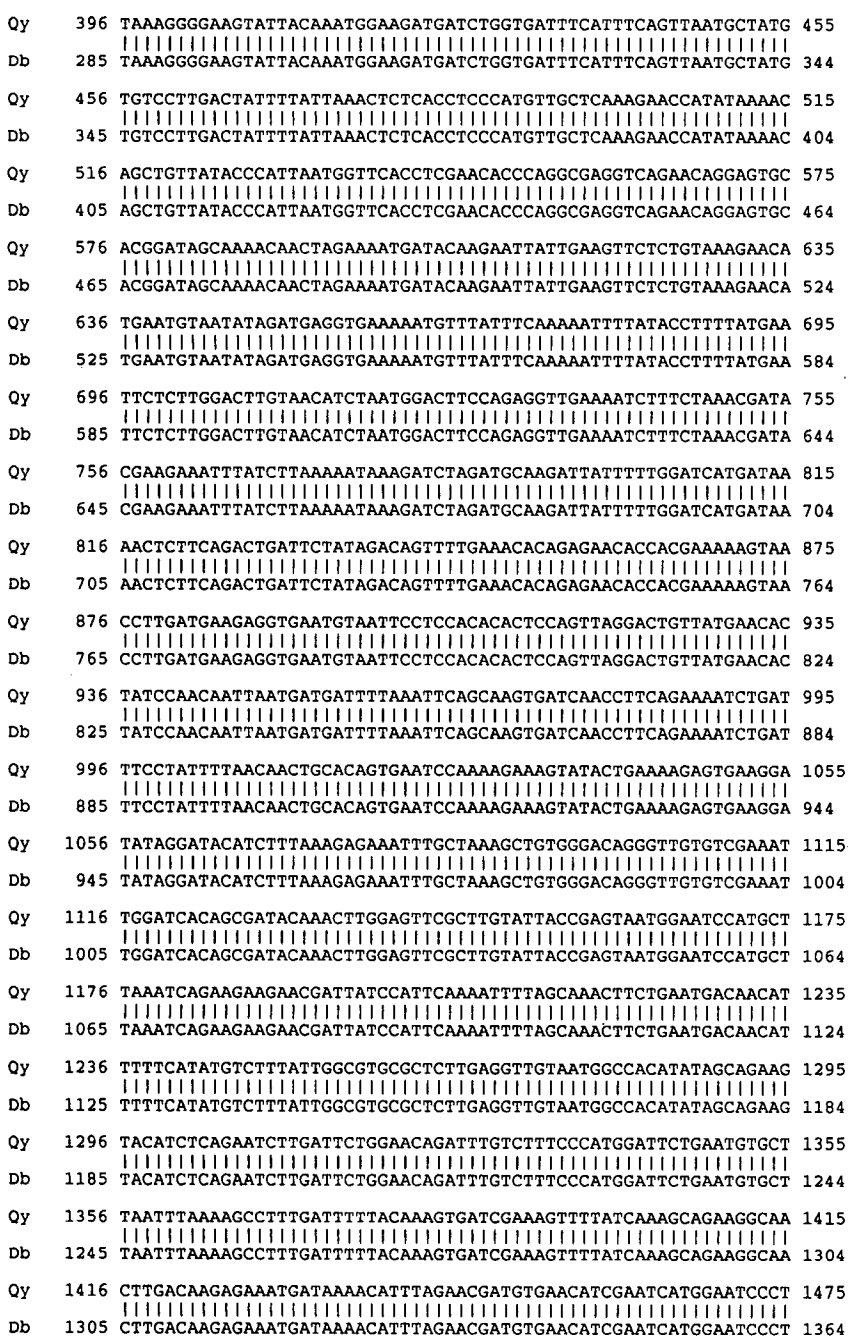
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ALIGNMENTS

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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


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  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
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;      TOPOLOGY:  not relevant
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US-08-038-760-2


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Qy    1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
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Db    1752 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1693

Qy    1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1692 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1633

Qy    1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
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Db   1632 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1573

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1513

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1453

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1393

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1333

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1273

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1213

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1153

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 1093

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 1033

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 973

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 913

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 853

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 793

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db    792 TACCTCAAACAAGGAAGAGAAA 771


RESULT   3
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match             87.0%;  Score 2242;  DB 2;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220
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Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT   4
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


  Query Match             87.0%;  Score 2242;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 284

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 344

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 404

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 464

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 524

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 584

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 644

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 704

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 764

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 824

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 884

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 944

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1004

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1064

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1124

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1184

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1244

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1304

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1364

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1424

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1484

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1485 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1544

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
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Db   1545 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1604

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1664

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1665 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1724

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1725 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1784

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1844

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1904

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1964

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2024
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Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
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Db   2025 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2084

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2144

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2204

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2264

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2324

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2325 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2384

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2385 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2444

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
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Db   2445 TACCTCAAACAAGGAAGAGAAA 2466
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RESULT   5
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match            87.0%;  Score 2242;  DB 4;  Length 3232;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3012 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 2953

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2952 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 2893

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2892 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 2833

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2832 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 2773

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2772 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 2713

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2712 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 2653

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 2593

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2592 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 2533

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 2473

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2472 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 2413

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2412 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 2353

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 2293

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2292 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 2233

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 2173

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 2113

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
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Db   2112 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 2053

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2052 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1993

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1992 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1933

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1932 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1873

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1872 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1813

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1812 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1753

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1693

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
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Db   1692 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1633

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
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Db   1632 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1573

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1513

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1453

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1393

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1333

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1273

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1213

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1153

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 1093

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 1033

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
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Db   1032 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 973

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
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Db    972 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 913

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 853

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 793

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db    792 TACCTCAAACAAGGAAGAGAAA 771


RESULT   6
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7
```

Query Match 87.0%; Score 2242; DB 4; Length 2995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy    2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy    2556 TACCTCAAACAAGGAAGAGAAA 2577
           |||||||||||||||||||||||
Db    2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT   7
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


  Query Match             87.0%;  Score 2242;  DB 4;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy     396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy     456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy     516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy     576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy     636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy     696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy     756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy     816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy     876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy     936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy     996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy    1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy    1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy    1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy    1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy    1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy    1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy    1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy    1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy    1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940
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Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||||
Db   2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT   8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


  Query Match             85.0%;  Score 2191;  DB 6;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2241;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
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Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815

Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875

Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935

Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995

Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055

Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115

Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175

Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235

Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295

Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355

Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415

Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475

Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535

Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595

Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655

Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715

Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775

Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835

Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895

Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1896 CCAAATTATGATGTGTTGCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955

Db   2241 CCAAATTATGATGTGTTGCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1956 CAAAATCATTGTAACAGGATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015

Db   2301 CAAAATCATTGTAACAGGATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075

Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135

Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195

Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255

Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315

Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375

Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2376 AAGTGCTGAAGGAAGCAAGCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435

Db   2721 AAGTGCTGAAGGAAGCAAGCCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495

Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555

Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577

Db   2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.1%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00039;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2494 CTGGCAGAAATGACTTCTACTCGAACAC 2521
           ||||||||||||||||||||||||||||
Db       1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-08-253-155A-92
; Sequence 92, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-92


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  11
US-08-625-209A-21
; Sequence 21, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-21


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  12
US-07-826-928A-15
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; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     952 ATGATTTTAAATTCAGCAAGTG 973
           ||||||||||||||||||||||
Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  13
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     952 ATGATTTTAAATTCAGCAAGTG 973
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Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  14
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2252 CAACACCAACAAAAATGACTCC 2273
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RESULT  15
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;    ANTI-SENSE:  no
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US-08-271-942A-22


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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 11:51:46 ; Search time 14294.3 Seconds
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Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

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49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2062	86.2	3232	5	I18496	I18496 Sequence 1
c 3	2062	86.2	3232	5	I18497	I18497 Sequence 2
4	2062	86.2	2994	5	I81465	I81465 Sequence 2
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11	198	8.3	693	5	I09384	I09384 Sequence 17
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19	163	6.8	252	10	HUMRB1777L	L49230 Homo sapien
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent EP 0259031.
ACCESSION I05311
VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
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BASE COUNT     1489 a    842 c    812 g   1454 t
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Query Match 86.2%; Score 2062; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SOURCE      Unknown.
  ORGANISM  Unknown.
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  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
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  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
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Db    765 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 824

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 884

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 944

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1004

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1064

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1124

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1184

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1244

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1304

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1364

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1424

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1484

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1485 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1544

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1545 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1604

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1664

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1665 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1724

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1725 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1784

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1844

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1904

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1964

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2024

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2084
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Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2144

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2204

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2205 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2264

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2324

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2325 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2384

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2385 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2444

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db   2445 TACCTCAAACAAGGAAGAGAAA 2466
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RESULT   3
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN
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  Query Match             86.2%;  Score 2062;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2832 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 2773

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2772 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 2713

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2712 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 2653

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 2593

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2592 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 2533

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 2473

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2472 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 2413

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2412 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 2353

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 2293

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2292 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 2233

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 2173

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 2113

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2112 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 2053

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2052 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1993

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1992 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1933

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1932 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1873

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1872 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1813

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1812 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1753

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1693

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1633

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1573

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1513

Qy   1650 GACCCTTTTCCAGCACACGCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 GACCCTTTTCCAGCACACGCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1453
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Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
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Db   1452 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1393

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1333

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1273

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1213

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1153

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 1093

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 1033

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 973

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 913

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 853

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 793

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
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Db    792 TACCTCAAACAAGGAAGAGAAA 771
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RESULT   4
I81465
LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
                     /organism="unknown"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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Query Match 86.2%; Score 2062; DB 5; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
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Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
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RESULT   5
HUMRB1MRNA
LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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Query Match 86.2%; Score 2062; DB 10; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
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Db   2180 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2239

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
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Db   2240 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2299

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
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Db   2360 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2419

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
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Db   2420 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2479

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
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Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
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Db   2540 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2599

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
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Db   2600 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2659

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
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Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
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Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
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Db   2780 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2839

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
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Db   2840 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2899

Qy   2370 TACCTCAAACAAGGAAGACAAA 2391
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Db   2900 TACCTCAAACAAGGAAGACAAA 2921
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RESULT   6
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
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COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
            provided by S.H.Friend, 10-FEB-1988.
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                     /map="13q14.2"
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BASE COUNT     1489 a    842 c    815 g   1454 t
ORIGIN
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Query Match 86.2%; Score 2062; DB 10; Length 4600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
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Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
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Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
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Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
Db   1146 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1205

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
Db   1206 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1265

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
Db   1266 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1325

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
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Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
Db   1386 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1445

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Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
Db   1566 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1625

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
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Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
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Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
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Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
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Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
Db   1986 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2045

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
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Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
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Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
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Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
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Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
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Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
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Db   2766 TACCTCAAACAAGGAAGAGAAA 2787


RESULT   7
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
            phosphoprotein associated with DNA binding activity
  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


  Query Match           86.2%;  Score 2062;  DB 10;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
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Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
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Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
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Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
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Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
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Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
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Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
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Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
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Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
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Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580
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Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
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Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
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Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
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Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
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Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
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Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
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Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
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Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
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Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
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Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
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Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
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Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
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Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
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Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
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Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
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Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
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Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
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Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
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Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
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Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
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Db   2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT   8
I09369
LOCUS       I09369       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
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BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


  Query Match             84.1%;  Score 2011;  DB 5;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
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Db    723 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 782

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
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Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
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Db    843 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 902

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
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Db    903 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 962

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    963 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1022

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
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Db   1023 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1082

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
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Db   1083 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1142
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Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
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Db   1143 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1202

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1203 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1262

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
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Db   1263 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1322

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
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Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
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Db   1383 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1442

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
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Db   1443 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1502

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
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Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
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Db   1563 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1622

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
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Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
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Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
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Db   1743 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1802

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
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Db   1803 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1862

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
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Db   1863 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1922

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
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Db   1923 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1982

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
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Db   1983 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2042

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
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Db   2043 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2102

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
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Db   2103 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2162

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
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Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
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Db   2283 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2342

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
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Db   2343 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2402

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2403 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2462

Qy   2070 ACCAACAAAAATGACTCGAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
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Db   2463 ACCAACAAAAATGACTCGAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2522

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
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Db   2523 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2582

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
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RESULT 9
HUMRBS
LOCUS HUMRBS 4740 bp mRNA PRI 12-JUL-1995
DEFINITION Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION M15400
VERSION M15400.1 GI:190958
KEYWORDS retinoblastoma susceptibility.
SOURCE Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 243 to 4740)
AUTHORS Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
TITLE Human retinoblastoma susceptibility gene: cloning, identification, and sequence
JOURNAL Science 235 (4794), 1394-1399 (1987)
MEDLINE 87149066
REFERENCE 2 (bases 1 to 4740)
AUTHORS Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and Lee,W.H.
TITLE Molecular mechanism of retinoblastoma gene inactivation in retinoblastoma cell line Y79
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
MEDLINE 88320373
COMMENT Draft entry and computer-readable copy of sequence in [1] kindly provided by R.Bookstein, 27-APR-1987.
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BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.
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Query Match 77.7%; Score 1858; DB 10; Length 4740;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2058; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATCGAAGATTATTTTTGGATCATGATAA 1160

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
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Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
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Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
Db   1281 TATCCAACAATTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
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Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069

Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129

Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189

Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249

Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309

Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369

Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391

Db   2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match             59.4%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy    373 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 432

Db    752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    433 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 492

Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    493 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 552

Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    553 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 612

Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy    613 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 672

Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy    673 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 732

Db   1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy    733 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 792

Db   1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy    793 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 852

Db   1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy    853 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 912

Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy    913 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 972

Db   1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy    973 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1032

Db   1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy   1033 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1092

Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1093 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1152

Db   1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy   1153 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1212

Db   1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy   1213 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1272

Db   1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy   1273 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1332

Db   1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy   1333 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1392

Db   1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy   1393 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1452

Db   1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy   1453 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1512

Db   1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy   1513 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1572

Db   1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy   1573 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1632

Db   1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010
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Qy   1633 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1692
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Db   2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy   1693 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy   1753 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 1812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy   1813 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 1872
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy   1873 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy   1933 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 1992
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy   1993 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy   2053 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2113 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2173 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2232
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2233 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2292
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Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2293 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2353 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2391
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Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN
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  Query Match             8.3%;  Score 198;  DB 5;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1106 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1165
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1166 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1226 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1285
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1286 CCCTTGCATGGCTCTCAG 1303
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Db    430 CCCTTGCATGGCTCTCAG 447
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RESULT  12
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
                     /number=16
     exon            250. .446
                     /note="retinoblastoma susceptibility gene"
                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN
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  Query Match             8.3%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1106 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1165
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1166 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1226 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1285
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1286 CCCTTGCATGGCTCTCAG 1303
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT 13
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
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                     /db_xref="taxon:9606"
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                     /bound_moiety="SP1"
                     /evidence=experimental
     protein_bind    1866. .1872
                     /bound_moiety="ATF"
                     /evidence=experimental
     exon            <2060. .2196
                     /number=1
     CDS             join(2060. .2196,5424. .5550,39446. .39561,41926. .42045,
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                     61730. .61807,64330. .64439,65364. .65441,70242. .70329,
                     73753. .73869,76430. .76486,76889. .76920,77001. .77077,
                     78083. .78279,149998. .150116,153208. .153353,156693. .156838,
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                     170372. .170402,173707. .173849,174361. .174410,
                     177005. .177078)
                     /codon_start=1
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAA53483.1"
                     /db_xref="GI:292421"
                     /translation="MPPKTPRKTAATAAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
                     IFIAAVDLDEMSFTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
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                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
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Qy   1106 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1165
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Qy   1166 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1225
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Db  78143 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 78202

Qy   1226 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1285
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Db  78203 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 78262

Qy   1286 CCCTTGCATGGCTCTCAG 1303
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Db  78263 CCCTTGCATGGCTCTCAG 78280


RESULT  14
HUMRB1501V
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
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                     /map="13q14.2"
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     intron          <1. .64
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                     /number=16
     exon            65. .260
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                     /number=17
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     mutation        66. .67
                     /gene="RB1"
                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
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Db    126 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 185

Qy   1228 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1287
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 245

Qy   1288 CTTGCATGGCTCTCAG 1303
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Db    246 CTTGCATGGCTCTCAG 261


RESULT  15
HUMRB4MU2
LOCUS       HUMRB4MU2     555 bp    DNA             PRI       05-OCT-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) gene from
            GOS561, exon 17, bases 77969-78523 in L11910.
ACCESSION   L41904
VERSION     L41904.1  GI:794013
KEYWORDS    mutation; retinoblastoma susceptibility protein.
SEGMENT     2 of 2
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
FEATURES             Location/Qualifiers
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                     /cell_line="GOS561"
                     /map="13q14.2"
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                     EMIKHLERCEH"
     mutation        282
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                     /note="c in wt/t in tumor GOS561 Arg->stop; G00-118-734"
                     /citation=[2]
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Qy   1106 GAAGTACATCTCAGAATGTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1165
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Db    115 GAAGTACATCTCAGAATGTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 174

Qy   1166 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1225
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Db    175 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 234

Qy   1226 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1272
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Db    235 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 281


Search completed: February 13, 2000, 11:56:44
Job time: 18700 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:55:27 ; Search time 9092.07 Seconds
(without alignments)
1070.151 Million cell updates/sec

Title: US-09-026-459A-42_COPY_7_2583
Perfect score: 2577
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2577

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	476	18.5	572	64	AL120941	AL120941 DKFZp762D
c	2	352	13.7	415	51	AI745644	AI745644 tr24b06.x
c	3	348	13.5	411	51	AI745643	AI745643 tr24b05.x
	4	257	10.0	285	33	AA382103	AA382103 EST95270
	5	204	7.9	304	32	AA361277	AA361277 EST70529
c	6	181	7.0	571	41	AI074792	AI074792 oy03a06.s
c	7	161	6.2	329	36	AA664676	AA664676 nu64f09.s

	8	156	6.1	456	30	AA210875 AA210875 zr88f11.r
c	9	132	5.1	171	38	AA765882 AA765882 oa14a06.s
	10	114	4.4	386	24	N25402 N25402 yx40c12.r1
	11	113	4.4	457	24	N41391 N41391 yw70g06.r1
	12	89	3.5	152	22	R57845 R57845 F6142 Fetal
	13	82	3.2	525	30	AA258255 AA258255 zr59g04.r
c	14	53	2.1	349	20	T24020 T24020 seq2177 3HF
	15	48	1.9	397	22	R70325 R70325 yj81b10.r1
	16	48	1.9	522	28	AA072780 AA072780 mm76a05.r
	17	42	1.6	986	89	AQ901300 AQ901300 HS_5234_A
c	18	35	1.4	914	38	AA763411 AA763411 vw54a04.r
c	19	35	1.4	871	38	AA763485 AA763485 vw54h01.r
	20	34	1.3	427	37	AA709628 AA709628 vv41c11.r
	21	31	1.2	284	59	AV111279 AV111279 AV111279
	22	31	1.2	174	72	AV302462 AV302462 AV302462
	23	27	1.0	472	46	AA955457 AA955457 UI-R-A1-e
c	24	26	1.0	405	39	AA861150 AA861150 ak36a12.s
	25	25	1.0	356	41	AI020392 AI020392 ub17a05.r
c	26	22	0.9	440	33	AA440741 AA440741 LD15614.5
	27	22	0.9	529	40	AA959709 AA959709 vw54a04.s
	28	22	0.9	615	40	AA959836 AA959836 vw54h01.s
c	29	22	0.9	332	44	AI259982 AI259982 LP03562.5
	30	22	0.9	832	49	AI646038 AI646038 vw54a10.x
	31	22	0.9	709	49	AI646097 AI646097 vw54h07.x
	32	22	0.9	586	59	AI770926 AI770926 606063D04
c	33	21	0.8	640	38	AA752076 AA752076 96AS1023
	34	21	0.8	219	38	AA752355 AA752355 96GS0852
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c	36	20	0.8	439	21	R12275 R12275 yf40f10.r1
c	37	20	0.8	424	21	R21339 R21339 yg50d05.r1
c	38	20	0.8	372	21	R21352 R21352 yg50f05.r1
c	39	20	0.8	351	21	T78368 T78368 yc99g02.r1
c	40	20	0.8	478	22	H06003 H06003 yl76c05.r1
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	42	20	0.8	712	38	AA392812 AA392812 LD11946.5
	43	20	0.8	175	39	AA825220 AA825220 oc66f12.s
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ALIGNMENTS

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DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
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ORIGIN
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Qy   1261 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1320
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Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1321 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1381 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1441 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1501 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1561 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1621 GTAAGATCTCCAAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1681 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1736
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT   2
AI745644/c
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
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            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


  Query Match             13.7%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 4e-148;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1931 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 1990
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy    1991 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2050
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy    2051 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy    2111 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy    2171 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy    2231 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .411
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219217"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


  Query Match             13.5%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-146;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1935 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 1994
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy    1995 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2054
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy    2055 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2114
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy    2115 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2174
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy    2175 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2234
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy    2235 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2282
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .285
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):107475"
                      /db_xref="taxon:9606"
                      /clone_lib="Activated T-cells II"
                      /cell_type="T-lymphocyte"
                      /dev_stage="adult"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             10.0%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-105;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1725 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy    1785 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1844
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy    1845 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy    1905 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy    1965 TGTAACAGCATACAAGG 1981
           ||||||||||||||||
Db     241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             7.9%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 2.2e-81;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1534 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy    1594 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1654 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1713
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1714 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1774 CGGCTAAATACACTT 1788
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AI074792/c
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


  Query Match             7.0%;  Score 181;  DB 41;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-71;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     85 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 309

Qy    145 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 249

Qy    205 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 189

Qy    265 G 265
          |
Db    188 G 188


RESULT   7
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.2%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-62;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1329 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1389 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1449 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1489
          |||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   8
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.1%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-60;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2422 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2482 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2542 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||||||||||||||||
Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180
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RESULT   9
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.1%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-49;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1124 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy   1184 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1244 TGTCTTTATTGG 1255
          ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT  10
N25402
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.4%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2377 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60

Qy   2437 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2490
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  11
N41391
LOCUS       N41391         457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g     128 t
ORIGIN


  Query Match             4.4%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 2e-40;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2313 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2373 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2425
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329
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RESULT  12
R57845
LOCUS       R57845         152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.5%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-29;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2147 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy    2207 ATATTTCACCCCTGAAGAGTCCATATAAA 2235
           |||||||||||||||||||||||||||||
Db      61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  13
AA258255
LOCUS       AA258255       525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             3.2%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-26;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2556 TACCTCAAACAAGGAAGAGAAA 2577
           |||||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  14
T24020/c
LOCUS       T24020         349 bp    mRNA            EST       01-AUG-1994
DEFINITION  seq2177 3HFLSK20 Homo sapiens cDNA clone 3HFLSK20-63 3', mRNA
            sequence.
ACCESSION   T24020
VERSION     T24020.1  GI:520260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   Soares,M.B.
  TITLE     Human infant brain library b4HB3MA cDNAs
```

```
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Bento Soares
            Columbia University
            Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
            10032
            Tel: 2129602313
            Fax: 2127813577
            Email: cuc@cuccfa.ccc.columbia.edu
            antisense Kanamycin
            Seq primer: M13 Reverse.
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                     weeks post-conception "
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ORIGIN


  Query Match             2.1%;  Score 53;  DB 20;  Length 349;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-13;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT  15
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VERSION     R70325.1  GI:843842
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 803
            High quality sequence stops: 324
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 803   Std Error: 0.00
            Seq primer: M13RP1
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                     /dev_stage="adult"
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                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot -
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      130 a     47 c     71 g    147 t      2 others
ORIGIN


  Query Match             1.9%;  Score 48;  DB 22;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 4e-11;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    287 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 334


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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	2062	86.2	3232	1	US-08-038-760-2	Sequence 2, Appli
	3	2062	86.2	2994	2	US-08-204-329-2	Sequence 2, Appli
	4	2062	86.2	3232	4	US-08-470-091-1	Sequence 1, Appli
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	6	2062	86.2	2995	4	US-08-959-638-7	Sequence 7, Appli
	7	2062	86.2	2994	4	US-08-482-627-4	Sequence 4, Appli
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	9	28	1.2	28	4	US-08-859-998-1097	Sequence 1097, Ap
	10	25	1.0	40	2	US-08-253-155A-92	Sequence 92, Appl
	11	25	1.0	40	2	US-08-625-209A-21	Sequence 21, Appl
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ALIGNMENTS

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US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


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Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
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Db   2145 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2204

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Db   2445 TACCTCAAACAAGGAAGAGAAA 2466
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RESULT 2
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.

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;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2

  Query Match             86.2%;  Score 2062;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2832 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 2773

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2772 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 2713

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2712 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 2653

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2652 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 2593

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2592 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 2533

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2532 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 2473

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2472 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 2413

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2412 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 2353

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2352 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 2293

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2292 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 2233

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2232 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 2173

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2172 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 2113

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2112 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 2053

Qy    1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2052 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1993

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1992 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1933

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1932 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1873

Qy    1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1872 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1813

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1812 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1753

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1752 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1693

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1692 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1633

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1632 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1573

Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1572 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1513

Qy    1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1512 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1453

Qy    1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1452 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1393

Qy    1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1392 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1333

Qy    1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1332 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1273

Qy    1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
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Db   1272 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1213

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1153

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 1093

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 1033

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 973

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 913

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 853

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 793

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db    792 TACCTCAAACAAGGAAGAGAAA 771


RESULT   3
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match             86.2%;  Score 2062;  DB 2;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy    930 TGGATCACAGCGATACAAAGTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 TGGATCACAGCGATACAAAGTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760
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Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
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Db   2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT 4
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,091
; FILING DATE: JUN-16-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..2469
US-08-470-091-1

Query Match 86.2%; Score 2062; DB 4; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 464

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 524

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     525 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 584

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 644

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     645 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 704

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     705 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 764

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     765 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 824

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     825 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 884

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     885 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 944

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     945 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1004

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1005 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1064

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1065 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1124

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1125 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1184

Qy    1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1185 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1244

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1245 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1304

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1305 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1364

Qy    1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1365 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1424

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1425 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1484

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1485 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1544

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1545 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1604

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1605 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1664
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Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1665 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1724

Qy    1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1725 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1784

Qy    1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1785 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1844

Qy    1770 CAAAATCATTGTAACAGGATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1845 CAAAATCATTGTAACAGGATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1904

Qy    1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1905 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1964

Qy    1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1965 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2024

Qy    1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2025 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2084

Qy    2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2085 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2144

Qy    2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2145 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2204

Qy    2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2205 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2264

Qy    2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2265 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2324

Qy    2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2325 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2384

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2385 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2444

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
           |||||||||||||||||||||||
Db    2445 TACCTCAAACAAGGAAGAGAAA 2466
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RESULT   5
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
```

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;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/470,091
;       FILING DATE:  JUN-16-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match             86.2%;  Score 2062;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2832 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 2773

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2772 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 2713

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2712 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 2653

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2652 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 2593

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2592 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 2533

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2532 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 2473

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2472 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 2413

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2412 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 2353

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2352 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 2293

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
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Db    2292 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 2233

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2232 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 2173

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2172 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 2113

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2112 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 2053

Qy    1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2052 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1993

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1992 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1933

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1932 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1873

Qy    1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1872 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1813

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1812 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1753

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1752 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1693

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1692 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1633

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1632 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1573

Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1572 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1513

Qy    1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1512 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1453

Qy    1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1452 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1393

Qy    1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1392 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1333

Qy    1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1332 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1273

Qy    1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1272 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1213

Qy    1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
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Db   1212 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1153

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 1093

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 1033

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 973

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 913

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 853

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 793

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db    792 TACCTCAAACAAGGAAGAGAAA 771


RESULT   6
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


  Query Match           86.2%;  Score 2062;  DB 4;  Length 2995;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700
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Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
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Db   2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT 7
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
; GENERAL INFORMATION:
; APPLICANT: Lee, Wen-Hwa
; APPLICANT: Lee, Eva Y-H.P
; TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
; TITLE OF INVENTION: and Regulator
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,627
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,947
; FILING DATE: 28-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..2924
US-08-482-627-4

Query Match 86.2%; Score 2062; DB 4; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
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Db    981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569

Db   1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629

Db   1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689

Db   1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

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Db   1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809

Db   1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869

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Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229

Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289

Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349

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Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409

Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469

Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529

Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

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Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

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Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709

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Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829

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Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889

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Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009

Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069

Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129

Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189

Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

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Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369

Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391

Db   2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT 8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: and Canji, Inc.
; TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
; TITLE OF INVENTION: Susceptibility Gene Product
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive
; CITY: San Diego
; STATE: California

```
;       COUNTRY:  USA
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10357
;       FILING DATE:  13-SEP-1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/121,108
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  FP-UC 1117
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2923
PCT-US94-10357-1


  Query Match             84.1%;  Score 2011;  DB 6;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy    1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy    1290 TGCATGGCTCTCAGATTCACGTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy    1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy    1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy    1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy    1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy    1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy    1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy    2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy    2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy    2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy    2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy    2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||||
Db    2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.2%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00044;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2308 CTGGCAGAAATGACTTCTACTCGAACAC 2335
           ||||||||||||||||||||||||||||
Db       1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-08-253-155A-92
; Sequence 92, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-92


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCCGCCCAAAACCCCCCGAAAAACG 27
           |||||||||||||||||||||||||
Db      16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  11
US-08-625-209A-21
; Sequence 21, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-21


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  12
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    766 ATGATTTTAAATTCAGCAAGTG 787
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  13
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
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;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    766 ATGATTTTAAATTCAGCAAGTG 787
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  14
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


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  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2066 CAACACCAACAAAAATGACTCC 2087
          ||||||||||||||||||||||
Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  15
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2066 CAACACCAACAAAAATGACTCC 2087
          ||||||||||||||||||||||
Db     22 CAACACCAACAAAAATGACTCC 1


Search completed: February 13, 2000, 17:15:09
Job time: 9189 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:55:34 ; Search time 9092.07 Seconds
(without alignments)
992.911 Million cell updates/sec

Title: US-09-026-459A-44_COPY_7_2397
Perfect score: 2391
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2391

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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102: gb_gss12:*
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104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		476	19.9	572	64	AL120941	AL120941 DKFZp762D
2	c	352	14.7	415	51	AI745644	AI745644 tr24b06.x
3	c	348	14.6	411	51	AI745643	AI745643 tr24b05.x
4		257	10.7	285	33	AA382103	AA382103 EST95270
5		204	8.5	304	32	AA361277	AA361277 EST70529
6	c	181	7.6	571	41	AI074792	AI074792 oy03a06.s
7	c	161	6.7	329	36	AA664676	AA664676 nu64f09.s

	8	156	6.5	456	30	AA210875 AA210875 zr88f11.r
c	9	132	5.5	171	38	AA765882 AA765882 oa14a06.s
	10	114	4.8	386	24	N25402 N25402 yx40c12.r1
	11	113	4.7	457	24	N41391 N41391 yw70g06.r1
	12	89	3.7	152	22	R57845 R57845 F6142 Fetal
	13	82	3.4	525	30	AA258255 AA258255 zr59g04.r
c	14	53	2.2	349	20	T24020 T24020 seq2177 3HF
	15	48	2.0	397	22	R70325 R70325 yj81b10.r1
	16	48	2.0	522	28	AA072780 AA072780 mm76a05.r
	17	42	1.8	986	89	AQ901300 AQ901300 HS_5234_A
c	18	35	1.5	914	38	AA763411 AA763411 vw54a04.r
c	19	35	1.5	871	38	AA763485 AA763485 vw54h01.r
	20	34	1.4	427	37	AA709628 AA709628 vv41c11.r
	21	31	1.3	284	59	AV111279 AV111279 AV111279
	22	31	1.3	174	72	AV302462 AV302462 AV302462
	23	27	1.1	472	46	AA955457 AA955457 UI-R-A1-e
c	24	26	1.1	405	39	AA861150 AA861150 ak36a12.s
	25	25	1.0	356	41	AI020392 AI020392 ub17a05.r
c	26	22	0.9	440	33	AA440741 AA440741 LD15614.5
	27	22	0.9	529	40	AA959709 AA959709 vw54a04.s
	28	22	0.9	615	40	AA959836 AA959836 vw54h01.s
c	29	22	0.9	332	44	AI259982 AI259982 LP03562.5
	30	22	0.9	832	49	AI646038 AI646038 vw54a10.x
	31	22	0.9	709	49	AI646097 AI646097 vw54h07.x
	32	22	0.9	586	59	AI770926 AI770926 606063D04
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	34	21	0.9	219	38	AA752355 AA752355 96GS0852
c	35	21	0.9	501	74	AV391000 AV391000 AV391000
c	36	20	0.8	439	21	R12275 R12275 yf40f10.r1
c	37	20	0.8	424	21	R21339 R21339 yg50d05.r1
c	38	20	0.8	372	21	R21352 R21352 yg50f05.r1
c	39	20	0.8	351	21	T78368 T78368 yc99g02.r1
c	40	20	0.8	478	22	H06003 H06003 yl76c05.r1
c	41	20	0.8	299	36	AA618388 AA618388 nq18h09.s
	42	20	0.8	712	38	AA392812 AA392812 LD11946.5
	43	20	0.8	175	39	AA825220 AA825220 oc66f12.s
c	44	20	0.8	631	39	AA827911 AA827911 od08g05.s
	45	20	0.8	353	99	AQ217005 AQ217005 HS_2262_B

ALIGNMENTS

RESULT 1
AL120941
LOCUS AL120941 572 bp mRNA EST 27-SEP-1999
DEFINITION DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762D143 5', mRNA sequence.
ACCESSION AL120941
VERSION AL120941.1 GI:5926942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948410.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES Location/Qualifiers
source 1. .572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762D143"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 180 a 128 c 98 g 166 t
ORIGIN

Query Match 19.9%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.8e-206;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1075 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1134
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Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1135 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1195 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1255 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1315 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1374
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Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1375 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1434
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Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1435 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1494
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Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1495 ACACAAGCAACCTCAGCGTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1550
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Db    421 ACACAAGCAACCTCAGCGTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
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RESULT 2
AI745644/c
LOCUS AI745644 415 bp mRNA EST 21-JUN-1999
DEFINITION tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI745644
VERSION AI745644.1 GI:5113932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137189.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

```
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             14.7%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 9e-150;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1745 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 1804
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy    1805 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 1864
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy    1865 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 1924
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy    1925 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 1984
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy    1985 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2044
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Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy    2045 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2096
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Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"
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                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


  Query Match             14.6%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 6e-148;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1749 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 1808
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Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy    1809 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 1868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy    1869 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 1928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy    1929 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 1988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy    1989 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy    2049 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2096
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             10.7%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-106;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1539 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1598
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy    1599 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1658
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy    1659 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1718
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy    1719 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1778
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy    1779 TGTAACAGCATACAAGG 1795
           ||||||||||||||||
Db     241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             8.5%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 2.4e-82;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1348 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1407
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy    1408 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1467
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1468 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1527
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1528 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1588 CGGCTAAATACACTT 1602
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AI074792/c
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo:"
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


  Query Match             7.6%;  Score 181;  DB 41;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-72;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     85 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 309

Qy    145 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 249

Qy    205 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 189

Qy    265 G 265
          |
Db    188 G 188


RESULT   7
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
            cDNA Library Preparation: David B. Krizman, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.7%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-63;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1143 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1203 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1263 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1303
          |||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   8
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.5%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-60;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2236 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2296 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2356 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||||||||||||||||
Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180


RESULT   9
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.5%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-49;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    938 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy    998 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1058 TGTCTTTATTGG 1069
          ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT  10
N25402
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.8%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2191 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60

Qy   2251 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2304
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  11
N41391
LOCUS       N41391         457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g     128 t
ORIGIN


  Query Match             4.7%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 6e-41;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2127 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2187 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2239
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329
```

```
RESULT  12
R57845
LOCUS       R57845         152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.7%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-30;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1961 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy    2021 ATATTTCACCCCTGAAGAGTCCATATAAA 2049
           |||||||||||||||||||||||||||||
Db      61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  13
AA258255
LOCUS       AA258255       525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             3.4%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-27;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
           |||||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  14
T24020/c
LOCUS       T24020         349 bp    mRNA            EST       01-AUG-1994
DEFINITION  seq2177 3HFLSK20 Homo sapiens cDNA clone 3HFLSK20-63 3', mRNA
            sequence.
ACCESSION   T24020
VERSION     T24020.1  GI:520260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   Soares,M.B.
  TITLE     Human infant brain library b4HB3MA cDNAs
```

```
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Bento Soares
            Columbia University
            Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
            10032
            Tel: 2129602313
            Fax: 2127813577
            Email: cuc@cuccfa.ccc.columbia.edu
            antisense Kanamycin
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="3HFLSK20-63"
                     /clone_lib="3HFLSK20"
                     /lab_host="E. coli"
                     /note="Vector: Lafmid K; Site_1: Not I; Site_2: EcoR I;
                     cDNA from polyA+ RNA from human fetal liver + spleen. 20
                     weeks post-conception "
BASE COUNT       98 a     73 c     59 g    118 t      1 others
ORIGIN


  Query Match             2.2%;  Score 53;  DB 20;  Length 349;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-13;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    213 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 297


RESULT  15
R70325
LOCUS       R70325        397 bp    mRNA            EST       01-JUN-1995
DEFINITION  yj81b10.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:155131 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   R70325
VERSION     R70325.1  GI:843842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 803
            High quality sequence stops: 324
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 803    Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1. .397
                     /organism="Homo sapiens"
                     /db_xref="GDB:569832"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155131"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      130 a     47 c     71 g    147 t      2 others
ORIGIN


  Query Match             2.0%;  Score 48;  DB 22;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-11;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    136 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 183
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 334


Search completed: February 13, 2000, 16:55:41
Job time: 15523 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 11:56:44 ; Search time 14294.3 Seconds
(without alignments)
-553.776 Million cell updates/sec

Title: US-09-026-459A-46_COPY_7_2613
Perfect score: 2607
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2607

Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
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10: gb_pr2:*
11: gb_pr3:*
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14: gb_sy:*
15: gb_un:*
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23: em_ov:*
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37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
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49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2061	79.1	4597	5	I05311	I05311 Sequence 1
2	2061	79.1	3232	5	I18496	I18496 Sequence 1
c 3	2061	79.1	3232	5	I18497	I18497 Sequence 2
4	2061	79.1	2994	5	I81465	I81465 Sequence 2
5	2061	79.1	4839	10	HUMRB1MRNA	L41870 Homo sapien
6	2061	79.1	4600	10	HUMRBA1RA	M33647 Human retin
7	2061	79.1	2994	10	HUMRBSA	M28419 Human retin
8	2010	77.1	4597	5	I09369	I09369 Sequence 1
9	1857	71.2	4740	10	HUMRBS	M15400 Human retin
10	1420	54.5	4580	5	A01444	A01444 H.sapiens D
11	279	10.7	426	11	AF043224	AF043224 Homo sapi
12	198	7.6	693	5	I09384	I09384 Sequence 17
13	198	7.6	693	9	HUMRBS15	M27858 Human retin
14	198	7.6	180388	9	HUMRETBLAS	L11910 Human retin
15	196	7.5	340	10	HUMRB1501V	L49220 Homo sapien
16	167	6.4	555	10	HUMRB4MU2	L41904 Homo sapien
17	165	6.3	935	5	I09389	I09389 Sequence 22
18	165	6.3	935	9	HUMRBS20	M27863 Human retin
19	165	6.3	420	10	HUMRB23EX	L41910 Homo sapien
20	163	6.3	252	10	HUMRB1777L	L49230 Homo sapien
21	155	5.9	555	10	HUMRB17MU2	L41924 Homo sapien
22	148	5.7	717	5	I09387	I09387 Sequence 20
23	148	5.7	717	9	HUMRBS18	L35147 Human retin
24	148	5.7	717	15	M27861	M27861 Figure 2. R
25	147	5.6	224	10	HUMRB1SDDL	L49225 Homo sapien
26	146	5.6	650	5	I09386	I09386 Sequence 19
27	146	5.6	650	9	HUMRBS17	M27860 Human retin
28	144	5.5	1310	9	HUMRBS22	M27865 Human retin
29	144	5.5	625	10	HUMRB25EX	L41912 Homo sapien
30	140	5.4	609	5	I09377	I09377 Sequence 10
31	140	5.4	609	9	HUMRBS08	L35146 Human retin
32	140	5.4	316	10	HUMRB08EX	L41896 Homo sapien
33	138	5.3	1008	5	I09370	I09370 Sequence 3
34	138	5.3	1050	9	HSRB1G	X16439 Human retin
35	138	5.3	1040	9	HUMRBS01	M27845 Human retin
36	138	5.3	480	9	HUMRBSY79	M19701 Human mutat
37	132	5.1	224	10	HUMRB1610K	L49223 Homo sapien
38	131	5.0	317	10	HUMRB17MUT	L41999 Homo sapien
39	130	5.0	704	5	I09371	I09371 Sequence 4
40	130	5.0	704	9	HUMRBS02	M27846 Human retin
41	130	5.0	410	10	HUMRB02EX	L41890 Homo sapien
42	125	4.8	350	10	HUMRB20MUU	L41996 Homo sapien
43	124	4.8	444	10	HUMRB04MUT	L41892 Homo sapien
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ALIGNMENTS

RESULT 1
I05311
LOCUS I05311 4597 bp PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent EP 0259031.
ACCESSION I05311
VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
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Query Match 79.1%; Score 2061; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
Db    724 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 783

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
Db    784 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 843

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
Db    844 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 903

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Db   1024 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1083

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
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Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
Db   1144 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1203

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
Db   1204 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1263

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
Db   1264 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1323

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
Db   1324 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1383

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
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Db   1564 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1623

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
Db   1624 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1683

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Db   1684 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1743

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
Db   1744 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1803

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
Db   1804 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1863

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Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
Db   1924 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1983

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
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Db   2044 ACCCTTTTCCAGCACACCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2103

Qy   1927 CAAATTATGATGTGTTCGATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
Db   2104 CAAATTATGATGTGTTCGATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2163

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
Db   2164 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2223

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
Db   2224 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2283

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
Db   2284 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2343

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
Db   2344 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2403

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Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
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RESULT   2
I18496
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


  Query Match             79.1%;  Score 2061;  DB 5;  Length 3232;
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Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
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Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
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Db     646 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 705

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
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Db     706 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 765

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
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Db     766 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 825

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Db     826 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 885

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Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
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Db    1426 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1485

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Db    1666 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1725

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Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
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Db    1786 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1845

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Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
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Qy    2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
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Qy    2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
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Db   2146 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2205

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Db   2266 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2325

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Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Db   2386 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2445

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RESULT   3
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


  Query Match             79.1%;  Score 2061;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
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Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
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Db   2411 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 2352

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
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Qy   1087 ATAGGATACATCTTTAAAGAGAAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2291 ATAGGATACATCTTTAAAGAGAAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 2232

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
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Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
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Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
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Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
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Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
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Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
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Db   1931 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1872

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Db   1871 GCATGGCTCTCAGATTCAGCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1812

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
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Db   1811 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1752

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
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Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
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Db   1691 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1632

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Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
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Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
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Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
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Db   1451 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1392

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Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
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Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
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Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
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Db   1031 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 972

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
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Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
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Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
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Db    791 ACCTCAAACAAGGAAGAGAAA 771
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RESULT   4
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LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
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Db    862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
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Db    982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
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Db   1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
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Db   1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
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Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
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Qy    967 ATCCAACAATTAATGATGATTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
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Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
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Db   1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
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Db   1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
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Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
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Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
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Db   1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1641

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
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Db   1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
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Db   1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
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Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Db   1822 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1881

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
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Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
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Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
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Db   2002 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
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Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
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Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
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Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
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Db   2902 ACCTCAAACAAGGAAGAGAAA 2922


RESULT   5
HUMRB1MRNA
LOCUS       HUMRB1MRNA    4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
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Query Match 79.1%; Score 2061; DB 10; Length 4600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    1987 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2046

Qy    1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
Db    2047 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2106

Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
Db    2107 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2166

Qy    1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
Db    2167 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2226

Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
Db    2227 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2286
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Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
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Db   2287 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2346

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Db   2347 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2406

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
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Db   2407 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2466

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
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Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
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Db   2527 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2586

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
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Db   2587 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2646

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
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Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Db   2707 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2766

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
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Db   2767 ACCTCAAACAAGGAAGAGAAA 2787
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RESULT   7
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
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                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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Query Match 79.1%; Score 2061; DB 10; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
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Db    862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
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Db    922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
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Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
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Db   1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
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Db   1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1221

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
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Db   1222 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
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Db   1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
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Db   1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
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Db   1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1521

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
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Db   1522 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581
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Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
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Db   1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1641

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
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Db   1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
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Db   1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
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Db   1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1821

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
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Db   1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1941

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
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Db   1942 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 2001

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
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Db   2002 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
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Db   2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 2121

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2181

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
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Db   2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2241

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
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Db   2242 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2301

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
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Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
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Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
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Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Db   2542 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2601

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
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Db   2602 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
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Db   2662 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2721

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
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Db   2722 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2781

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
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Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
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RESULT   8
I09369
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ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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ORIGIN


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Db     784 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 843

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
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Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
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Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
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Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
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Db    1024 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1083

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
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Db    1084 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1143
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Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
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Db   1144 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1203

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
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Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
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Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
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Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
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Db   1444 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1503

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1563

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
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Db   1564 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1623

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
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Db   1624 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1683

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Db   1684 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1743

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
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Db   1744 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1803

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
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Db   1804 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1863

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1923

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
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Db   1924 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1983

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
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Db   1984 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2043

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
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Db   2044 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2103

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
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Db   2104 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2163

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
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Db   2164 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2223

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
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Db   2224 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2283

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
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Db   2284 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2343

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Db   2344 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2403

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2463

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2464 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2523

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   2584 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGAAGGA 2643

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2644 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2703

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2763

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2764 ACCTCAAACAAGGAAGAGAAA 2784
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RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
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                MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
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                IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.
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Query Match 71.2%; Score 1857; DB 10; Length 4740;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2057; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
Db     862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
Db     922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
Db     982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
Db     1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
Db     1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATCGAAGATTATTTTTGGATCATGATAAA 1161

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
Db     1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1221

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
Db     1222 CTTGATGAAGAGGTGAATATAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
Db     1282 ATCCAACAATTAATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

Qy     1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
Db     1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy     1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
Db     1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy     1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
Db     1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1521

Qy     1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
Db     1522 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

Qy     1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
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Qy     1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
Db     1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701

Qy     1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
Db     1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

Qy     1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
Db     1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1821

Qy     1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Qy     1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
Db     1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1941

Qy     1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
Db     1942 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 2001

Qy     1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
Db     2002 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

Qy     1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
Db     2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 2121

Qy     1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
Db     2122 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2181

Qy     1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
Db     2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2241

Qy     1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
Db     2242 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2301

Qy     1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
Db     2302 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2361

Qy     2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
Db     2362 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2421

Qy     2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
Db     2422 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2481

Qy     2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Db   2482 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2541

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286

Db   2542 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2601

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346

Db   2602 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406

Db   2662 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2721

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466

Db   2722 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2781

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526

Db   2782 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2841

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586

Db   2842 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2901

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607

Db   2902 ACCTCAAACAAGGAAGAGAAA 2922


RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
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BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match           54.5%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

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Db    752 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    649 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 708

Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    709 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 768

Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    769 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 828

Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy    829 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 888

Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy    889 ACACCACGAAAAAGTAAGCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 948

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Qy    949 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1008

Db   1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy   1009 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1068

Db   1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231

Qy   1069 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1128

Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

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Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1309 GCCACATATAGCAGAAGTAGATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1368

Db   1471 GCCACATATAGCAGAAGTAGATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy   1369 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1428

Db   1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

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Qy   1489 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1548

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Qy   1549 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1608

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Qy   1609 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1668

Db   1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy   1669 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1728

Db   1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy   1729 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1788

Db   1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy   1789 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1848

Db   1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010
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Qy   1849 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy   1909 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy   1969 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy   2029 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2088
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy   2089 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy   2149 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2208
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Db   2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy   2209 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2268
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Db   2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy   2269 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2328
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Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2329 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2388
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Db   2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2389 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2448
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Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2449 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2508
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Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2509 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2568
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Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2569 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2607
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Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
AF043224
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
     exon            <1. .7
                     /gene="RB1"
                     /number=5
     CDS             <1. .137
                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
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     exon            77. .192
                     /gene="RB1"
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     exon            193. .312
                     /gene="RB1"
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     exon            313. .350
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     exon            351. .418
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                     /gene="RB1"
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BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN
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Qy    264 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     75 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 134

Qy    324 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 194

Qy    384 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 254

Qy    444 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 314

Qy    504 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGAT 542
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Db    315 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGAT 353
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RESULT  12
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.7e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1322 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1382 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1442 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1501
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1502 CCCTTGCATGGCTCTCAG 1519
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  13
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
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     exon            250. .446
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                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN

  Query Match             7.6%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1322 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1382 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1442 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1501
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Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1502 CCCTTGCATGGCTCTCAG 1519
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Db    430 CCCTTGCATGGCTCTCAG 447


RESULT  14
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
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  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
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                     /number=1
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                     61730. .61807,64330. .64439,65364. .65441,70242. .70329,
                     73753. .73869,76430. .76486,76889. .76920,77001. .77077,
                     78083. .78279,149998. .150116,153208. .153353,156693. .156838,
                     160730. .160834,161997. .162110,162204. .162367,
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                     /protein_id="AAA53483.1"
                     /db_xref="GI:292421"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
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                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
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     intron          39562. .41925
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     exon            44668. .44706
                     /number=5
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     intron          45867. .56852
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  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1322 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1381
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Db  78083 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 78142

Qy   1382 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1441
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Db  78143 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 78202

Qy   1442 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1501
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Db  78203 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 78262

Qy   1502 CCCTTGCATGGCTCTCAG 1519
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Db  78263 CCCTTGCATGGCTCTCAG 78280


RESULT  15
HUMRB1501V
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES              Location/Qualifiers
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ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 5.3e-94;
  Matches  196;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Search completed: February 13, 2000, 12:02:00
Job time: 19016 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 17:15:09 ; Search time 404.96 Seconds
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Searched: 214294 seqs, 59861208 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	6	2061	79.1	2995	4	US-08-959-638-7	Sequence 7, Appli
	7	2061	79.1	2994	4	US-08-482-627-4	Sequence 4, Appli
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ALIGNMENTS

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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


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; Sequence 2, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.

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;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             79.1%;  Score 2061;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
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Db    2471 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 2412

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2411 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 2352

Qy    1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2351 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 2292

Qy    1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2291 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 2232

Qy    1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2231 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 2172

Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2171 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 2112

Qy    1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2111 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 2052

Qy    1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2051 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1992

Qy    1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1991 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1932

Qy    1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1931 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1872

Qy    1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1871 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1812

Qy    1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1811 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1752

Qy    1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1751 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1692

Qy    1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1691 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1632

Qy    1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1631 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1572

Qy    1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1571 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1512

Qy    1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1511 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1452

Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1451 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1392

Qy    1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1391 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1332

Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1331 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 1272

Qy    2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
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Db   1271 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 1212

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 1152

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 1092

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 1032

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 972

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 912

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 852

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 792

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db    791 ACCTCAAACAAGGAAGAGAAA 771


RESULT   3
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match             79.1%;  Score 2061;  DB 2;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1221

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1222 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
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Db   1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1521

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1522 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1641

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761
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Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1821

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1822 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1881

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1941

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1942 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 2001

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2002 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 2121

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2181

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2241

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2301

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2361

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2421

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2422 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2481

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2482 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2541

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2542 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2601

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2602 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2662 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2721

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2722 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2781

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2782 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2841

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2842 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2901

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2902 ACCTCAAACAAGGAAGAGAAA 2922


RESULT   4
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


  Query Match             79.1%;  Score 2061;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 465

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 525

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    526 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 585

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 645

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 705

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 765

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 825

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 885

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 945

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1005

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1065

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1125

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1185

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1245

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1305

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1365

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Db   1366 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1425

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1485

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
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Db   1486 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1545

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1605

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1665
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Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1725

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1785

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1845

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1905

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 1965

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1966 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2025

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2085

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2145

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2205

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2265

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2325

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2385

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Db   2386 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2445

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2446 ACCTCAAACAAGGAAGAGAAA 2466
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RESULT   5
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
```

```
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/470,091
;       FILING DATE:  JUN-16-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match             79.1%;  Score 2061;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2831 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 2772

Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2771 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 2712

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2711 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 2652

Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2651 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 2592

Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2591 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 2532

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2531 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 2472

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2471 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 2412

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2411 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 2352

Qy    1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2351 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 2292

Qy    1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2291 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 2232

Qy    1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2231 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 2172

Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2171 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 2112

Qy    1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2111 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 2052

Qy    1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2051 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1992

Qy    1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1991 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1932

Qy    1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1931 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1872

Qy    1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1871 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1812

Qy    1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1811 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1752

Qy    1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1751 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1692

Qy    1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1691 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1632

Qy    1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1631 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1572

Qy    1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1571 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1512

Qy    1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1511 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1452

Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1451 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1392

Qy    1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1391 AAAATCATTGTAACAGCATAGAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1332

Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1331 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 1272

Qy    2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1271 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 1212

Qy    2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Db   1211 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 1152

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 1092

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 1032

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 972

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 912

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 852

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Db    851 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 792

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db    791 ACCTCAAACAAGGAAGAGAAA 771


RESULT   6
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


  Query Match             79.1%;  Score 2061;  DB 4;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
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Db    862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
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Db    982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
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Db   1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
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Db   1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
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Db   1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1221

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
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Db   1222 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
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Db   1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
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Db   1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
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Db   1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1521

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
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Db   1522 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
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Db   1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1641

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701
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Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
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Db   1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
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Db   1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1821

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Db   1822 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1881

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
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Db   1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1941

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1942 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 2001

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
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Db   2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 2121

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
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Db   2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2241

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2301

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2361

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Db   2362 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2421

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Db   2422 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2481

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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Db   2482 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2541

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
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Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
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Db   2602 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

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Db   2662 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2721

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2722 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2781

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2782 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2841

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
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Db   2902 ACCTCAAACAAGGAAGAGAAA 2922


RESULT   7
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


  Query Match             79.1%;  Score 2061;  DB 4;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
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Db    862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
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Db    922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
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Db    982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786

Db   1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

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Db   1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906

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Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966

Db   1222 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026

Db   1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

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Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626

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Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046

Db   2302 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2361

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106

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Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526

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Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586

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Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607

Db   2902 ACCTCAAACAAGGAAGAGAAA 2922


RESULT   8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
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;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


  Query Match             77.1%;  Score 2010;  DB 6;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2060;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1221

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1222 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

Qy    1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy    1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy    1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1521

Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1522 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

Qy    1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1641

Qy    1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701

Qy    1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

Qy    1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1821

Qy    1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1822 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1881

Qy    1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1941

Qy    1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1942 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 2001

Qy    1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2002 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

Qy    1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 2121

Qy    1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2122 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2181

Qy    1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2241

Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2242 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2301

Qy    1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2302 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2361

Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2362 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2421

Qy    2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2422 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2481

Qy    2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2482 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2541

Qy    2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2542 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2601

Qy    2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2602 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

Qy    2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2662 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2721

Qy    2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    2722 AGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGGA 2781

Qy    2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2782 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2841

Qy    2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2842 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2901

Qy    2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db    2902 ACCTCAAACAAGGAAGAGAAA 2922


RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.1%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00045;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2524 CTGGCAGAAATGACTTCTACTCGAACAC 2551
           ||||||||||||||||||||||||||||
Db       1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-08-253-155A-92
; Sequence 92, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-92


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCCGCCCAAAACCCCCCGAAAAACG 27
           |||||||||||||||||||||||||
Db      16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  11
US-08-625-209A-21
; Sequence 21, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-21


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCCGCCCAAAACCCCCCGAAAAACG 27
           |||||||||||||||||||||||||
Db      16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  12
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     982 ATGATTTTAAATTCAGCAAGTG 1003
           ||||||||||||||||||||||
Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  13
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
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;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     982 ATGATTTTAAATTCAGCAAGTG 1003
           ||||||||||||||||||||||
Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  14
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2282 CAACACCAACAAAAATGACTCC 2303
           ||||||||||||||||||||||
Db      22 CAACACCAACAAAAATGACTCC 1


RESULT  15
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
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Qy    2282 CAACACCAACAAAAATGACTCC 2303
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Search completed: February 13, 2000, 17:16:09
Job time: 9249 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 12:02:00 ; Search time 14294.3 Seconds
(without alignments)
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Title: US-09-026-459A-48_COPY_7_2619
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Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

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49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1885	72.1	4597	5	I05311	I05311 Sequence 1
2	1885	72.1	3232	5	I18496	I18496 Sequence 1
c 3	1885	72.1	3232	5	I18497	I18497 Sequence 2
4	1885	72.1	2994	5	I81465	I81465 Sequence 2
5	1885	72.1	4839	10	HUMRB1MRNA	L41870 Homo sapien
6	1885	72.1	4600	10	HUMRBA1RA	M33647 Human retin
7	1885	72.1	2994	10	HUMRBSA	M28419 Human retin
8	1834	70.2	4597	5	I09369	I09369 Sequence 1
9	1684	64.4	4740	10	HUMRBS	M15400 Human retin
10	1349	51.6	4580	5	A01444	A01444 H.sapiens D
11	338	12.9	426	11	AF043224	AF043224 Homo sapi
12	198	7.6	693	5	I09384	I09384 Sequence 17
13	198	7.6	693	9	HUMRBS15	M27858 Human retin
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18	165	6.3	935	9	HUMRBS20	M27863 Human retin
19	165	6.3	420	10	HUMRB23EX	L41910 Homo sapien
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25	147	5.6	224	10	HUMRB1SDDL	L49225 Homo sapien
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34	132	5.1	224	10	HUMRB1610K	L49223 Homo sapien
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent EP 0259031.
ACCESSION I05311
VERSION I05311.1 GI:591083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4597)
AUTHORS Dryja,T.P. and Friend,S.

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  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
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BASE COUNT     1489 a    842 c    812 g   1454 t
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Query Match 72.1%; Score 1885; DB 5; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
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Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
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Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
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VERSION     I18496.1  GI:1598851
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
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  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
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Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
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Db   1542 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1601

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1602 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1661

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1662 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1721

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1722 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1781

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1782 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1841

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1842 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1901

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1902 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1961

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1962 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2021

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2022 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2081

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2082 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2141

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2142 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2201

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2202 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2261

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2262 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2321

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2322 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2381

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2382 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2441
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Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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Db   2442 GGATACCTCAAACAAGGAAGAGAAA 2466


RESULT   3
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


  Query Match             72.1%;  Score 1885;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2655 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 2596

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2595 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 2536

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2535 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 2476

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2475 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 2416

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2415 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 2356

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2355 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 2296

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2295 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 2236

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2235 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 2176

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2175 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 2116

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2115 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 2056

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2055 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1996

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1995 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1936

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1935 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1876

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1875 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1816

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1815 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1756

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1755 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1696

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1695 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1636

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1635 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1576

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1575 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1516

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1515 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1456

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1455 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1396

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1395 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1336

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1335 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1276

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1275 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 1216

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1215 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 1156

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1155 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 1096

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1095 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 1036

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1035 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 976

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    975 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 916
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Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    915 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 856

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    855 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 796

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db    795 GGATACCTCAAACAAGGAAGAGAAA 771


RESULT   4
I81465
LOCUS       I81465       2994 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
                     /organism="unknown"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


  Query Match             72.1%;  Score 1885;  DB 5;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
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Db   1038 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 1097

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1157

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1217

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1277

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1337

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1397

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1457

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db   1458 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1517

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1577

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1637

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db   1638 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1697

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1757

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1817

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1877

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1937

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1997

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 2057

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 2117

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2177

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2237

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2238 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2297

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2298 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2357

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2358 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2417

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Db   2418 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2477

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db   2478 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2537

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RESULT 5
HUMRB1MRNA
LOCUS HUMRB1MRNA 4839 bp mRNA PRI 05-MAY-1995
DEFINITION Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and mutations.
ACCESSION L41870
VERSION L41870.1 GI:793994
KEYWORDS retinoblastoma protein; retinoblastoma susceptibility.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS McGee,T.L., Yandell,D.W. and Dryja,T.P.
TITLE Structure and partial genomic sequence of the human retinoblastoma susceptibility gene
JOURNAL Gene 80 (1), 119-128 (1989)
MEDLINE 90006771
REFERENCE 2 (sites)
AUTHORS Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
TITLE Detection of heterozygous mutations in the RB1 gene in retinoblastoma patients using single-strand conformation polymorphism analysis and polymerase chain reaction sequencing
JOURNAL Oncogene 7 (7), 1445-1451 (1992)
MEDLINE 92319557
REFERENCE 3 (sites)
AUTHORS Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
TITLE Oncogenic point mutations in exon 20 of the RB1 gene in families showing incomplete penetrance and mild expression of the retinoblastoma phenotype
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
MEDLINE 92335261
REFERENCE 4 (sites)
AUTHORS Onadim,Z., Hogg,A. and Cowell,J.K.
TITLE Mechanisms of oncogenesis in patients with familial retinoblastoma
JOURNAL Br. J. Cancer 68 (5), 958-964 (1993)
MEDLINE 94031584
REFERENCE 5 (sites)
AUTHORS Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
TITLE Molecular mechanisms of oncogenic mutations in tumors from patients with bilateral and unilateral retinoblastoma
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
MEDLINE 93348271
REFERENCE 6 (sites)
AUTHORS Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J., Cowell,J.K. and Kaye,F.J.
TITLE Partial inactivation of the RB product in a family with incomplete penetrance of familial retinoblastoma and benign retinal tumors
JOURNAL Oncogene 9 (5), 1321-1326 (1994)
MEDLINE 94203660
COMMENT Mutation data provided by Dr. B.L.Gallie,

Hospital for Sick Children
555 Univ. Ave.
Toronto ONT W5G 1X8
Canada
Ph: 416 813-5868
FAX: 416 813-4989
E-mail: brenda@hafiz.eric.on.ca.

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RESULT   6
HUMRBA1RA
LOCUS       HUMRBA1RA    4600 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma associated (RB1) mRNA, complete cds.
ACCESSION   M33647 J02994
VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
SOURCE      Homo sapiens (clone: p4.7R) cDNA to mRNA.
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
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COMMENT     Draft entry and computer-readable copy of sequence for [1] kindly
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ORIGIN


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Qy     789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
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Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
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Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
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Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
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Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
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HUMRBSA
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DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
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VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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BASE COUNT 974 a 618 c 593 g 809 t
ORIGIN

Query Match 72.1%; Score 1885; DB 10; Length 2994;
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Matches 1885; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
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RESULT   8
I09369
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SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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ORIGIN


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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1559

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1619

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
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Db   1620 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1679

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1739

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
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Db   1740 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1799

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1859

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1919

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1979

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2039

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2099

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2159

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2219

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
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Db   2220 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2279

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Db   2280 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2339

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db   2340 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2399

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2459

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2519

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2579
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Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
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Db   2580 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGA 2639

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2699

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2759

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2760 GGATACCTCAAACAAGGAAGAGAAA 2784


RESULT   9
HUMRBS
LOCUS       HUMRBS       4740 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
            provided by R.Bookstein, 27-APR-1987.
FEATURES             Location/Qualifiers
     source          1. .4740
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                     /db_xref="taxon:9606"
                     /clone="RB-[1,5]"
                     /dev_stage="foetus"
                     /tissue_type="retina"
                     /map="13q14.2"
     mRNA            <1. .4740
                     /note="rbs mRNA"
     gene            139. .2925
                     /gene="RB1"
     CDS             139. .2925
                     /gene="RB1"
                     /note="retinoblastoma susceptibility protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA69807.1"
                     /db_xref="GI:190959"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPEEDPEQDSGPEDLPL
                     VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
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                     LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
                     MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKQLENDTRIIEV
                     LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLKNKDLDRR
                     LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIIPPHTPVRTVMNTIQQLMMILNSA
                     SDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGV
                     RLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDS
                     GTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSD
                     SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                     TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWT
                     LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
                     RVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
                     IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


  Query Match             64.4%;  Score 1684;  DB 10;  Length 4740;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1784;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    828 AAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAAC 887
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1137 AAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAAC 1196

Qy    888 ACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACAC 947
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   1197 ACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATATAATTCCTCCACACAC 1256

Qy    948 TCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAG 1007
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   1257 TCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCTGCAAG 1316

Qy   1008 TGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGA 1067
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1317 TGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGA 1376

Qy   1068 AAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGC 1127
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1377 AAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGC 1436

Qy   1128 TGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTA 1187
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1437 TGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTA 1496

Qy   1188 TTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTT 1247
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1497 TTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTT 1556

Qy   1248 TAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGT 1307
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1557 TAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGT 1616

Qy   1308 TGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTC 1367
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1617 TGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTC 1676

Qy   1368 TTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGA 1427
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1677 TTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGA 1736

Qy   1428 AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATG 1487
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1737 AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATG 1796

Qy   1488 TGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTAT 1547
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Db   1797 TGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTAT 1856

Qy   1548 TAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAA 1607
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Db   1857 TAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAA 1916

Qy   1608 TCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCC 1667
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1917 TCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCC 1976

Qy   1668 AAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAAC 1727
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1977 AAAGAAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAAC 2036
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Qy   1728 CTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAA 1787
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2037 CTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAA 2096

Qy   1788 AGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCA 1847
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2097 AGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCA 2156

Qy   1848 CCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGA 1907
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2157 CCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGA 2216

Qy   1908 ACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAA 1967
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2217 ACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAA 2276

Qy   1968 AGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCA 2027
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2277 AGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCA 2336

Qy   2028 TGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTAT 2087
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2337 TGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTAT 2396

Qy   2088 AGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTC 2147
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Db   2397 AGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTC 2456

Qy   2148 CACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCC 2207
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Db   2457 CACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCC 2516

Qy   2208 TAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATA 2267
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Db   2517 TAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATA 2576

Qy   2268 TAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGT 2327
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Db   2577 TAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGT 2636

Qy   2328 ATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATG 2387
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Db   2637 ATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATG 2696

Qy   2388 TAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAA 2447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2697 TAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAA 2756

Qy   2448 AAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 2507
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Db   2757 AAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 2816

Qy   2508 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAA 2567
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2817 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAA 2876

Qy   2568 GCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||||||||||||||||||||||
Db   2877 GCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT  10
A01444
LOCUS       A01444       4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
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BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN
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  Query Match           51.6%;  Score 1349;  DB 5;  Length 4580;
  Best Local Similarity  99.6%;  Pred. No. 0;
  Matches 1839;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;

Qy    768 GGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGC 827
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Db    925 GGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGC 984

Qy    828 AAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAAC 887
          |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db    985 AAGATTATTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAAC 1044

Qy    888 ACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACAC 947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045 ACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACAC 1104

Qy    948 TCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAG 1007
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Db   1105 TCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAG 1164

Qy   1008 TGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGA 1067
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 TGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGA 1224

Qy   1068 AAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGC 1127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 AAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGC 1284

Qy   1128 TGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTA 1187
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 TGT-GGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTA 1343

Qy   1188 TTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTT 1247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 TTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTT 1403

Qy   1248 TAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGT 1307
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Db   1404 TAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGT 1463

Qy   1308 TGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTC 1367
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Db   1464 TGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTC 1523

Qy   1368 TTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGA 1427
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Db   1524 TTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGA 1583

Qy   1428 AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATG 1487
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Db   1584 AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATG 1643

Qy   1488 TGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTAT 1547
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Db   1644 TGAACATCGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTAT 1703

Qy   1548 TAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAA 1607
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Qy   1608 TCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCC 1667
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Qy   1668 AAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAAC 1727
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Qy   1728 CTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAA 1787
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Qy   1788 AGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCA 1847
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Db   1944 AGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCA 2003

Qy   1848 CCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGA 1907
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Db   2004 CCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGA 2063

Qy   1908 ACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAA 1967
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Db   2064 ACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAA 2123

Qy   1968 AGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCA 2027
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Db   2124 AGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCA 2183

Qy   2028 TGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTAT 2087
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Db   2184 TGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTAT 2243

Qy   2088 AGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTC 2147
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2244 AGTGTTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTC 2303

Qy   2148 CACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCC 2207
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Db   2304 CACCAGGCCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCC 2362

Qy   2208 TAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATA 2267
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Db   2363 TAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATA 2422

Qy   2268 TAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGT 2327
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Db   2423 TAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGT 2482

Qy   2328 ATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATG 2387
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Qy   2388 TAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAA 2447
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Db   2543 TAACAGCGACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAA 2602

Qy   2448 AAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 2507
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Db   2603 AAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 2662

Qy   2508 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAA 2567
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Db   2663 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAA 2722

Qy   2568 GCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2613
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Db   2723 GCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768


RESULT 11
AF043224
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LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
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                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
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                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
                     "
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                     /gene="RB1"
                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
                     /gene="RB1"
                     /number=5
     exon            351. .418
                     /gene="RB1"
                     /number=6
     exon            419. .>426
                     /gene="RB1"
                     /number=7
BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN


  Query Match           12.9%;  Score 338;  DB 11;  Length 426;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-170;
  Matches  338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    264 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 323
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Db      75 GGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGT 134

Qy     324 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     135 TGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 194

Qy     384 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     195 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 254

Qy     444 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     255 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 314

Qy     504 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 563
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     315 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 374

Qy     564 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 601
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Db     375 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAG 412


RESULT  12
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.6%;  Score 198;  DB 5;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy    1388 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1447
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Db     310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy    1448 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1507
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Db     370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy    1508 CCCTTGCATGGCTCTCAG 1525
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Db     430 CCCTTGCATGGCTCTCAG 447


RESULT  13
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
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     exon            250. .446
                     /note="retinoblastoma susceptibility gene"
                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.6%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-95;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1328 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1387
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Db     250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy    1388 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1447
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Db     310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy    1448 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1507
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Db     370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy    1508 CCCTTGCATGGCTCTCAG 1525
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Db     430 CCCTTGCATGGCTCTCAG 447


RESULT  14
HUMRETBLAS
LOCUS       HUMRETBLAS 180388 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility gene exons 1-27, complete cds.
ACCESSION   L11910
VERSION     L11910.1  GI:292420
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma gene;
            retinoblastoma protein; retinoblastoma susceptibility; tumor
            supressor gene.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
            retinoblastoma and osteosarcoma
  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
REFERENCE   2  (sites)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
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          Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   5  (sites)
  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
            retinoblastoma gene
  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
REFERENCE   6  (bases 1 to 180388)
  AUTHORS   Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R., Tucker,S.,
            Yandell,D.W. and Dryja,T.P.
  TITLE     Complete genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Genomics 17 (3), 535-543 (1993)
  MEDLINE   94063891
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     satellite       102921. .102959
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     intron          150117. .153207
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     exon            153208. .153353
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     intron          153354. .156692
                     /number=19
     exon            156693. .156838
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     satellite       156895. .156976
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                     /number=21
     intron          160835. .161996
                     /number=21
     exon            161997. .162110
                     /number=22
     intron          162111. .162203
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     intron          162368. .170371
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Qy   1328 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  78083 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 78142

Qy   1388 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1447
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  78143 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 78202

Qy   1448 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1507
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Db  78203 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 78262

Qy   1508 CCCTTGCATGGCTCTCAG 1525
           ||||||||||||||||||
Db  78263 CCCTTGCATGGCTCTCAG 78280


RESULT  15
HUMRB1501V
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES              Location/Qualifiers
     source           1. .340
                      /organism="Homo sapiens"
                      /isolate="Patient G364"
                      /db_xref="taxon:9606"
                      /cell_type="leukocyte"
                      /map="13q14.2"
     gene             1. .340
                      /gene="RB1"
     intron           <1. .64
                      /gene="RB1"
                      /note="G00-118-734"
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     mutation         66. .67
                      /gene="RB1"
                      /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                      premature stop at AA 518; G00-118-734"
     intron           261. .>340
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                      /note="G00-118-734"
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BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.9e-94;
  Matches  196;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1330 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 125

Qy   1390 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 185

Qy   1450 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 245

Qy   1510 CTTGCATGGCTCTCAG 1525
           ||||||||||||||||
Db    246 CTTGCATGGCTCTCAG 261


Search completed: February 13, 2000, 12:06:52
Job time: 19308 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:55:48 ; Search time 9092.07 Seconds
(without alignments)
1085.101 Million cell updates/sec

Title: US-09-026-459A-48_COPY_7_2619
Perfect score: 2613
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2613

Scoring table: OLIGO_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	476	18.2	572	64	AL120941	AL120941 DKFZp762D
c	2	352	13.5	415	51	AI745644	AI745644 tr24b06.x
c	3	348	13.3	411	51	AI745643	AI745643 tr24b05.x
	4	257	9.8	285	33	AA382103	AA382103 EST95270
	5	204	7.8	304	32	AA361277	AA361277 EST70529
c	6	181	6.9	571	41	AI074792	AI074792 oy03a06.s
c	7	161	6.2	329	36	AA664676	AA664676 nu64f09.s

	8	156	6.0	456	30	AA210875 AA210875 zr88f11.r
c	9	132	5.1	171	38	AA765882 AA765882 oa14a06.s
	10	114	4.4	386	24	N25402 N25402 yx40c12.r1
	11	113	4.3	457	24	N41391 N41391 yw70g06.r1
	12	89	3.4	152	22	R57845 R57845 F6142 Fetal
	13	82	3.1	525	30	AA258255 AA258255 zr59g04.r
c	14	53	2.0	349	20	T24020 T24020 seq2177 3HF
	15	48	1.8	397	22	R70325 R70325 yj81b10.r1
	16	48	1.8	522	28	AA072780 AA072780 mm76a05.r
	17	42	1.6	986	89	AQ901300 AQ901300 HS_5234_A
	18	38	1.5	472	46	AA955457 AA955457 UI-R-A1-e
c	19	35	1.3	914	38	AA763411 AA763411 vw54a04.r
c	20	35	1.3	871	38	AA763485 AA763485 vw54h01.r
	21	34	1.3	427	37	AA709628 AA709628 vv41c11.r
c	22	33	1.3	462	48	AI606529 AI606529 vb27g08.y
	23	33	1.3	832	49	AI646038 AI646038 vw54a10.x
	24	33	1.3	709	49	AI646097 AI646097 vw54h07.x
	25	33	1.3	575	49	AI662832 AI662832 vb27g08.x
	26	31	1.2	284	59	AV111279 AV111279
	27	31	1.2	174	72	AV302462 AV302462
	28	29	1.1	615	40	AA959836 AA959836 vw54h01.s
c	29	26	1.0	405	39	AA861150 AA861150 ak36a12.s
	30	26	1.0	529	40	AA959709 AA959709 vw54a04.s
	31	25	1.0	356	41	AI020392 AI020392 ub17a05.r
c	32	24	0.9	492	33	AA396353 AA396353 vb27g08.r
c	33	22	0.8	440	33	AA440741 AA440741 LD15614.5
c	34	22	0.8	332	44	AI259982 AI259982 LP03562.5
	35	22	0.8	586	59	AI770926 AI770926 606063D04
c	36	21	0.8	640	38	AA752076 AA752076 96AS1023
	37	21	0.8	219	38	AA752355 AA752355 96GS0852
c	38	21	0.8	501	74	AV391000 AV391000 AV391000
c	39	20	0.8	439	21	R12275 R12275 yf40f10.r1
c	40	20	0.8	424	21	R21339 R21339 yg50d05.r1
c	41	20	0.8	372	21	R21352 R21352 yg50f05.r1
c	42	20	0.8	351	21	T78368 T78368 yc99g02.r1
c	43	20	0.8	478	22	H06003 H06003 yl76c05.r1
c	44	20	0.8	299	36	AA618388 AA618388 nq18h09.s
	45	20	0.8	574	103	AQ498524 AQ498524 HS_5120_B

ALIGNMENTS

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RESULT   1
AL120941
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


  Query Match           18.2%;  Score 476;  DB 64;  Length 572;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-205;
  Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1297 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1356
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Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1357 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1416
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Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1417 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1476
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Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1477 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1537 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1597 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1656
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Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1657 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1716
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Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1717 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476


RESULT   2
AI745644/c
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
```

```
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


  Query Match             13.5%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-149;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1967 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 2026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy   2027 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy   2087 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy   2147 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy   2207 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2266
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Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy   2267 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2318
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Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


  Query Match             13.3%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-147;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1971 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2030
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy   2031 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2090
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy   2091 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy   2151 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy   2211 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy   2271 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             9.8%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-106;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1761 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy    1821 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy    1881 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy    1941 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy    2001 TGTAACAGCATACAAGG 2017
           ||||||||||||||||
Db     241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             7.8%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 5.4e-82;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1570 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy    1630 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1690 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1749
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1750 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1810 CGGCTAAATACACTT 1824
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AI074792/c
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


  Query Match             6.9%;  Score 181;  DB 41;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-71;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     85 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 309

Qy    145 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 249

Qy    205 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 189

Qy    265 G 265
          |
Db    188 G 188


RESULT   7
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbtp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.2%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-62;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1365 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1425 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1485 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1525
          |||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   8
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.0%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-60;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2458 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2518 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2578 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||||||||||||
Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180
```

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RESULT   9
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.1%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 3e-49;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1160 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy   1220 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1280 TGTCTTTATTGG 1291
          ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT  10
N25402
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.4%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2413 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60

Qy   2473 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  11
N41391
LOCUS       N41391         457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g     128 t
ORIGIN


  Query Match             4.3%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-41;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329
```

```
RESULT  12
R57845
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN
```

```
  Query Match             3.4%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-30;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2183 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy   2243 ATATTTCACCCCTGAAGAGTCCATATAAA 2271
          |||||||||||||||||||||||||||||
Db     61 ATATTTCACCCCTGAAGAGTCCATATAAA 89
```

```
RESULT  13
AA258255
LOCUS       AA258255      525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN
```

```
  Query Match             3.1%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-26;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2532 GGCAGAAATGACTTCTAGTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCAGAAATGACTTCTAGTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy   2592 TACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||
Db     61 TACCTCAAACAAGGAAGAGAAA 82
```

```
RESULT  14
T24020/c
LOCUS       T24020        349 bp    mRNA            EST       01-AUG-1994
DEFINITION  seq2177 3HFLSK20 Homo sapiens cDNA clone 3HFLSK20-63 3', mRNA
            sequence.
ACCESSION   T24020
VERSION     T24020.1  GI:520260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   Soares,M.B.
  TITLE     Human infant brain library b4HB3MA cDNAs
```

```
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Bento Soares
            Columbia University
            Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
            10032
            Tel: 2129602313
            Fax: 2127813577
            Email: cuc@cuccfa.ccc.columbia.edu
            antisense Kanamycin
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="3HFLSK20-63"
                     /clone_lib="3HFLSK20"
                     /lab_host="E. coli"
                     /note="Vector: Lafmid K; Site_1: Not I; Site_2: EcoR I;
                     cDNA from polyA+ RNA from human fetal liver + spleen. 20
                     weeks post-conception "
BASE COUNT       98 a     73 c     59 g    118 t      1 others
ORIGIN


  Query Match             2.0%;  Score 53;  DB 20;  Length 349;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-13;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    213 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 297


RESULT  15
R70325
LOCUS       R70325        397 bp    mRNA            EST       01-JUN-1995
DEFINITION  yj81b10.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:155131 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   R70325
VERSION     R70325.1  GI:843842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 803
            High quality sequence stops: 324
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 803   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1. .397
                     /organism="Homo sapiens"
                     /db_xref="GDB:569832"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155131"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      130 a     47 c     71 g    147 t      2 others
ORIGIN


  Query Match             1.8%;  Score 48;  DB 22;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-11;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    136 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 183
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 334


Search completed: February 13, 2000, 16:55:55
Job time: 15537 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 17:16:09 ; Search time 404.96 Seconds
(without alignments)
772.508 Million cell updates/sec

Title: US-09-026-459A-48_COPY_7_2619
Perfect score: 2613
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2613

Scoring table: OLIGO_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1885	72.1	3232	1	US-08-038-760-1	Sequence 1, Appli
c	2	1885	72.1	3232	1	US-08-038-760-2	Sequence 2, Appli
	3	1885	72.1	2994	2	US-08-204-329-2	Sequence 2, Appli
	4	1885	72.1	3232	4	US-08-470-091-1	Sequence 1, Appli
c	5	1885	72.1	3232	4	US-08-470-091-2	Sequence 2, Appli
	6	1885	72.1	2995	4	US-08-959-638-7	Sequence 7, Appli
	7	1885	72.1	2994	4	US-08-482-627-4	Sequence 4, Appli
	8	1834	70.2	2994	6	PCT-US94-10357-1	Sequence 1, Appli
	9	28	1.1	28	4	US-08-859-998-1097	Sequence 1097, Ap
	10	25	1.0	40	2	US-08-253-155A-92	Sequence 92, Appl
	11	25	1.0	40	2	US-08-625-209A-21	Sequence 21, Appl
	12	22	0.8	52	1	US-07-826-928A-15	Sequence 15, Appl
	13	22	0.8	52	1	US-07-826-928A-36	Sequence 36, Appl
c	14	22	0.8	22	1	US-08-271-946A-22	Sequence 22, Appl
c	15	22	0.8	22	1	US-08-271-942A-22	Sequence 22, Appl
c	16	22	0.8	22	6	PCT-US95-08604-22	Sequence 22, Appl
c	17	22	0.8	22	6	PCT-US95-08606-22	Sequence 22, Appl
	18	20	0.8	48	1	US-07-826-928A-13	Sequence 13, Appl
	19	20	0.8	633	1	US-08-234-783-1	Sequence 1, Appli
	20	20	0.8	633	1	US-08-456-907-1	Sequence 1, Appli
c	21	20	0.8	44	2	US-08-253-155A-93	Sequence 93, Appl
c	22	20	0.8	44	2	US-08-625-209A-22	Sequence 22, Appl
	23	20	0.8	633	6	PCT-US95-05523-1	Sequence 1, Appli
	24	19	0.7	2095	2	US-08-336-408B-3	Sequence 3, Appli
c	25	19	0.7	2952	2	US-08-306-691B-54	Sequence 54, Appl
c	26	19	0.7	276	3	US-08-712-948-3	Sequence 3, Appli
c	27	19	0.7	3509	3	US-08-817-436A-1	Sequence 1, Appli
c	28	19	0.7	6530	4	US-08-146-930-1	Sequence 1, Appli
	29	19	0.7	2095	6	PCT-US91-00399-3	Sequence 3, Appli
c	30	19	0.7	6530	6	PCT-US93-03993-1	Sequence 1, Appli
c	31	19	0.7	4008	6	PCT-US95-11808-5	Sequence 5, Appli
c	32	18	0.7	37	1	US-07-826-928A-14	Sequence 14, Appl
c	33	18	0.7	37	1	US-07-826-928A-35	Sequence 35, Appl
	34	18	0.7	3879	1	US-08-530-010-1	Sequence 1, Appli
	35	18	0.7	3879	2	US-08-484-101B-1	Sequence 1, Appli
c	36	18	0.7	18	3	US-08-511-836C-2	Sequence 2, Appli
c	37	18	0.7	2850	3	US-08-224-482-7	Sequence 7, Appli
c	38	18	0.7	747	3	US-08-679-765-2	Sequence 2, Appli
	39	18	0.7	4534	4	US-08-935-450-1	Sequence 1, Appli
c	40	18	0.7	747	4	US-09-196-525-2	Sequence 2, Appli
c	41	18	0.7	3760	4	US-08-724-354D-1	Sequence 1, Appli
c	42	17	0.7	2009	1	US-07-958-222A-1	Sequence 1, Appli
c	43	17	0.7	1037	1	US-08-240-124-1	Sequence 1, Appli
c	44	17	0.7	28	1	US-07-941-523-12	Sequence 12, Appl
	45	17	0.7	90	1	US-08-123-702-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE: 19930325
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..2469
US-08-038-760-1

Query Match 72.1%; Score 1885; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
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Db 582 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 641

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Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
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Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
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Db    702 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 761

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    762 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 821

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
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Db    822 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 881

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
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Db    882 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 941

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
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Db    942 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1001

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db   1002 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1061

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
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Db   1062 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1121

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
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Db   1122 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1181

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db   1182 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1241

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
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Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
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Db   1362 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1421

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
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Db   1422 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1481

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1482 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1541

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
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Db   1542 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1601

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1602 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1661

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1662 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1721
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Qy   1869 CTGGACCCTTTTCCAGGACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
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Db   1722 CTGGACCCTTTTCCAGGACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1781

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1782 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1841

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Db   1842 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1901

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
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Db   1902 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1961

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Db   1962 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2021

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db   2022 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2081

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
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Db   2082 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2141

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2142 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2201

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
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Db   2202 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2261

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
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Db   2262 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2321

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
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Db   2322 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2381

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
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Db   2382 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2441

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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Db   2442 GGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT   2
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             72.1%;  Score 1885;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
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Qy     789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
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Db    2595 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 2536

Qy     849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
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Db    2535 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 2476

Qy     909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
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Db    2475 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 2416

Qy     969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
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Db    2415 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 2356

Qy    1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
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Db    2355 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 2296

Qy    1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
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Db    2295 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 2236

Qy    1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db    2235 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 2176

Qy    1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
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Db    2175 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 2116

Qy    1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
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Db    2115 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 2056

Qy    1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db    1995 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1936

Qy    1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
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Db    1935 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1876

Qy    1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
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Db    1875 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1816

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Db    1815 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1756

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Db    1695 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1636

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Qy    1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
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Db    1515 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1456

Qy    1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1455 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1396

Qy    1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Qy    2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
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Db    1335 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1276

Qy    2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Db    1275 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 1216

Qy    2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db    1215 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 1156

Qy    2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1155 TGGAGGGAACATCTATATTTGACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 1096

Qy    2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1095 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 1036

Qy    2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1035 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 976

Qy    2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     975 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 916

Qy    2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
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Db    915 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 856

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588

Db    855 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 796

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613

Db    795 GGATACCTCAAACAAGGAAGAGAAA 771


RESULT   3
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match             72.1%;  Score 1885;  DB 2;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788

Db   1038 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 1097

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848

Db   1098 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1157

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908

Db   1158 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1217

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968

Db   1218 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1277

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028

Db   1278 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1337

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088

Db   1338 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1397

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148

Db   1398 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1457

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208

Db   1458 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1517

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268

Db   1518 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1577

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328

Db   1578 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1637

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388

Db   1638 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1697

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448

Db   1698 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1757

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508

Db   1758 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1817

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568

Db   1818 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1877

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628

Db   1878 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1937

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688

Db   1938 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1997

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748

Db   1998 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 2057

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808

Db   2058 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 2117

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868

Db   2118 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2177

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928

Db   2178 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2237

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988

Db   2238 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2297
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Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2298 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2357

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2358 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2417

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2418 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2477

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2478 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2537

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2538 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2597

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2598 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2657

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2658 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2717

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2718 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2777

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2778 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2837

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2838 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2897

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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Db   2898 GGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   4
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


  Query Match            72.1%;  Score 1885;  DB 4;  Length 3232;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
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Db    582 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 641

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    642 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 701

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    702 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 761

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    762 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 821

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    822 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 881

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    882 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 941

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    942 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1001

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1002 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1061

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1062 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1121

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1122 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1181

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1182 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1241

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1242 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1301

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1302 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1361

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1362 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1421

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1422 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1481

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1482 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1541

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
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Db   1542 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1601

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
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Db   1602 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1661

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1662 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1721

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1722 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1781

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1782 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1841

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1842 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1901

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1902 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1961

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1962 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2021

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db   2022 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2081

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2082 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2141

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2142 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2201

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2202 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2261

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2262 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2321

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2322 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2381
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Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2382 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2441

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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Db   2442 GGATACCTCAAACAAGGAAGAGAAA 2466


RESULT   5
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Jai
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match           72.1%;  Score 1885;  DB 4;  Length 3232;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
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Db   2655 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 2596

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
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Db   2595 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 2536

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
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Db   2535 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 2476
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Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
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Db   2475 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 2416

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
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Db   2415 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 2356

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
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Db   2355 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 2296

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
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Db   2295 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 2236

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db   2235 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 2176

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
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Db   2175 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 2116

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
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Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db   2055 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1996

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
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Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
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Db   1935 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1876

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
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Db   1875 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1816

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
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Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
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Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1695 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1636

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1635 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1576

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1575 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1516

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1515 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1456

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
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Db   1455 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1396
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Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Db   1395 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1336

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
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Db   1335 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1276

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Db   1275 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 1216

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db   1215 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 1156

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
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Db   1155 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 1096

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1095 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 1036

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
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Db   1035 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 976

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
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Db    975 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 916

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    915 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 856

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
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Db    855 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 796

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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Db    795 GGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   6
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7

  Query Match             72.1%;  Score 1885;  DB 4;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
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Db    1098 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1157

Qy     849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
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Db    1158 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1217

Qy     909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
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Db    1218 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1277

Qy     969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1278 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1337

Qy    1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
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Db    1338 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1397

Qy    1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1398 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1457

Qy    1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1458 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1517

Qy    1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
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Db    1518 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1577

Qy    1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
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Db    1578 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1637

Qy    1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db    1638 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1697

Qy    1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1698 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1757

Qy    1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
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Db    1758 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1817

Qy    1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
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Db    1818 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1877

Qy    1569 AGGACCAACTGATCACGTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1878 AGGACCAACTGATCACGTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1937

Qy    1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
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Db    1938 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1997

Qy    1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1998 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 2057

Qy    1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
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Db    2058 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 2117

Qy    1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
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Db    2118 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2177

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Db    2178 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2237

Qy    1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2238 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2297

Qy    1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2298 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2357

Qy    2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
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Db    2358 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2417

Qy    2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Db    2418 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2477

Qy    2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db    2478 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2537

Qy    2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
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Db    2538 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2597

Qy    2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
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Db    2598 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2657

Qy    2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
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Db    2658 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2717

Qy    2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
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Db    2718 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2777
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Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
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Db   2778 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2837

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
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Db   2838 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2897

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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RESULT   7
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


  Query Match             72.1%;  Score 1885;  DB 4;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 1097

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1157

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1217

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1277

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
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Db   1278 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1337

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1397

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
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Db   1398 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1457

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db   1458 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1517

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
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Db   1518 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1577

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
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Db   1578 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1637

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db   1638 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1697

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
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Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
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Db   1758 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1817

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1877

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
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Db   1878 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1937

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1997

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 2057

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 2117

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2177

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2237

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
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Db   2238 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2297

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2298 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2357

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2358 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2417

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2418 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2477

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2478 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2537

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2538 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2597

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2598 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2657

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2658 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2717

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2718 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2777

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2778 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2837

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
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Db   2838 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2897

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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Db   2898 GGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


  Query Match             70.2%;  Score 1834;  DB 6;  Length 2994;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1884;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 1097

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1157

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1217

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1277

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
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Db   1278 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1337

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1397

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
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Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db   1458 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1517

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1577

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1637

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db   1638 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1697

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1757
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Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1817

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1877

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1937

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
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Db   1938 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1997

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
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Db   1998 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 2057

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 2117

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2177

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2237

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2238 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2297

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Db   2298 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2357

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
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Db   2358 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2417

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Db   2418 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2477

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db   2478 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2537

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
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Db   2538 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2597

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2598 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2657

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2658 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2717

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   2718 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGA 2777

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2778 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2837

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2838 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2897

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2898 GGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1097:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1097

Query Match 1.1%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2530 CTGGCAGAAATGACTTCTACTCGAACAC 2557
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Db      1 CTGGCAGAAATGACTTCTACTCGAACAC 28
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RESULT 10
US-08-253-155A-92
; Sequence 92, Application US/08253155A
; Patent No. 5691147
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno

```
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-92


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  11
US-08-625-209A-21
; Sequence 21, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-21


  Query Match             1.0%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  12
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15
```

```
  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     988 ATGATTTTAAATTCAGCAAGTG 1009
           ||||||||||||||||||||||
Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  13
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     988 ATGATTTTAAATTCAGCAAGTG 1009
           ||||||||||||||||||||||
Db      31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  14
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2288 CAACACCAACAAAAATGACTCC 2309
           ||||||||||||||||||||||
Db      22 CAACACCAACAAAAATGACTCC 1


RESULT  15
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
```

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;       ZIP:  10598-4412
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS 5.0
;       SOFTWARE:  Word Perfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/271,942A
;       FILING DATE:  08-JUL-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marina T. Larson
;       REGISTRATION NUMBER:  32,038
;       REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (914) 245-3252
;       TELEFAX:  (914) 962-4330
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  22
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
;     HYPOTHETICAL:  no
;     ANTI-SENSE:  no
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  human
;     FEATURE:
;       NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2288 CAACACCAACAAAAATGACTCC 2309
           ||||||||||||||||||||||
Db      22 CAACACCAACAAAAATGACTCC 1


Search completed: February 13, 2000, 17:17:08
Job time: 9308 sec
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 16:55:41 ; Search time 9092.07 Seconds
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Title: US-09-026-459A-46_COPY_7_2613
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Scoring table: OLIGO_NUC

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105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		476	18.3	572	64	AL120941	AL120941 DKFZp762D
c 2		352	13.5	415	51	AI745644	AI745644 tr24b06.x
c 3		348	13.3	411	51	AI745643	AI745643 tr24b05.x
4		257	9.9	285	33	AA382103	AA382103 EST95270
5		204	7.8	304	32	AA361277	AA361277 EST70529
c 6		181	6.9	571	41	AI074792	AI074792 oy03a06.s
c 7		161	6.2	329	36	AA664676	AA664676 nu64f09.s

	8	156	6.0	456	30	AA210875 AA210875 zr88f11.r
c	9	132	5.1	171	38	AA765882 AA765882 oa14a06.s
	10	114	4.4	386	24	N25402 N25402 yx40c12.r1
	11	113	4.3	457	24	N41391 N41391 yw70g06.r1
	12	89	3.4	152	22	R57845 R57845 F6142 Fetal
	13	82	3.1	525	30	AA258255 AA258255 zr59g04.r
c	14	53	2.0	349	20	T24020 T24020 seq2177 3HF
	15	48	1.8	397	22	R70325 R70325 yj81b10.r1
	16	48	1.8	522	28	AA072780 AA072780 mm76a05.r
	17	42	1.6	986	89	AQ901300 AQ901300 HS_5234_A
	18	38	1.5	472	46	AA955457 AA955457 UI-R-A1-e
c	19	35	1.3	914	38	AA763411 AA763411 vw54a04.r
c	20	35	1.3	871	38	AA763485 AA763485 vw54h01.r
	21	34	1.3	427	37	AA709628 AA709628 vv41c11.r
c	22	33	1.3	462	48	AI606529 AI606529 vb27g08.y
	23	33	1.3	832	49	AI646038 AI646038 vw54a10.x
	24	33	1.3	709	49	AI646097 AI646097 vw54h07.x
	25	33	1.3	575	49	AI662832 AI662832 vb27g08.x
	26	31	1.2	284	59	AV111279 AV111279 AV111279
	27	31	1.2	174	72	AV302462 AV302462 AV302462
	28	29	1.1	615	40	AA959836 AA959836 vw54h01.s
c	29	26	1.0	405	39	AA861150 AA861150 ak36a12.s
	30	26	1.0	529	40	AA959709 AA959709 vw54a04.s
	31	25	1.0	356	41	AI020392 AI020392 ub17a05.r
c	32	24	0.9	492	33	AA396353 AA396353 vb27g08.r
c	33	22	0.8	440	33	AA440741 AA440741 LD15614.5
c	34	22	0.8	332	44	AI259982 AI259982 LP03562.5
	35	22	0.8	586	59	AI770926 AI770926 606063D04
c	36	21	0.8	640	38	AA752076 AA752076 96AS1023
	37	21	0.8	219	38	AA752355 AA752355 96GS0852
c	38	21	0.8	501	74	AV391000 AV391000 AV391000
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c	40	20	0.8	424	21	R21339 R21339 yg50d05.r1
c	41	20	0.8	372	21	R21352 R21352 yg50f05.r1
c	42	20	0.8	351	21	T78368 T78368 yc99g02.r1
c	43	20	0.8	478	22	H06003 H06003 yl76c05.r1
c	44	20	0.8	299	36	AA618388 AA618388 nq18h09.s
	45	20	0.8	574	103	AQ498524 AQ498524 HS_5120_B

ALIGNMENTS

RESULT 1
AL120941
LOCUS AL120941 572 bp mRNA EST 27-SEP-1999
DEFINITION DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762D143 5', mRNA sequence.
ACCESSION AL120941
VERSION AL120941.1 GI:5926942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948410.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762D143"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 180 a 128 c 98 g 166 t
ORIGIN

Query Match 18.3%; Score 476; DB 64; Length 572;
Best Local Similarity 100.0%; Pred. No. 7.6e-205;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1291 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 60

Qy   1351 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 120

Qy   1411 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 180

Qy   1471 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 240

Qy   1531 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

Qy   1591 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 360

Qy   1651 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 420

Qy   1711 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 476
```

RESULT 2
AI745644/c
LOCUS AI745644 415 bp mRNA EST 21-JUN-1999
DEFINITION tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI745644
VERSION AI745644.1 GI:5113932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137189.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

```
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a      75 c      87 g     135 t
ORIGIN


  Query Match             13.5%;  Score 352;  DB 51;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 1e-148;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1961 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 2020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 AAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTC 356

Qy    2021 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 2080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 ATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTA 296

Qy    2081 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 2140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 TAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTT 236

Qy    2141 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 CCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 176

Qy    2201 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 2260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCAT 116

Qy    2261 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2312
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 ATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   3
AI745643/c
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


  Query Match             13.3%;  Score 348;  DB 51;  Length 411;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-147;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1965 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     411 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 352

Qy    2025 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 292

Qy    2085 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 232

Qy    2145 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 172

Qy    2205 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2264
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     171 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 112

Qy    2265 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 2312
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     111 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64


RESULT   4
AA382103
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


  Query Match             9.9%;  Score 257;  DB 33;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-105;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1755 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1814
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 60

Qy   1815 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 1874
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTT 120

Qy   1875 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 1934
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTAT 180

Qy   1935 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1994
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 240

Qy   1995 TGTAACAGCATACAAGG 2011
           ||||||||||||||||
Db    241 TGTAACAGCATACAAGG 257
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RESULT   5
AA361277
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


  Query Match             7.8%;  Score 204;  DB 32;  Length 304;
  Best Local Similarity   99.6%;  Pred. No. 9.9e-82;
  Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1564 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 109

Qy   1624 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1683
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 169
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Qy   1684 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1743
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    170 CGTGTAAATTCTACTGCAAATGCAGAGNCACAAGCAACCTCAGCCTTCCAGACCCAGAAG 229

Qy   1744 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 289

Qy   1804 CGGCTAAATACACTT 1818
          |||||||||||||||
Db    290 CGGCTAAATACACTT 304


RESULT   6
AI074792/c
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


  Query Match             6.9%;  Score 181;  DB 41;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-71;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     85 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAG 309
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Qy    145 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 TTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGAT 249

Qy    205 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 189

Qy    265 G 265
          |
Db    188 G 188


RESULT   7
AA664676/c
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


  Query Match             6.2%;  Score 161;  DB 36;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-62;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1359 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 1418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 GTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGAT 236

Qy   1419 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 1478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    235 CGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACG 176

Qy   1479 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 1519
          |||||||||||||||||||||||||||||||||||||||
Db    175 ATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAG 135


RESULT   8
AA210875
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


  Query Match             6.0%;  Score 156;  DB 30;  Length 456;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-60;
  Matches  156;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2452 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAA 84

Qy   2512 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 TTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATG 144

Qy   2572 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||||||||||||||||
Db    145 AATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 180
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RESULT   9
AA765882/c
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2415   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


  Query Match             5.1%;  Score 132;  DB 38;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-49;
  Matches  132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1154 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 1213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    171 AGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAG 112

Qy   1214 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    111 AAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 52

Qy   1274 TGTCTTTATTGG 1285
          ||||||||||||
Db     51 TGTCTTTATTGG 40


RESULT  10
N25402
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


  Query Match             4.4%;  Score 114;  DB 24;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 60

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 114


RESULT  11
N41391
LOCUS       N41391         457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g     128 t
ORIGIN


  Query Match             4.3%;  Score 113;  DB 24;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-40;
  Matches  113;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2343 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 276

Qy   2403 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 2455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTG 329
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RESULT  12
R57845
LOCUS       R57845         152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


  Query Match             3.4%;  Score 89;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-29;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2177 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 60

Qy    2237 ATATTTCACCCCTGAAGAGTCCATATAAA 2265
           |||||||||||||||||||||||||||||
Db      61 ATATTTCACCCCTGAAGAGTCCATATAAA 89


RESULT  13
AA258255
LOCUS       AA258255       525 bp    mRNA            EST       06-AUG-1997
DEFINITION  zr59g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667734 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AA258255
VERSION     AA258255.1  GI:1893417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1393412.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 662   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:667734"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      150 a     89 c    107 g    179 t
ORIGIN


  Query Match             3.1%;  Score 82;  DB 30;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-26;
  Matches   82;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2526 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2585
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 60

Qy    2586 TACCTCAAACAAGGAAGAGAAA 2607
           |||||||||||||||||||||||
Db      61 TACCTCAAACAAGGAAGAGAAA 82


RESULT  14
T24020/c
LOCUS       T24020         349 bp    mRNA            EST       01-AUG-1994
DEFINITION  seq2177 3HFLSK20 Homo sapiens cDNA clone 3HFLSK20-63 3', mRNA
            sequence.
ACCESSION   T24020
VERSION     T24020.1  GI:520260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   Soares,M.B.
  TITLE     Human infant brain library b4HB3MA cDNAs
```

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  JOURNAL   Unpublished (1994)
COMMENT     Contact: Bento Soares
            Columbia University
            Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
            10032
            Tel: 2129602313
            Fax: 2127813577
            Email: cuc@cuccfa.ccc.columbia.edu
            antisense Kanamycin
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="3HFLSK20-63"
                     /clone_lib="3HFLSK20"
                     /lab_host="E. coli"
                     /note="Vector: Lafmid K; Site_1: Not I; Site_2: EcoR I;
                     cDNA from polyA+ RNA from human fetal liver + spleen. 20
                     weeks post-conception "
BASE COUNT       98 a     73 c     59 g    118 t      1 others
ORIGIN


  Query Match             2.0%;  Score 53;  DB 20;  Length 349;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-13;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    213 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 265
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Db    349 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 297


RESULT  15
R70325
LOCUS       R70325        397 bp    mRNA            EST       01-JUN-1995
DEFINITION  yj81b10.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:155131 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   R70325
VERSION     R70325.1  GI:843842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 803
            High quality sequence stops: 324
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 803   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
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                     /db_xref="GDB:569832"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155131"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      130 a     47 c     71 g    147 t      2 others
ORIGIN


  Query Match             1.8%;  Score 48;  DB 22;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-11;
  Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    136 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 183
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Db    287 AGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGT 334


Search completed: February 13, 2000, 16:55:48
Job time: 15530 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 12:06:52 ; Search time 14294.3 Seconds
(without alignments)
-591.374 Million cell updates/sec

Title: US-09-026-459A-50_COPY_7_2790
Perfect score: 2784
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2784

Scoring table: OLIGO_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
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36: em_ba1:*
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42: gb_htg4:*
43: gb_htg5:*
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47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2682	96.3	2994	5	I81465	I81465 Sequence 2
2	2682	96.3	4839	10	HUMRB1MRNA	L41870 Homo sapien
3	2682	96.3	4600	10	HUMRBA1RA	M33647 Human retin
4	2682	96.3	2994	10	HUMRBSA	M28419 Human retin
5	2562	92.0	4597	5	I05311	I05311 Sequence 1
6	2511	90.2	4597	5	I09369	I09369 Sequence 1
7	2448	87.9	3232	5	I18496	I18496 Sequence 1
c 8	2448	87.9	3232	5	I18497	I18497 Sequence 2
9	2208	79.3	4740	10	HUMRBS	M15400 Human retin
10	1420	51.0	4580	5	A01444	A01444 H.sapiens D
11	265	9.5	426	11	AF043224	AF043224 Homo sapi
12	207	7.4	480	9	HUMRBSY79	M19701 Human mutat
13	198	7.1	693	5	I09384	I09384 Sequence 17
14	198	7.1	693	9	HUMRBS15	M27858 Human retin
15	198	7.1	180388	9	HUMRETBLAS	L11910 Human retin
16	196	7.0	340	10	HUMRB1501V	L49220 Homo sapien
17	167	6.0	555	10	HUMRB4MU2	L41904 Homo sapien
18	165	5.9	935	5	I09389	I09389 Sequence 22
19	165	5.9	935	9	HUMRBS20	M27863 Human retin
20	165	5.9	420	10	HUMRB23EX	L41910 Homo sapien
21	163	5.9	252	10	HUMRB1777L	L49230 Homo sapien
22	155	5.6	555	10	HUMRB17MU2	L41924 Homo sapien
23	148	5.3	717	5	I09387	I09387 Sequence 20
24	148	5.3	717	9	HUMRBS18	L35147 Human retin
25	148	5.3	717	15	M27861	M27861 Figure 2. R
26	147	5.3	224	10	HUMRB1SDDL	L49225 Homo sapien
27	146	5.2	650	5	I09386	I09386 Sequence 19
28	146	5.2	650	9	HUMRBS17	M27860 Human retin
29	145	5.2	609	5	I09377	I09377 Sequence 10
30	145	5.2	609	9	HUMRBS08	L35146 Human retin
31	145	5.2	316	10	HUMRB08EX	L41896 Homo sapien
32	144	5.2	1310	9	HUMRBS22	M27865 Human retin
33	144	5.2	625	10	HUMRB25EX	L41912 Homo sapien
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35	138	5.0	1050	9	HSRB1G	X16439 Human retin
36	138	5.0	1040	9	HUMRBS01	M27845 Human retin
37	132	4.7	224	10	HUMRB1610K	L49223 Homo sapien
38	131	4.7	317	10	HUMRB17MUT	L41999 Homo sapien
39	130	4.7	704	5	I09371	I09371 Sequence 4
40	130	4.7	704	9	HUMRBS02	M27846 Human retin
41	130	4.7	410	10	HUMRB02EX	L41890 Homo sapien
42	125	4.5	350	10	HUMRB20MUU	L41996 Homo sapien
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ALIGNMENTS

RESULT 1
I81465
LOCUS I81465 2994 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 2 from patent US 5710255.
ACCESSION I81465
VERSION I81465.1 GI:3209762
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2994)
AUTHORS Shepard,H.Michael and Wen,S.Fen.

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  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .2994
                     /organism="unknown"
BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN

  Query Match           96.3%;  Score 2682;  DB 5;  Length 2994;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2782;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy     841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
Db     979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038

Qy      901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
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Qy     1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
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Qy     1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
Db     1459 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1518

Qy     1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
Db     1519 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1578

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Db     1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1698

Qy     1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
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Db     1759 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1818

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Qy     1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
Db     1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1998

Qy     1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
Db     1999 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 2058

Qy     1921 CCATTGAAATCTACCTCTGTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
Db     2059 CCATTGAAATCTACCTCTGTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 2118

Qy     1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
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Db    2119 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2178

Qy    2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
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Db    2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418

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Qy    2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718

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Db    2899 GATACCTCAAACAAGGAAGAGAAA 2922


RESULT   2
HUMRB1MRNA
LOCUS       HUMRB1MRNA   4839 bp    mRNA            PRI       05-MAY-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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VERSION     M33647.1  GI:190945
KEYWORDS    retinoblastoma protein.
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
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Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
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Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
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Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
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Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
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Qy    781 GCACGGATAGCAAAACAAGTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
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Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
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Qy    901 AATTCTCTTGGACTTGTAAGATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
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Db   1624 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1683

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Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Db   1744 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1803

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Db   1804 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1863

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

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Db   2224 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2283

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Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Db   2524 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2583

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640

Db   2584 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2643

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Db   2644 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2703

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

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Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784

Db   2764 GATACCTCAAACAAGGAAGAGAAA 2787
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RESULT   4
HUMRBSA
LOCUS       HUMRBSA      2994 bp    mRNA            PRI       12-JUL-1995
DEFINITION  Human retinoblastoma susceptibility protein mRNA, complete cds.
ACCESSION   M28419
VERSION     M28419.1  GI:190962
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility protein.
SOURCE      Homo sapiens retinoblastoma cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  JOURNAL   Nature 329 (6140), 642-645 (1987)
  MEDLINE   88014238
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN
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Query Match 96.3%; Score 2682; DB 10; Length 2994;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2782; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
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Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
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Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
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Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
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Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
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Db   2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
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Db   2419 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2478

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
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Db   2479 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2538

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2598

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
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Db   2599 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2658

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
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Db   2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
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Db   2719 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2778

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
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Db   2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2838

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2839 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898

Qy-  2761 GATACCTCAAACAAGGAAGAGAAA 2784
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Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   5
I05311
LOCUS       I05311       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN
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Query Match 92.0%; Score 2562; DB 5; Length 4597;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2662; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
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Db    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
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Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
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Db    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
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Db    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
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Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
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Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
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Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
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Db   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
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Db   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
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Db   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
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Db   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
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Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
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Db   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
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Db   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
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Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
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Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
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Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
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Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
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Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
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Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
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Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
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Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
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Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

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Db   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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RESULT   6
I09369
LOCUS       I09369       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent WO 8906703.
ACCESSION   I09369
VERSION     I09369.1  GI:587899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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          Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    841 c    813 g   1454 t
ORIGIN


  Query Match             90.2%;  Score 2511;  DB 5;  Length 4597;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2661;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
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Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

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Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
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Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
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Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
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Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
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Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
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Db   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
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Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
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Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGAA 2640

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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Db   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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RESULT   7
I18496
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN
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Query Match             87.9%;  Score 2448;  DB 5;  Length 3232;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    337 ATGTCGTTCACTTTTAGTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     19 ATGTCGTTCACTTTTAGTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 78

Qy    397 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 138

Qy    457 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 198

Qy    517 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 258

Qy    577 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 318

Qy    637 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 378

Qy    697 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 756
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 438

Qy    757 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 498

Qy    817 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 558

Qy    877 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 618

Qy    937 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 678

Qy    997 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 738

Qy   1057 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 798

Qy   1117 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 858

Qy   1177 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 918

Qy   1237 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 978

Qy   1297 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1038

Qy   1357 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1416
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Db   1039 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1098

Qy   1417 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1476

Db   1099 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1158

Qy   1477 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1536

Db   1159 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1218

Qy   1537 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1596

Db   1219 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1278

Qy   1597 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1656

Db   1279 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1338

Qy   1657 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1716

Db   1339 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1398

Qy   1717 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1776

Db   1399 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1458

Qy   1777 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1836

Db   1459 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1518

Qy   1837 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1896

Db   1519 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1578

Qy   1897 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1956

Db   1579 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1638

Qy   1957 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2016

Db   1639 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1698

Qy   2017 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2076

Db   1699 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1758

Qy   2077 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2136

Db   1759 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1818

Qy   2137 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2196

Db   1819 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1878

Qy   2197 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2256

Db   1879 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1938

Qy   2257 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2316

Db   1939 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 1998

Qy   2317 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2376

Db   1999 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2058

Qy   2377 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2436

Db   2059 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2118

Qy   2437 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2496

Db   2119 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2178

Qy   2497 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2556

Db   2179 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2238

Qy   2557 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2616

Db   2239 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2298

Qy   2617 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2676

Db   2299 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2358

Qy   2677 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2736

Db   2359 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2418

Qy   2737 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784

Db   2419 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT   8
I18497/c
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN
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  Query Match             87.9%;  Score 2448;  DB 5;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    337 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 396

Db   3218 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 3159

Qy    397 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 456

Db   3158 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 3099

Qy    457 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 516

Db   3098 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 3039

Qy    517 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 576

Db   3038 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 2979

Qy    577 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 636

Db   2978 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 2919

Qy    637 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 696

Db   2918 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 2859
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Qy    697 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 756
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Db   2858 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 2799

Qy    757 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2798 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 2739

Qy    817 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2738 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 2679

Qy    877 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2678 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 2619

Qy    937 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2618 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 2559

Qy    997 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2558 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 2499

Qy   1057 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2498 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 2439

Qy   1117 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2438 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 2379

Qy   1177 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1236
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Db   2378 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 2319

Qy   1237 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1296
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Db   2318 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 2259

Qy   1297 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1356
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Qy   1417 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1476
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Qy   1477 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1536
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Qy   1657 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1716
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RESULT 9
HUMRBS
LOCUS HUMRBS 4740 bp mRNA PRI 12-JUL-1995
DEFINITION Human retinoblastoma susceptibility mRNA, complete cds.
ACCESSION M15400

```
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable copy of sequence in [1] kindly
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                     RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
                     KMNDSMDTSNKEEK"
BASE COUNT     1508 a    887 c    862 g   1483 t
ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.
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Query Match 79.3%; Score 2208; DB 10; Length 4740;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2408; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    373 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 432
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Db    511 GAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTT 570

Qy    433 GATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAA 492
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Qy    493 TTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 552
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Qy    553 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 612
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Qy    613 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGAC 672
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Qy    733 CCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCA 792
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Qy    853 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 912
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Qy    973 TATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAG 1032
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Qy   1033 ACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAA 1092
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Qy   1153 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1212
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 GGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2790

Qy   2653 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2791 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2850

Qy   2713 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAAC 2910

Qy   2773 AAGGAAGAGAAA 2784
          ||||||||||||
Db   2911 AAGGAAGAGAAA 2922


RESULT  10
A01444
LOCUS       A01444     · 4580 bp    DNA             PAT       18-FEB-1993
DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


  Query Match           51.0%;  Score 1420;  DB 5;  Length 4580;
  Best Local Similarity 99.6%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy    766 GGTCAGAACAGGAGTGCAGGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 GGTCAGAACAGGAGTGCAGGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 811

Qy    826 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    812 ATTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 871

Qy    886 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    872 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGCGGTTGAA 931

Qy    946 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    932 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 991

Qy   1006 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    992 TTTTTGCATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1051

Qy   1066 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1052 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1111

Qy   1126 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1112 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1171

Qy   1186 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1172 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1231
```

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Qy   1246 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1232 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT-GGA 1290

Qy   1306 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1350

Qy   1366 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1410

Qy   1426 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1470

Qy   1486 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1545
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1471 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCAGGAACAGATTTGTCTTTCCCA 1530

Qy   1546 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1590

Qy   1606 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1650

Qy   1666 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1725
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CGAATCATGGAATCCTTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1710

Qy   1726 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1770

Qy   1786 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1845
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1830

Qy   1846 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1890

Qy   1906 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1965
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1950

Qy   1966 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2010

Qy   2026 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2070

Qy   2086 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2130

Qy   2146 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2190

Qy   2206 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2265
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   2191 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGTTC 2250

Qy   2266 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2310

Qy   2326 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2385
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 CCCCCTACCTTG-CACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2369

Qy   2386 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2429

Qy   2446 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2489

Qy   2506 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2549

Qy   2566 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2625
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 GACCGTGTGCTCTAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2609

Qy   2626 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2669

Qy   2686 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2670 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2729

Qy   2746 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||||||||||||||||||
Db   2730 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2768
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RESULT  11
AF043224
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
     exon            <1. .7
                     /gene="RB1"
                     /number=5
     CDS             <1. .137
                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
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                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
                     "
     exon            8. .76
                     /gene="RB1"
                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
                     /gene="RB1"
                     /number=5
     exon            351. .418
                     /gene="RB1"
                     /number=6
     exon            419. .>426
                     /gene="RB1"
                     /number=7
BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN
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Query Match 9.5%; Score 265; DB 11; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.4e-130;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     337 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 207

Qy     397 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 267

Qy     457 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 327

Qy     517 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 387

Qy     577 GTTTCTTGGATCACATTTTTATTAG 601
           |||||||||||||||||||||||||
Db     388 GTTTCTTGGATCACATTTTTATTAG 412
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RESULT  12
HUMRBSY79
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
```

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COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
                     /note="mutated retinoblastoma protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.
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Query Match 7.4%; Score 207; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.6e-99;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     606 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 665
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 AGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 333

Qy     666 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 725
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGC 393

Qy     726 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 785
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 TGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG 453

Qy     786 GATAGCAAAACAACTAGAAAATGATAC 812
           ||||||||||||||||||||||||||
Db     454 GATAGCAAAACAACTAGAAAATGATAC 480
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RESULT  13
I09384
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN
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Query Match 7.1%; Score 198; DB 5; Length 693;
Best Local Similarity 100.0%; Pred. No. 1.1e-94;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1499 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1558
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1559 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 369

Qy   1619 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 1678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT 429

Qy   1679 CCCTTGCATGGCTCTCAG 1696
          ||||||||||||||||||
Db    430 CCCTTGCATGGCTCTCAG 447


RESULT 14
HUMRBS15
LOCUS       HUMRBS15      693 bp    DNA          PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
                     /number=16
     exon            250. .446
                     /note="retinoblastoma susceptibility gene"
                     /number=17
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


  Query Match             7.1%;  Score 198;  DB 9;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-94;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1499 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 1558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATG 309

Qy   1559 TGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAG 1618
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RESULT 15
HUMRETBLAS

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ACCESSION   L11910
VERSION     L11910.1  GI:292420
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REFERENCE   1  (sites)
  AUTHORS   Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A., Rapaport,J.M.,
            Albert,D.M. and Dryja,T.P.
  TITLE     A human DNA segment with properties of the gene that predisposes to
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  JOURNAL   Nature 323 (6089), 643-646 (1986)
  MEDLINE   87039336
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  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
            tumors: organization of the sequence and its encoded protein
            [published erratum appears in Proc Natl Acad Sci U S A 1988
            Apr;85(7):2234]
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
  MEDLINE   88097427
REFERENCE   3  (sites)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   4  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
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  AUTHORS   Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and Dryja,T.P.
  TITLE     Oncogenic germ-line mutations in Sp1 and ATF sites in the human
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  JOURNAL   Nature 353 (6339), 83-86 (1991)
  MEDLINE   91351319
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  TITLE     Complete genomic sequence of the human retinoblastoma
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  JOURNAL   Genomics 17 (3), 535-543 (1993)
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GenCore version 4.5
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Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

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RESULT   2
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; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7
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  Matches 2782;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db    139 ATGCCGCCCAAAACCCCCCGAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 198

Qy     61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
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Db    199 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 258

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
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Db    259 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 318

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
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Db    319 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 378

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
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Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db    439 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 498

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
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Db    499 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 558

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
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Db    559 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 618

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
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Db    619 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 678

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
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Db    739 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 798

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
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Db    799 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 858

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
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Db    859 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 918

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Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
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Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
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Db   1099 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1158

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Db   1219 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1278

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Db   1279 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
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Db   2839 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922


RESULT   3
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
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;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


  Query Match             94.5%;  Score 2631;  DB 4;  Length 2994;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2781;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 198

Qy     61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    199 CCGGCACCGCCGCCGCCGCCCCCTCCGGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 258

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 318

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 378

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 438

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db    439 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 498

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 558

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 618

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 678

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 738

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 798

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 858

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 918

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 978

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 1098

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1158

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1218

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1278

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1398

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1458

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1518

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1578

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
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Db   1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1698

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1758

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1818

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1878

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1998

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 2058

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 2118

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2178

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2238

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2298

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2358

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2478

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2538

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2598

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2599 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2658

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2719 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2778

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2838

Qy   2701 CTGGCAGAAATGACTTGTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2839 CTGGCAGAAATGACTTGTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||||
Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922


RESULT   4
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


  Query Match             92.7%;  Score 2580;  DB 6;  Length 2994;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2780;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 ATGCCGCCCAAAACCCCGCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 ATGCCGCCCAAAACCCCGCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 198

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     199 CCGGCACCGCCGCCGCCGCCCCCTCCGGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 258
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Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 318

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 378

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 438

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db    439 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 498

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 558

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 618

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 678

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 738

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 798

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 858

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 918

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 978

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 1098

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1158

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1218

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1278

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1398

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1458

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1518

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1578

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1698

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1758

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1818

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1878

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ACTGCAGCAGATATGTATCTT▪CTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1998

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 2058

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 2118

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
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Db   2119 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2178

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2238

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2298

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2358

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
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Db   2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
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Db   2419 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2478

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2538

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2598

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2599 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2658

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   2719 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGAA 2778

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2838

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2839 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   5
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


  Query Match             87.9%;  Score 2448;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    337 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     19 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 78

Qy    397 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 138

Qy    457 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 198

Qy    517 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 258

Qy    577 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 318

Qy    637 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 378

Qy    697 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 756
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 438

Qy    757 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 816
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Db    439 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 498

Qy    817 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 558

Qy    877 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 936
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Db    559 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 618

Qy    937 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 678

Qy    997 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 738

Qy   1057 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 798

Qy   1117 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 858

Qy   1177 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1236
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Db    859 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 918

Qy   1237 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 978

Qy   1297 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1356
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Db    979 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1038

Qy   1357 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1416
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Db   1039 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1098

Qy   1417 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1158

Qy   1477 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1218

Qy   1537 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1278

Qy   1597 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1338

Qy   1657 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1398

Qy   1717 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1458

Qy   1777 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1836
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Db   1459 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1518

Qy   1837 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1578

Qy   1897 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1638

Qy   1957 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1698

Qy   2017 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1758

Qy   2077 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1818

Qy   2137 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2196
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Db   1819 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1878

Qy   2197 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1938

Qy   2257 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 1998

Qy   2317 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2376
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Db   1999 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2058

Qy   2377 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2118

Qy   2437 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2496
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Db   2119 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2178

Qy   2497 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2238

Qy   2557 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2298

Qy   2617 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2676
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Db   2299 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2358

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Db   2359 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2418

Qy   2737 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT   6
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
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;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             87.9%;  Score 2448;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 396
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Db    3218 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 3159

Qy     397 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3158 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 3099

Qy     457 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3098 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 3039

Qy     517 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3038 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 2979

Qy     577 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2978 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 2919

Qy     637 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2918 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 2859

Qy     697 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2858 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 2799

Qy     757 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2798 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 2739

Qy     817 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2738 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 2679

Qy     877 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2678 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 2619

Qy     937 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2618 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 2559

Qy     997 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2558 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 2499

Qy    1057 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2498 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 2439

Qy    1117 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2438 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 2379

Qy    1177 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2378 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 2319

Qy    1237 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2318 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 2259

Qy    1297 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2258 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 2199

Qy    1357 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2198 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 2139

Qy    1417 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2138 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 2079

Qy    1477 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2078 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 2019

Qy    1537 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2018 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1959

Qy    1597 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1958 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1899

Qy    1657 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1716
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1898 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1839

Qy    1717 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1776
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1838 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1779

Qy    1777 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1778 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1719

Qy    1837 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1718 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1659

Qy    1897 ACCTCAGCCTTCCAGACGCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1658 ACCTCAGCCTTCCAGACGCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1599

Qy    1957 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2016
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1598 AAAGTGTATCGGCTAGCGTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1539

Qy    2017 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2076
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1538 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1479

Qy    2077 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1478 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1419

Qy    2137 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1418 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1359

Qy    2197 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1358 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1299

Qy    2257 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1298 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 1239

Qy    2317 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1238 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 1179
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Qy   2377 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1178 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 1119

Qy   2437 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 1059

Qy   2497 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 999

Qy   2557 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 939

Qy   2617 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 879

Qy   2677 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 819

Qy   2737 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771


RESULT   7
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


  Query Match             87.9%;  Score 2448;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    337 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     19 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 78

Qy    397 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 138

Qy    457 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 198

Qy    517 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 258

Qy    577 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 318

Qy    637 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 378

Qy    697 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 756
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 438

Qy    757 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 498

Qy    817 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 558

Qy    877 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 618

Qy    937 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 678

Qy    997 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 738

Qy   1057 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 798

Qy   1117 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 858

Qy   1177 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 918

Qy   1237 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    919 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 978

Qy   1297 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1038

Qy   1357 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1098

Qy   1417 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1158

Qy   1477 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1218

Qy   1537 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1278

Qy   1597 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1338

Qy   1657 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1398

Qy   1717 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1458

Qy   1777 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1518

Qy   1837 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1578

Qy   1897 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1638

Qy   1957 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1698

Qy   2017 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1758

Qy   2077 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1818

Qy   2137 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1878

Qy   2197 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1938

Qy   2257 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 1998

Qy   2317 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2058
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Qy   2377 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2118

Qy   2437 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2178

Qy   2497 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2238

Qy   2557 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2298

Qy   2617 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2358

Qy   2677 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2359 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2418

Qy   2737 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT   8
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match            87.9%;  Score 2448;  DB 4;  Length 3232;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     337 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3218 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 3159

Qy     397 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3158 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 3099

Qy     457 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3098 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 3039

Qy     517 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3038 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 2979

Qy     577 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2978 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 2919

Qy     637 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2918 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 2859

Qy     697 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2858 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 2799

Qy     757 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2798 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 2739

Qy     817 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2738 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 2679

Qy     877 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2678 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 2619

Qy     937 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2618 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 2559

Qy     997 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2558 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 2499

Qy    1057 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2498 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 2439

Qy    1117 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2438 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 2379

Qy    1177 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2378 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 2319

Qy    1237 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2318 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 2259

Qy    1297 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2258 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 2199

Qy    1357 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2198 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 2139

Qy    1417 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2138 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 2079

Qy    1477 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2078 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 2019

Qy    1537 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2018 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1959

Qy    1597 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1958 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1899

Qy    1657 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1716
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1898 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1839

Qy    1717 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1776
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1838 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1779

Qy    1777 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1778 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1719

Qy    1837 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1718 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1659

Qy    1897 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1658 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1599

Qy    1957 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2016
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1598 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1539

Qy    2017 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2076
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1538 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1479

Qy    2077 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1478 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1419

Qy    2137 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1418 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1359

Qy    2197 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1358 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1299

Qy    2257 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1298 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 1239

Qy    2317 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1238 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 1179

Qy    2377 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2436
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Db   1178 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 1119

Qy   2437 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 1059

Qy   2497 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 999

Qy   2557 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 939

Qy   2617 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2676
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 879

Qy   2677 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 819

Qy   2737 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.0%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00051;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2701 CTGGCAGAAATGACTTGTACTCGAACAC 2728
          ||||||||||||||||||||||||||||
Db      1 CTGGCAGAAATGACTTGTACTCGAACAC 28


RESULT  10
US-08-253-155A-92
; Sequence 92, Application US/08253155A
; Patent No. 5691147
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  CDK4 Binding Proteins
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/253,155A
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MII-028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  92:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
US-08-253-155A-92


  Query Match             0.9%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db      16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  11
US-08-625-209A-21
; Sequence 21, Application US/08625209A
; Patent No. 5756671
;  GENERAL INFORMATION:
;    APPLICANT:  Gyuris, Jeno
;    APPLICANT:  Lamphere, Lou
;    APPLICANT:  Draetta, Giulio
;    TITLE OF INVENTION:  Cdc37 Cell-Cyle Regulatory Protein,
```

```
;    TITLE OF INVENTION:  and Uses Related Thereto
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley, Hoag & Eliot
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/625,209A
;      FILING DATE:  01-APR-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  MIV048.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-625-209A-21


  Query Match             0.9%;  Score 25;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCCGCCCAAAACCCCCCGAAAAACG 27
          |||||||||||||||||||||||||
Db     16 GCCGCCCAAAACCCCCCGAAAAACG 40


RESULT  12
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1159 ATGATTTTAAATTCAGCAAGTG 1180
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Db     31 ATGATTTTAAATTCAGCAAGTG 52


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; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
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US-07-826-928A-36

Query Match 0.8%; Score 22; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 31 ATGATTTTAAATTCAGCAAGTG 52

RESULT 14
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; Sequence 22, Application US/08271946A
; Patent No. 5545527
; GENERAL INFORMATION:
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,946A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
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US-08-271-946A-22

Query Match 0.8%; Score 22; DB 1; Length 22;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 22, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,942A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 23 of human RB1 gene
US-08-271-942A-22

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 CAACACCAACAAAAATGACTCC 1

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 17:05:38 ; Search time 404.96 Seconds
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Perfect score: 2622
Sequence: 1 ATGGATTTTACTGCATTATG.....CCTCAAACAAGGAAGAGAAA 2622

Scoring table: OLIGO_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	2619	99.9	2995	4	US-08-959-638-7	Sequence 7, Appli
	3	2619	99.9	2994	4	US-08-482-627-4	Sequence 4, Appli
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	7	2460	93.8	3232	4	US-08-470-091-1	Sequence 1, Appli
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	10	22	0.8	52	1	US-07-826-928A-15	Sequence 15, Appl
	11	22	0.8	52	1	US-07-826-928A-36	Sequence 36, Appl
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c	16	20	0.8	44	2	US-08-253-155A-93	Sequence 93, Appl
c	17	20	0.8	44	2	US-08-625-209A-22	Sequence 22, Appl
c	18	18	0.7	37	1	US-07-826-928A-14	Sequence 14, Appl
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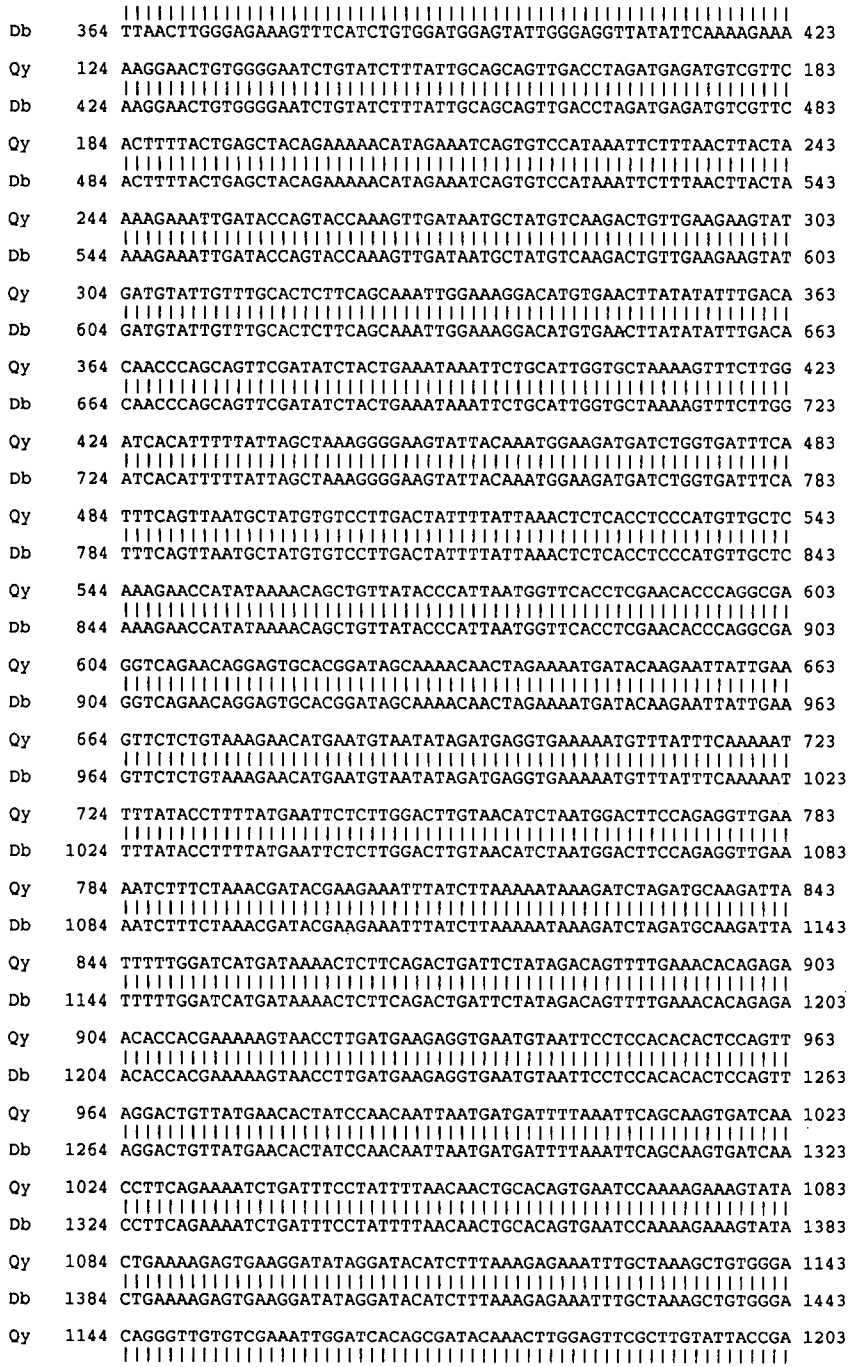
ALIGNMENTS

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RESULT 1
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; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match             99.9%;  Score 2619;  DB 2;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db 2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

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Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   2
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7

  Query Match             99.9%;  Score 2619;  DB 4;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
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Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 3
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
; GENERAL INFORMATION:
; APPLICANT: Lee, Wen-Hwa
; APPLICANT: Lee, Eva Y-H.P
; TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
; TITLE OF INVENTION: and Regulator
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,627
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,947
; FILING DATE: 28-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.

```
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  P-UC 1707
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2924
US-08-482-627-4


  Query Match             99.9%;  Score 2619;  DB 4;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
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Db    844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy    1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy    1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy    2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy    2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy    2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy    2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy    2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy    2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy    2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy    2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy    2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy    2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db    2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   4
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


  Query Match             97.9%;  Score 2568;  DB 6;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2618;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy     424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy     484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy     544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy     604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963
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Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
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Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 5
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

```
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


  Query Match             93.8%;  Score 2460;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    163 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy    223 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy    283 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy    343 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy    403 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy    463 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy    523 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy    583 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy    643 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy    703 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy    763 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy    823 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy    883 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy    943 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy   1003 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy   1063 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy   1123 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy   1183 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy   1243 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy   1303 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy   1363 GGAACAGATTTGTCTTTGCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGAACAGATTTGTCTTTGCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1423 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1483 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy   1543 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy   1603 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy   1663 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy   1723 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1782
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Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1783 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy   1843 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1903 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   1963 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   2023 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   2083 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2142
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Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2143 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2203 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2263 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2323 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2383 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2443 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2503 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2563 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466


RESULT   6
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             93.8%;  Score 2460;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     163 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy     223 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy     283 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 342
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy     343 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 402
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy     403 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 462
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy     463 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 522
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy     523 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 582
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy     583 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 642
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy     643 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 702
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy     703 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 762
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Db   2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy    763 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy    823 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy    883 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy    943 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy   1003 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy   1063 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy   1123 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1182
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Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy   1183 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1242
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Db   2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy   1243 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1302
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Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy   1303 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy   1363 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1422
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Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1423 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1483 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1543 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1603 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy   1663 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy   1723 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1783 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551
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Qy   1843 CTTCTGTCTGAGCACCGAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1550 CTTCTGTCTGAGCACCGAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1903 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy   1963 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   2023 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311

Qy   2083 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2143 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy   2203 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy   2263 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2323 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2383 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2443 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2503 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2563 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   7
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/470,091
;       FILING DATE:  JUN-16-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  19..2469
US-08-470-091-1


  Query Match             93.8%;  Score 2460;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    163 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy    223 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy    283 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy    343 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy    403 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy    463 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy    523 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy    583 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy    643 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy    703 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 762
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Db    547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy    763 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy    823 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy    883 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy    943 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy   1003 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy   1063 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy   1123 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy   1183 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy   1243 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1302
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Db   1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy   1303 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy   1363 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1423 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1483 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy   1543 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy   1603 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy   1663 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1722
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Db   1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy   1723 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1783 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1842
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Db    1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy    1843 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy    1903 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1962
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy    1963 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy    2023 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy    2083 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2142
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Db    1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy    2143 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2202
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Db    1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy    2203 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy    2263 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy    2323 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy    2383 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy    2443 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2502
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Db    2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy    2503 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy    2563 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466


RESULT   8
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


  Query Match             93.8%;  Score 2460;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     163 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy     223 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 282
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy     283 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 342
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy     343 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 402
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy     403 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 462
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy     463 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 522
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy     523 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 582
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy     583 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 642
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy     643 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 702
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy     703 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 762
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631
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Qy    763 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy    823 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy    883 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 942
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Db   2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy    943 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy   1003 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy   1063 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy   1123 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy   1183 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy   1243 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy   1303 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy   1363 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy   1423 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy   1483 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy   1543 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy   1603 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy   1663 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy   1723 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy   1783 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551
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Qy   1843 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy   1903 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy   1963 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy   2023 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311

Qy   2083 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy   2143 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy   2203 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy   2263 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy   2323 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2383 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2443 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2503 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2563 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
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;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.1%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2539 CTGGCAGAAATGACTTCTACTCGAACAC 2566
          ||||||||||||||||||||||||||||
Db      1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    997 ATGATTTTAAATTCAGCAAGTG 1018
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Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  11
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.8%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    997 ATGATTTTAAATTCAGCAAGTG 1018
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Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  12
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2297 CAACACCAACAAAAATGACTCC 2318
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Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  13
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.8%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2297 CAACACCAACAAAAATGACTCC 2318
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Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  14
PCT-US95-08604-22/c
; Sequence 22, Application PC/TUS9508604
;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  HSC Reasearch and Development Limitied Partnership
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  125
;    CORRESPONDENCE ADDRESS:
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;       ADDRESSEE:  Oppedahl & Larson
;       STREET:  1992 Commerce Street, Suite 309
;       CITY:  Yorktown Heights
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10598-4412
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS 5.0
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;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/08604
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/271,942
;       FILING DATE:  08-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marina T. Larson
;       REGISTRATION NUMBER:  32,038
;       REFERENCE/DOCKET NUMBER:  VGEN.P-003-WO
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (914) 245-3252
;       TELEFAX:  (914) 962-4330
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  22
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
;     HYPOTHETICAL:  no
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;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  human
;     FEATURE:
;       NAME/KEY:  primer for exon 23 of human RB1 gene
PCT-US95-08604-22


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;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Capatos, Denis
;    APPLICANT:  Matthews, David E.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
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Date: Feb 13, 2000  3:52 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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; Patent No. 5710255
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;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
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              Ratio:  1.000                 Gaps:      0
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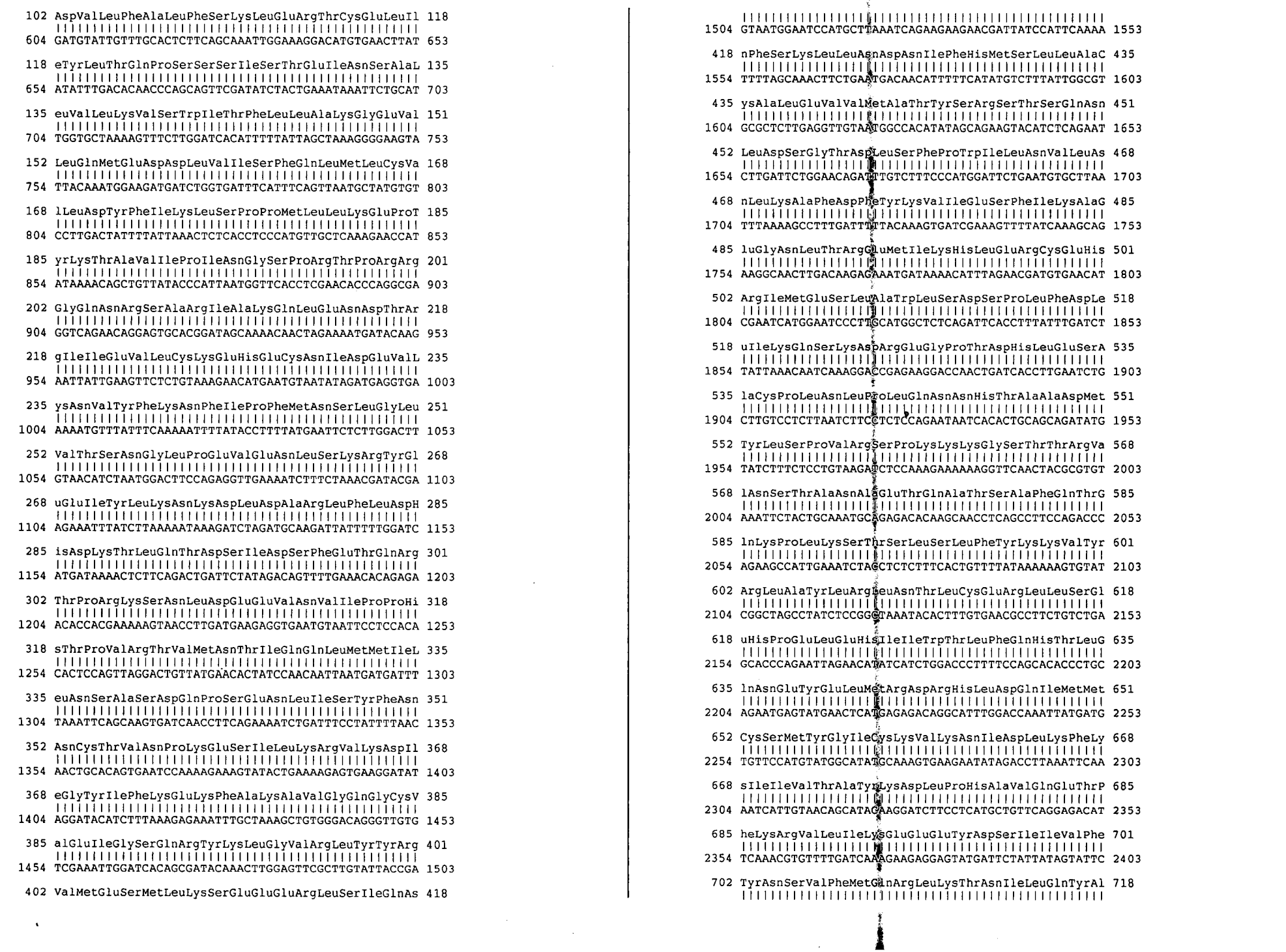
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seq_documentation_block:
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
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;      TOPOLOGY:  linear
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     168 lLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProT 185
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
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;      LOCATION:  19..2469
US-08-038-760-1


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; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
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US-08-038-760-2


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 Align seg 1/1  to reverse of: US-08-038-760-2  from: 1  to: 3232

      55 AspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIleGl 71
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGA 3181

      71 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 88
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    3180 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 3131

      88 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 104
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    3130 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 3081

     105 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 121
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    3080 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 3031

     121 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 138
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    3030 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 2981

     138 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 154
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2980 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

     155 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 171
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 2881

     171 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2880 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 2831

     188 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 204
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2830 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 2781

     205 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 221
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2780 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 2731

     221 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 238
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2730 AGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTT 2681

     238 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 254
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    2680 ATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

     255 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 271
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 2581

     271 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 288
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2580 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 2531

     288 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 304
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2530 CTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGA 2481

     305 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVa 321
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2480 AAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGT 2431

     321 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 338
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2430 TAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAG 2381

     338 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 354
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2380 CAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

     355 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 371
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACAT 2281

     371 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 388
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2280 CTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTG 2231

     388 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 404
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2230 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 2181

     405 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2180 TCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAA 2131

     421 sLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuG 438
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2130 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 2081

     438 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 454
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    2080 AGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

     455 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 471
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGC 1981

     471 aPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnL 488
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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 488 euThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 504
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1930 TGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATG 1881

 505 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGl 521
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1880 GAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACA 1831

 521 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 538
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 538 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 554
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1680 TGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCAT 1631

 588 euLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 604
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1630 TGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCC 1581

 605 TyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGl 621
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1580 TATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGA 1531

 621 uLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluT 638
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1480 ATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

 655 TyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleVa 671
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 738 heProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 754
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1180 TTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

 755 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 771
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAAT 1081

 771 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 788
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1080 GACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTT 1031
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 788 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 804
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 805 LeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysLe 821
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 980 CTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACT 931

 821 uArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuP 838
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 930 ACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCC 881

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seq_documentation_block:
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
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;      LOCATION:  19..2469
US-08-470-091-1


alignment_scores:
            Quality:  820.00              Length:    820
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x US-08-470-091-1   ..

 Align seg 1/1  to: US-08-470-091-1  from: 1  to: 3232

      55 AspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIleGl 71
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       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGA 56

      71 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 88
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

      88 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 104
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     105 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 121
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     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

     121 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 138
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

     138 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 154
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

     155 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 171
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     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 356

     171 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 188
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

     188 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 204
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

     205 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 221
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     457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

     221 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 238
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     507 AGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTT 556

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     255 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 271
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 656

     271 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 288
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

     288 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 304
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     321 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 338
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     355 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 371
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     371 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 388
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     957 CTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTG 1006

     388 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 404
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     405 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 421
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     421 sLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuG 438
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    1107 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 1156

     438 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 454
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    1157 AGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

     455 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 471
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     471 aPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnL 488
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     488 euThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 504
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     505 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGl 521
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     521 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 538
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     538 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 554
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     555 ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerTh 571
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    1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTAC 1556

     571 rAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProL 588
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    1557 TGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCAT 1606

     588 euLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 604
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    605 TyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGl 621
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seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236

;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 2581

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; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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     168 lLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProT 185
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     185 yrLysThrAlaValIleProIleAsnGlySerProArgThrProArgArg 201
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     202 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrAr 218
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     904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAG 953

     218 gIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGluValL 235
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 954 AATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGA 1003

 235 ysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeu 251
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1004 AAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTT 1053

 252 ValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGl 268
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1054 GTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGA 1103

 268 uGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspH 285
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1104 AGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATC 1153

 285 isAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 301
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1154 ATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

 302 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHi 318
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 318 sThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleL 335
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 335 euAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsn 351
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 352 AsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspIl 368
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 368 eGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysV 385
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1404 AGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTG 1453

 385 alGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
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1454 TCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

 402 ValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAs 418
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 418 nPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaC 435
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1554 TTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGT 1603

 435 ysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsn 451
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 452 LeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAs 468
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 535 laCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMet 551
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1904 CTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATG 1953

 552 TyrLeuSerProValArgSerProLysLysLysGlySerThrThrArgVa 568
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1954 TATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGT 2003

 568 lAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrG 585
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 585 lnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyr 601
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 618 uHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuG 635
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 668 sIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrP 685
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 685 heLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValPhe 701
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2354 TCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

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2454 TTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCC 2503

 735 roTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyr 751
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 752 IleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThrPr 768
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 768 oThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerP 785
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2604 AACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCAT 2653

 785 heGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSer 801
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2654 TCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

 802 AspArgValLeuLysArgSerAlaGluGlySerAsnProProLysPro 817
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; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


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; Sequence 1, Application US/07878960
; Patent No. 5444164
;  GENERAL INFORMATION:
;    APPLICANT:  Purchio, Anthony F.
;    APPLICANT:  Skonier, John
;    APPLICANT:  Neubauer, Michael G.
;    TITLE OF INVENTION:  TGF-BETA INDUCED GENE AND PROTEIN
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/878,960
;      FILING DATE:  05-MAY-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/833,835
;      FILING DATE:  05-FEB-1992
;      NAME:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sorrentino, Joseph M.
;      REGISTRATION NUMBER:  32,598
;      REFERENCE/DOCKET NUMBER:  ON0092-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206/728-4800
;      TELEFAX:  206/727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2691 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  LUNG
;      CELL TYPE:  ADENOCARCINOMA
;      CELL LINE:  A549
US-07-878-960-1


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seq_documentation_block:
; Sequence 11, Application US/07891942G
; Patent No. 5679511
;  GENERAL INFORMATION:
;    APPLICANT:  Kwon, Byoung Se
;    TITLE OF INVENTION:  cDNA CLONES FOR HUMAN TYROSINASE AND FOR
;    TITLE OF INVENTION:  A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christopher A. Michaels, Barnard, Brown &
;      ADDRESSEE:  Michaels
;      STREET:  306 East State Street; Suite 220
;      CITY:  Ithaca
;      STATE:  NY
;      COUNTRY:  USA
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;       ZIP:  14850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/891,942G
;       FILING DATE:  01-JUN-1992
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  06/915,753
;       FILING DATE:  06-OCT-1986
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/362,847
;       FILING DATE:  07-JUN-1989
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Michaels, Christopher A
;       REGISTRATION NUMBER:  34,390
;       REFERENCE/DOCKET NUMBER:  IND1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  607-273-1711
;       TELEFAX:  607-273-2609
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2397 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-07-891-942G-11


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seq_documentation_block:
; Sequence 1, Application US/07675211
; Patent No. 5219737
;  GENERAL INFORMATION:
;     APPLICANT:  KAJIYAMA, NAOKI
;     APPLICANT:  NAKANO, EIICHI
;     TITLE OF INVENTION:  MUTANT LUCIFERASE OF A FIREFLY, MUTANT
;     TITLE OF INVENTION:  LUCIFERASE GENES, NOVEL RECOMBINANT DNAS CONTAINING THE
;     TITLE OF INVENTION:  GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  PENNIE & EDMONDS
;       STREET:  1155 AVENUE OF THE AMERICAS
;       CITY:  NEW YORK
;       STATE:  N.Y.
;       COUNTRY:  U.S.A
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/675,211
;       FILING DATE:  19910326
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MISROCK, S. LESLIE
;       REGISTRATION NUMBER:  18,872
;       REFERENCE/DOCKET NUMBER:  7005-026-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-9741
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1644 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Luciola cruciata
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1644
US-07-675-211-1


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seq_documentation_block:
; Sequence 1, Application US/07903047
; Patent No. 5229285
;  GENERAL INFORMATION:
;     APPLICANT:  Kajiyama, Naoki
;     APPLICANT:  Nakano, Eiichi
;     TITLE OF INVENTION:  Thermostable Luciferase Of Firefly,
;     TITLE OF INVENTION:  Thermostable Luciferase Gene Of Firefly, No. 5229285el Reco
;     TITLE OF INVENTION:  DNA, And Process For The Preparation Of Thermostable
;     TITLE OF INVENTION:  Luciferase Of Firefly
;     NUMBER OF SEQUENCES:  11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Pennie & Edmonds
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/903,047
;       FILING DATE:  19920623
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Misrock, S. Leslie
;       REGISTRATION NUMBER:  18,872
;       REFERENCE/DOCKET NUMBER:  7005-048
;     TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  212 790-9090
;       TELEFAX:  212 869-8864/9741
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1644 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
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;     MOLECULE TYPE:  cDNA to mRNA
US-07-903-047-1


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seq_documentation_block:
; Sequence 1, Application US/07767135
; Patent No. 5234811
;  GENERAL INFORMATION:
;     APPLICANT:  Beutler, Ernest
;     APPLICANT:  Sorge, Joseph A
;     TITLE OF INVENTION:  An Assay for a New Gaucher Disease
;     TITLE OF INVENTION:  Mutation
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  The Scripps Research Institute, Office of
;       ADDRESSEE:  Patent Counsel
;       STREET:  3366 No. 5234811th Torrey Pines Court, Suite 240
;       CITY:  La Jolla
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/767,135
;       FILING DATE:  19910927
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bingham, Douglas A
;       REGISTRATION NUMBER:  32,457
;       REFERENCE/DOCKET NUMBER:  SCR0422P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-554-2937
;       TELEFAX:  619-554-6312
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7620 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
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;       NAME/KEY:  exon
;       LOCATION:  356..611
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;       LOCATION:  3564..4116
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;     FEATURE:
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US-07-767-135-1


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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-841-652-1

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; Patent No. 5266459
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    TITLE OF INVENTION:  GAUCHER'S DISEASE: DETECTION OF A NEW
;    TITLE OF INVENTION:  MUTATION IN INTRON 2 OF THE GLUCOCEREBROSIDASE GENE
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5266459th Torrey Pines Road, TPC 8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/841,652
;      FILING DATE:  19920224
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0670P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7620 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
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;       OTHER INFORMATION:  /function= "Intron 9"
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US-07-841-652-1


alignment_scores:
            Quality:    7.00              Length:      7
              Ratio:  1.000                Gaps:       0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x US-07-841-652-1/rev   ..

 Align seg 1/1  to reverse of: US-07-841-652-1  from: 1  to: 7620

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Date: Feb 13, 2000  4:00 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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Search information block:
Query: US-09-026-459A-43
Query length: 859
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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
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US-08-038-760-2

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             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
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;       FILING DATE:  14-JUL-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  RENEE A. FITTS
;       REGISTRATION NUMBER:  35,136
;       REFERENCE/DOCKET NUMBER:  16930-000400US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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              Ratio:  1.000                Gaps:      0
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 Align seg 1/1  to: US-08-204-329-2  from: 1  to: 2994

     113 SerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPh 129
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     682 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 781

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     782 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 831

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     832 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 881

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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     882 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 931

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
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     313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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    1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

     329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
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    1382 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1431

     363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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    1432 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1481

     379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
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    1482 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1531

     396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
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    1532 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

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     429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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    1682 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1731

     463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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     546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
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     563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
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    2082 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACAC 2131

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seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-470-091-1

seq_documentation_block:
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


alignment_scores:
            Quality:  747.00              Length:    747
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x US-08-470-091-1   ..

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     226 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 275

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     276 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 325

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     326 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 375

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
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     376 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 425

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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     426 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 475

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 229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
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 246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
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 263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
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 279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
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 296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
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 313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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 346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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 363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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 396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
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 413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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 429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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 446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
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 463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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 563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
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 596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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1676 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1725
 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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 746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


alignment_scores:
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             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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seq_documentation_block:
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


alignment_scores:
            Quality:  747.00              Length:    747
              Ratio:  1.000                 Gaps:      0
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     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
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     932 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
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     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
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     279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
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; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
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;      LOCATION:  139..2924
US-08-482-627-4

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;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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     413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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    1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

     429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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    1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1681

     446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
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 479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
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 546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
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 646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
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2282 AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 2331

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2332 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2381

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2432 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2481

 713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
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 746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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2682 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAG 2731

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seq_documentation_block:
; Sequence 1, Application US/07915246
; Patent No. 5401836
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris L.
;    APPLICANT:  Fallis, Lynne
;    APPLICANT:  Bellmare, Guy
;    APPLICANT:  Boivin, Rodolphe
;    TITLE OF INVENTION:  A BRASSICA REGULATORY SEQUENCE FOR
;    TITLE OF INVENTION:  ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held, and Malloy
;      STREET:  500 W. Madison St. 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/915,246
;      FILING DATE:  19920716
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien, Donald J.
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  91 P 1125
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312 707-8889
;      TELEFAX:  312 707-9155
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1505 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Brassica napus
;      STRAIN:  Westar
;      DEVELOPMENTAL STAGE:  Somatic
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US-07-915-246-1


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seq_documentation_block:
; Sequence 1, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
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;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
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seq_documentation_block:
; Sequence 3, Application US/08234783
; Patent No. 5622835
; GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
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;       ADDRESSEE:  Howson and Howson
;       STREET:  Spring House Corporate Cntr, PO Box 457
;       CITY:  Spring House
;       STATE:  Pennsylvania
;       COUNTRY:  USA
;       ZIP:  19477
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/456,907
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/234,783
;       FILING DATE:  28-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST48AUSA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9200
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  633 base pairs
;       TYPE:  nucleic acid
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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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US-08-456-907-3


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seq_documentation_block:
; Sequence 5, Application US/08246982A
; Patent No. 5686288
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/246,982A
;      FILING DATE:  May 20, 1994
;      CLASSIFICATION:  435
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Jorge, A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  0609.3880002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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seq_documentation_block:
; Sequence 5, Application US/08453265
; Patent No. 5693757
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,265
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0609.3880003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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US-08-453-265-5


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 Align seg 1/1  to: US-08-453-265-5  from: 1  to: 10366

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About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-1998 Compugen Ltd.

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Search information block:
Query: US-09-026-459A-2_COPY_370_928
Query length: 559
Database: EST:*
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Database length: 1887831982
Search time (sec): 602.370000

score_list:

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gb_est19:AA763411	-	1040.00	2026.95	3.9e-104	914	! AA763411 vw54a04.r1 Soares mous
gb_est19:AA763485	-	1008.50	1965.28	1.1e-100	871	! AA763485 vw54h01.r1 Soares mous
gb_est38:AL120941	+	882.00	1720.49	4.6e-87	572	! AL120941 DKFZp762D143_r1 762 (s
gb_est9:AA072780	+	815.50	1590.16	8.3e-80	522	! AA072780 mm76a05.r1 Stratagene
gb_est32:C82304	+	681.50	1319.83	9.5e-65	799	! C82304 C82304 Leukocyte of Japa
gb_est32:AI745644	-	613.00	1192.69	1.1e-57	415	! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643	-	609.00	1184.90	3.1e-57	411	! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est13:AA361277	+	504.00	981.11	7.0e-46	304	! AA361277 EST70529 T-cell lymphc
gb_est22:AI020392	+	503.00	977.14	1.2e-45	356	! AI020392 ub17a05.r1 Stratagene
gb_est14:AA382103	+	490.00	954.25	2.2e-44	285	! AA382103 EST95270 Activated T-c
gb_est17:AA664676	-	328.50	633.12	1.7e-26	329	! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est5:N25402	+	314.00	602.42	8.6e-25	386	! N25402 yx40c12.r1 Soares melanc
gb_est11:AA210875	+	272.00	517.27	4.8e-20	456	! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est5:N41391	+	267.00	507.36	1.7e-19	457	! N41391 yw70g06.r1 Soares_placen
gb_est36:AI931087	+	263.50	507.24	1.7e-19	267	! AI931087 fc77c03.y1 Zebrafish W
gb_est10:AA179202	+	250.50	474.60	1.1e-17	462	! AA179202 zp45e01.r1 Stratagene
gb_est34:AI807601	-	238.50	449.21	3.0e-16	527	! AI807601 we43d04.x1 NCI_CGAP_Lu
gb_est19:AA765882	-	238.00	462.46	5.4e-17	171	! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est21:AA992582	-	237.50	449.43	2.9e-16	443	! AA992582 ot97f01.s1 Soares_tota
gb_est26:AI337125	-	237.50	448.33	3.3e-16	483	! AI337125 qx83a07.x1 NCI_CGAP_GC
gb_est27:AI459215	-	237.50	447.32	3.8e-16	523	! AI459215 tk11a05.x1 NCI_CGAP_Lu
gb_est29:AI620692	-	237.50	447.20	3.8e-16	528	! AI620692 tu85g09.x1 NCI_CGAP_Ga
gb_est30:AI656871	-	237.50	445.99	4.5e-16	581	! AI656871 tt48c10.x1 NCI_CGAP_GC
gb_est5:N38772	-	237.00	444.56	5.4e-16	602	! N38772 yy42g02.s1 Soares melanc
gb_est1:T16945	-	231.50	439.84	9.8e-16	370	! T16945 NIB2045 Normalized infan
gb_est15:AA480678	-	230.50	437.70	1.3e-15	375	! AA480678 ne24e06.s1 NCI_CGAP_Co
gb_est25:AI248936	-	229.50	436.23	1.6e-15	360	! AI248936 qh67h05.x1 Soares_feta
gb_est26:AI333590	-	228.50	430.33	3.3e-15	491	! AI333590 qq06h02.x1 Soares_NhHM
gb_est19:AA744758	-	214.00	400.43	1.5e-13	541	! AA744758 ny71c01.s1 NCI_CGAP_GC
gb_gss14:AQ509204	+	210.00	394.09	3.5e-13	478	! AQ509204 nbxb0094G15r CUGI Rice
gb_est24:AI240076	-	207.00	392.25	4.4e-13	346	! AI240076 qh44f07.x1 Soares_NFL_
gb_est42:AV302462	+	205.00	397.00	2.4e-13	174	! AV302462 AV302462 RIKEN full-le
gb_est31:AI680908	+	203.50	379.58	2.2e-12	545	! AI680908 tx42f09.x1 NCI_CGAP_Lu
gb_est20:AA885217	-	201.00	381.66	1.7e-12	313	! AA885217 am34d06.s1 Soares_NFL_
gb_est36:AI917628	-	201.00	380.61	2.0e-12	340	! AI917628 wi36a12.x1 NCI_CGAP_Co
gb_est33:AV111279	+	200.00	380.91	1.9e-12	284	! AV111279 AV111279 Mus musculus
gb_est25:AI288993	-	192.50	361.16	2.4e-11	419	! AI288993 ql86g01.x1 Soares_NhHM
gb_est12:AA312113	+	187.00	348.28	1.2e-10	491	! AA312113 EST182807 Jurkat T-cel
gb_est3:R46603	-	183.50	343.06	2.4e-10	429	! R46603 yg51g11.s1 Soares infant
gb_est44:AW209660	+	181.50	335.83	6.1e-10	556	! AW209660 ul45f01.y1 Rashbass mo
gb_est4:H20728	+	175.00	325.79	2.2e-09	445	! H20728 ym47c11.r1 Soares infant
gb_est20:AA861150	-	170.50	318.09	5.9e-09	405	! AA861150 ak36a12.s1 Soares_t
gb_est3:R57845	+	164.00	317.64	6.3e-09	152	! R57845 F6142 Fetal heart Hom
gb_est15:AA497926	+	163.00	298.87	7.0e-08	573	! AA497926 vi74c08.r1 Stratage
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seq_name: gb_est19:AA763411

seq_documentation_block:
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DEFINITION vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION AA763411
VERSION AA763411.1 GI:2813158
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 914)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Jan 14, 1998 this sequence version replaced gi:1798537.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:661286
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 422.
FEATURES Location/Qualifiers
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/clone_lib="Soares mouse mammary gland NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 257 a 178 c 217 g 261 t 1 others
ORIGIN

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Quality: 1040.00 Length: 273
Ratio: 4.177 Gaps: 2
Percent Similarity: 91.209 Percent Identity: 80.952

alignment_block:
US-09-026-459A-2_COPY_370_928 x AA763411/rev ..

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812 CCCCCCACCCCGGTTTGGGCTGTTTTGGAACCTATCCAACAATTTATTGT 763

 18 tIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrP 35
    :|||||||||||||||:::|||:::|||||||||   |||   |||
762 GATTTTAAACTCCGCCAATGACCGCCCCTCAGAATNTCTGTT.TCCCTCT 714

 35 heAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLys 51
    |||   :::      ||||||||||||      |||||||||   |||
713 CTAATATTGCGCCCGGTAACCCCAAAGAAATTCCCCTAAAGCGGGT.AAG 665

 52 AspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGl 68
    |||:::|||:::|||:::||||||||||||      ::::::      ||
664 GACGTTGGGCACATCCTTAAAGAGAAGTTTCTA...ACGCTGTGGCCAGG 618

 68 yCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrT 85
    |||||||   ||||||   ||||||||||||||   ||||||   ||||
617 CTGTGTGACCATCGGAGTACAGCGATATAAACTTTGAGTCCGATCGTATT 568

 85 yrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIle 101
    ||||||||||||||||||||||:::||||||||||||||||||||||||
567 ACCGTGTGATGGAATCCATGCTTAGATCAGAAGAAGAACGTTTGTCCATT 518

102 GlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLe 118
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517 CAGAATTTTAGCAAACTCCTAAATGACAACATCTTTCATATGTCTTTACT 468

118 uAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerG 135
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467 GGCCTGTGCTCTTGAAGTTGTAATGGCTACGTATAGCAGAAGTACATTGC 418

135 lnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnVal 151
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417 AGCATCTTGATTCTGGAACAGATTTGTCCTTCCCGTGGATTCTGAACGTA 368

152 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLy 168
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367 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATTGAAAGTTTTATCAA 318

168 sAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysG 185
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317 AGTGGAAGCCAACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTG 268

185 luHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPhe 201
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267 AGCATCGAATCATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTT 218

202 AspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGl 218
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217 GATCTCATTAAGCAGTCCAAGGATGGAGAAGGACCT...GATAACCTTGA 171

218 uSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaA 235
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170 ACCTGCTTGTCCTCTCAGCCTGCCTCTCCAGGGTAACCATACTGCAGCAG 121

235 spMetTyrLeuSerProValArgSerProLysLysLysGlySerThrThr 251
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252 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGl 268
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268 nThrGlnLysProLeuLys 274
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 20 TACTCAGAAGCCATTGAAA 2

seq_name: gb_est19:AA763485

seq_documentation_block:
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);; mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
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                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


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 Percent Similarity:  86.813   Percent Identity: 75.824

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AA763485/rev   ..

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    817 CCCCCCACATCCAGTTGGGCCGTTTTTGATACTACTCCACCATTAGGGGG 768

     18 tIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrP 35
        :::|||   |||   |||   :::|||||||||||||||:::      |
    767 GTTTTTAATTTCCCCAAGTATCAGCCCATCCGAAAATCTTGTTCCCTCCT 718

     35 heAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLys 51
        ||:::         :::   ||||||:::::::::|||      :::
    717 TCCATATTGTCCCGTTACCTCCAAAGAACAATCTCCTAGGAGCTTAAAGG 668
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     52 AspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGl 68
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    667 TTGTCTGCCCACCCTTTAAAAGAGAGGGTTCTTAACGCTGTGGGCCAGGG 618

     68 yCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrT 85
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    617 CTGTGTTGACATCGGAGTACAGCGATATACACTTGGAGTCCGATTGTATT 568

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    102 GlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLe 118
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    517 CAGAATTTTAGCACACTCCTAAATGACAACATCTTTCATATGTCTNTACT 468

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    367 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATTGAAAGTTTTATCAA 318

    168 sAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysG 185
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    317 AGTGGAAGCCAACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTG 268

    185 luHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPhe 201
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    120 ATATGTATCTTTCTCCTCTAAGATCTCCAAAGAAAAGAACTTCCACTACA 71

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seq_name: gb_est38:AL120941

seq_documentation_block:
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DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES              Location/Qualifiers
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BASE COUNT      180 a    128 c     98 g    166 t
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alignment_block:
 US-09-026-459A-2_COPY_370_928 x AL120941   ..

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    137 uAspSerGlyThrAspLeuSerProTrpIleLeuAsnValLeuAsnL 154
        ||||||||||||||||||||||||||||||||||||||||||||||||
     51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

    154 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 170
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150

    171 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 187
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    151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

    187 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 204
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

    204 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 220
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

    221 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 237
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

    237 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 254
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

    254 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 270
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450
```

```
     271 LysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrAr 287
         ||||||||||||||||||||||||   ||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTC.CTGTTTTATAAAAAAGTGTATCG 499

     287 gLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluH 304
         ||||||||||||||||||||   ||||||||||||||||||   ||||
     500 GCTAGCCTATCTCCGGCTAAATCA.CTTTGTGAACGCCTTCTGCT.GAGC 547

     304 isProGluLeuGluHisIleIleTrp 312
         ||||||||||||  ||||||||||||
     548 ACCCAGAATTAGA.CATATCATCTGG 572

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:  815.50            Length:    175
              Ratio:  4.797               Gaps:      2
 Percent Similarity:  97.143   Percent Identity: 92.000

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AA072780   ..
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     340 TyrGlyIleCysLysVal LysAsnIleAspLeuLysPheLysIleIleVa 356
         ||||||||||||||||| |||||||||||||||||||||||||||||||||
       3 TATGGCATCTGCAAGGTGAAGAACATCGACCTCAAGTTCAAAATCATCGT 52

     356 lThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArgV 373
         |||||||||||||||||||||||||:::|||||||||||||||||||||
      53 CACTGCCTACAAGGATCTTCCTCACGCTGCCCAGGAGACCTTTAAACGTG 102

     373 alLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSer 389
         ||||||||:::|||||||:::|||||||||||||||||||||||||||||
     103 TTTTGATCAGAGAAGAGGAGTTTGATTCCATTATAGTATTCTATAACTCC 152

     390 ValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrAr 406
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     153 GTTTTCATGCAGAGACTAAAAACAAATATTTTACAGTATGCCTCCACCAG 202

     406 gProProThrLeuSerProIleProHisIleProArgSerProTyrLysP 423
         |||||||||||||||||||||||||||||||||||||||||||||||||
     203 GCCTCCTACCTTGTCACGAATAGCTCACATTCCTCGAAGCCCTTACAAGT 252

     423 heProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 439
         ||   ||||||||||||||||||||||||||||||||||||||||||||||
     253 TTTCTAGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCC 302

     440 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 456
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     303 CTAAAGAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAAT 352

     456 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 473
         |||||||||||||||||||||||||||||||||||||||||||||||||
     353 GACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACAT 402

     473 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 489
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     403 CTGAAAAGTTCCAGAAATAAACCAGATGGTGTGTAATAGTGACAGAGTG 452

     490 LeuLysArgSerAlaGluGlySer.AsnProProLysProLeuLysLysL 506
         ||||||:::      :::   ::: :::|||||||||||||||||||||
     453 CTCAAAGAAGTGCTGAAG...GCGGCAACCCCCCAAACCACTGAAGAAGC 499

     506 euArgPheAspIleGluGlySer 513
         |||||:::||||||||||||:::
     500 TGCGGCTTGACATCGAGGGAGCC 522

seq_name: gb_est32:C82304

seq_documentation_block:
LOCUS       C82304        799 bp    mRNA            EST       10-JUN-1999
DEFINITION  C82304 Leukocyte of Japanese flounder i Paralichthys olivaceus cDNA
            clone WC10-6, mRNA sequence.
ACCESSION   C82304
VERSION     C82304.1  GI:5039540
KEYWORDS    EST.
SOURCE      flounder.
  ORGANISM  Paralichthys olivaceus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
            Pleuronectiformes; Pleuronectoidei; Bothidae; Paralichthys.
REFERENCE   1  (bases 1 to 799)
  AUTHORS   Nam,B., Katagiri,T., Hong,Y., Hirono,I. and Aoki,T.
  TITLE     A survey of expressed genes in the leukocyte of Japanese flounder
            (Paralychthys olivaceus) infected with Hirame rhabdo virus
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 22, 1998 this sequence version replaced gi:3247348.
            Contact: Takashi Aoki
            Genetics and Biochemistry
            Tokyo University of Fisheries
            Konan, 4-5-7, Minato 108, Japan
            Tel: 03-5463-0556
            Fax: 03-5463-0690
            Email: ad95217@s4201.tokyo-u-fish.ac.jp
```

```
          clone WC10-6: similar to chicken retinoblastoma (GDRETINB).
FEATURES             Location/Qualifiers
     source          1. .799
                     /organism="Paralichthys olivaceus"
                     /db_xref="taxon:8255"
                     /clone="WC10-6"
                     /clone_lib="Leukocyte of Japanese flounder i"
                     /sex="Female"
                     /cell_type="leukocyte infected with Hirame r"
BASE COUNT      200 a    218 c    189 g    192 t
ORIGIN


alignment_scores:
            Quality:  681.50             Length:    274
              Ratio:  3.292                Gaps:      7
 Percent Similarity:  75.547   Percent Identity: 54.380

alignment_block:
 US-09-026-459A-2_COPY_370_928 x C82304   ..

 Align seg 1/1  to: C82304  from: 1  to: 799

      44 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 60
         :::::::::|||||||||:::::   ::::::      |||:::|||::
       1 CAAGACATGCTGAAGCGTTTGGAGACATTCAATCAGGCGTTTAGTGAAAG 50

      60 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 77
         :|||:::::::|||||||||      |||:::   :::|||:::||||||:
      51 TTTTGGTCAGGCAGTCGGCCCGCGCTGTATCGTACTTGGAAAGCAGCGAT 100

      77 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 93
         ::   ||||||||||||||||||||:::|||||||||:::|||||||||
     101 TTACCCTCGGAGTACGACTGTATTATAAAGTCATGGAGGCAATGTTGAAA 150

      94 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 110
         |||||||||:::|||||||||:::|||||||||||||||||||||||||
     151 TCGGAAGAGAAGCGACTGTCTGTGCAAAATTTCAGTAAACTCCTCAATGA 200

     110 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 127
         |:::   ||||||   |||||||||||||||||||||||||||||||||
     201 CTCCACATTCCACACATCACTTTTGGCCTGTGCTTTGGAGGTGGTCATGG 250

     127 laThrTyrSerArgSerThrSerGln..................... 135
         ||:::|||::::::|||      :::
     251 CAGCATATGGAGAGAGCTGTTTTAAGGCTGGAGGATACAACCATGGCGGT 300

     136 AsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLe 152
         :::   ::::::|||||||||:::   ||||||||||||||:::|||::
     301 GGGGACTCAGCTGGGACAGATGTTTGTTTCCCCTGGATACTGGATGTGTT 350

     152 uAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysA 169
         :||||||   |||||||||||||||||||||||||||||||||||||||||
     351 TAACCTCGCCGCCTTTGACTTCTACAAAGTTATCGAGAGCTTCATCAAGG 400

     169 laGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGlu 185
         ||      :::|||:::::::::::::::|||||||||||   ||||||
     401 CCTACCCCACACTGAGCAAAGATATTGTCAAACATCTGGAGACTTGCGAG 450

     186 HisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAs 202
         :::   |||||||||   :::||||||   :::   |||||||||||||||
     451 AACCTCATCATGGAGAGGATTGCATGGAGAACAGGCTCCCCGCTATTTGA 500

     202 pLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluS 219
         ||||:::|||||||:::   |||            :::::::::::::|||:
     501 CCTGCTGAAACAGGAGCATGACAGCGG....ACAGCAGAACAGGTGGAGA 546

     219 erAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAsp 235
         ::   :::   :::|||   |||||||||:::|||||||||||||||||||
     547 CCCCAGCCAGTTTCAACCAACCACTGCAGCACAACCACACCGCAGCTGAC 596

     236 MetTyrLeuSerProValArg.................SerProLysLy 246
         :::|||||||||||||||||||                  |||:::::
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     597 CTATATCTGTCCCCTGTGCGTCCGGGCCATCGTGTTTTGCCTCCTGAGTC 646

     246 sLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnA 263
         :  |||:::         |||||||||                  :::|
     647 TCCAGGCACG.........GTCAACTCT.................CATG 669

     263 laThrSerAlaPheGlnThrGlnLysProLeu.LysSerThr........ 276
         ||:::|||         ||||||   |||    :::||||||
     670 CTTCCTCTCACGCGCCAACCCAGCCGCCTACCCAGATCCACGACACTCCA 719

     277 .......SerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrL 291
                 ||||||||||||||||||||||||:::|||||||||||||||
     720 AGTCCACTCTCTCAGCCTTTTCTATAAAAAATTGTACCGTCTTGCCTACA 769

     291 euArgLeuAsnThrLeuCys 297
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     770 CGAGGCTGAAGATACTCTGC 789

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
            Quality:  613.00             Length:    122
              Ratio:  5.108                Gaps:      0
 Percent Similarity:  98.361   Percent Identity: 96.721
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alignment_block:
 US-09-026-459A-2_COPY_370_928 x AI745644/rev   ..

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     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     361 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 378
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     378 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 394
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     395 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 411
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     411 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 428
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     428 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 444
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     445 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 461
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     461 gIleLeuValSerIle 466
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      63 GTGTGTGTTTTCTCTT 48

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
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                     /db_xref="taxon:9606"
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                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
            Quality:  609.00             Length:    121
              Ratio:  5.118                Gaps:      0
 Percent Similarity:  98.347   Percent Identity: 96.694

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     346 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 362
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     362 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 379
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     379 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 395
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     396 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 412
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     412 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 429
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTGGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     429 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 445
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     446 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIl 462
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGGTG 61

     462 eLeuValSerIle 466
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      60 TGTGTTTTCTCTT 48

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
```

```
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


alignment_scores:
            Quality:  504.00            Length:    101
              Ratio:  5.040               Gaps:      0
 Percent Similarity:  99.010   Percent Identity: 98.020

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     196 SerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGl 212
         |||||||||||||||||||||||||||||||||||||||||||||||||  ||
       2 TCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGANGG 51

     212 yProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnA 229
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      52 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGA 101

     229 snAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLys 245
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     102 ATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAG 151

     246 LysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGl 262
         ||||||||||||||||||||||||||||||||||||||||||||||:::||
     152 AAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGNCACA 201

     262 nAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuS 279
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 AGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTT 251

     279 erLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThr 295
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     252 CACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA 301

     296 Leu 296
         |||
     302 CTT 304

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS       AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION  ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AI020392
VERSION     AI020392.1  GI:3234728
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:  503.00            Length:    105
              Ratio:  4.837               Gaps:      0
 Percent Similarity:  99.048   Percent Identity: 93.333

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356
```

```
     455 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 471
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     471 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 488
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     488 rgValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLys 504
         ||||||||||||||||||||||||||:::||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGCGGCAACCCCCCCAAACCACTGAAA 152

     505 LysLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHi 521
         ||||||||||||||||||||||||:::||||||||||||||||||||||||
     153 AAGCTGCGCTTTGACATCGAGGGAGCCGATGAAGCAGATGGGAGTAAACA 202

     521 sLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerT 538
         |||||||:::|||||||||||||||||||||||||||||||||||||||||
     203 TCTCCCAGCGGAGTCCAAATTCCAACAGAAACTGGCAGAAATGACTTCCA 252

     538 hrArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSer 554
         ||||||||||||||||||||||:::|||||||:::|||   |||:::|||
     253 CTCGAACACGAATGCAAAAGCAGAGAATGAATGAGAGCAAGGATGTCTCA 302

     555 AsnLysGluGluLys 559
         ||||||||||||||||
     303 AACAAGGAGGAAAAG 317

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
            Quality:  490.00             Length:     94
              Ratio:  5.269                Gaps:      0
 Percent Similarity:  98.936   Percent Identity: 98.936

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     276 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 292
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     292 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 309
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCGTTCTGTCTGAGCACCCAGAATTAGAAC 101

     309 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 325
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     326 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 342
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     342 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 359
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     359 yrLysAspLeuProHisAlaValGlnGluThr 369
         |||||   |||||||||||||||||||||||||
     252 ACAAGGGTCTTCCTCATGCTGTTCAGGAGACA 283

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
```

```
          Tel: (301) 496-1550
          Email: Robert_Strausberg@nih.gov
          Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
          Ph.D.
           cDNA Library Preparation: David B. Krizman, Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html

          Seq primer: -40m13 fwd. ET from Amersham
          High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a      62 c      65 g     108 t
ORIGIN


alignment_scores:
            Quality:  328.50              Length:     98
              Ratio:  4.212                 Gaps:      1
 Percent Similarity:  79.592   Percent Identity: 69.388

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     133 ThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLe 149
         |||||||||||||||||||||||||||||||   ||||||||||||||||||
     327 ACATCTCAGAATCTCGATTCTGGAACAGATTGGTCTTTCCCATGGATTCT 278

     149 uAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerP 166
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     277 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTT 228

     166 heIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGlu 182
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     227 TTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAA 178

     183 ArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer..... 196
         ||||||||||||||||||||||||||||||||||||||||
     177 CGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGTGATCCT 128

     197 .............AspSerProLeuPheAspLeuIleLysGlnSerLysA 209
                     :::      :::::::::      |||:::::::   :
     127 GCCTTATCCTGGAGAAAGAAATGTTATGCAAGAGGCCAAGAAGAAGCTAA 78

     209 spArgGluGlyProThrAspHisLeuGluSerAlaCysProLeu 223
         ::::::::::::      |||          |||      ||||||
      77 ACAAACAAGCCATGATGGATTCCCATCTCAGCTTATTACCATTG 34

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a      78 c      87 g      96 t      11 others
ORIGIN


alignment_scores:
            Quality:  314.00              Length:     66
              Ratio:  5.065                 Gaps:      0
 Percent Similarity:  93.939   Percent Identity: 93.939

alignment_block:
 US-09-026-459A-2_COPY_370_928 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     493 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 509
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     509 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 526
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     526 erLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMet 542
         |||||||||||||||   ||||||   ||||||||||||||||||||||
     101 CCAAATTTCAGCAGNNACTGGCAGANATGACTTCTACTCGAACACGAATG 150

     543 GlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 558
```

```
        ||||||||   ||||||||||||||||||||||||   ||||||||
    151 CAAAAGCAGANNATGAATGATAGCATGGATACCTCANACAAGGAAGAG 198

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


alignment_scores:
            Quality:  272.00             Length:     57
              Ratio:  4.857                Gaps:      1
 Percent Similarity:  98.246   Percent Identity: 98.246

alignment_block:
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 Align seg 1/1  to: AA210875  from: 1  to: 456

     504 LysLysLeuArg.PheAspIleGluGlySerAspGluAlaAspGlySerL 520
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      12 AAAAAACTACGCTTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTA 61

     520 ysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThr 536
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      62 AACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACT 111

     537 SerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspTh 553
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     112 TCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATAC 161

     553 rSerAsnLysGluGluLys 559
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     162 CTCAAACAAGGAAGAGAAA 180

seq_name: gb_est5:N41391

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DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


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            Quality:  267.00             Length:     83
              Ratio:  3.560                Gaps:      7
 Percent Similarity:  90.361   Percent Identity: 83.133

alignment_block:
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     218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

     488 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 505
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

     505 ysLeuArgPhe.AspIleGluGlySerAspGluAla.AspGlySerLysH 521
         |||||||||||| |||||||||||||||||||||| ||||||||||||
     318 AACTACGCTTTGGATATTGAAGGATCAGATGAAGCCAGATGGAAGTAAAC 367

     521 isLeuProGly.GluSerLysPhe...GlnGlnLysLeu.AlaGluMetT 536
         |||||||||||| ||||||::::::   :::|||||||||| ||||||||||
     368 ATCTCCCAGGAGGAGTCCCAAATTTCCAGCCAGAAACTGGGCAGAAATGA 417

     536 hrSer.Thr...ArgThrArgMetGlnLysGlnLysMet 547
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seq_name: gb_est36:AI931087

seq_documentation_block:
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DEFINITION  fc77c03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to
            TR:Q98966 Q98966 RETINOBLASTOMA PROTEIN. ;, mRNA sequence.
ACCESSION   AI931087
VERSION     AI931087.1  GI:5667051
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
            Cyprinoidea; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 267)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2947971.
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 241.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:7955"
                     /clone_lib="Zebrafish WashU MPIMG EST"
                     /sex="mixed"
                     /tissue_type="26 somite embryos, adult livers, shield
                     stage embryos"
                     /lab_host="XL1-blue MRF"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
                     strand cDNA was primed with a Not I - oligo(dT)15 primer
                     [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT3'];
                     double-stranded cDNA was ligated to Sal I adaptors (BRL),
                     digested with Not I and cloned into the Not I and Sal I
                     sites of the pSPORT1 vector (BRL). Library was constructed
                     by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
                     Institut fuer Molekulare Genetik,Berlin). cDNAs for EST
                     analysis were selected following oligonucleotide
                     hybridization fingerprinting of arrayed clones from
                     zebrafish late somitogenesis (26 ss), adult liver or
                     embryonic shield stage (5.6 h) libraries.  Fingerprint
                     data were used to computationally cluster cDNAs, and a
                     single cDNA from each cluster was chosen for sequencing.
                     In some cases multiple members of the same cluster were
                     sequenced to assess clustering parameters or single clones
                     were sequenced additional times to assess quality
                     control."
BASE COUNT       66 a     70 c     72 g     58 t      1 others
ORIGIN


alignment_scores:
            Quality:  263.50              Length:     84
              Ratio:  3.819                Gaps:      1
 Percent Similarity:  82.143   Percent Identity: 61.905

alignment_block:
 US-09-026-459A-2_COPY_370_928 x AI931087   ..

 Align seg 1/1  to: AI931087  from: 1  to: 267

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     157 eAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuT 174
         :|||   ||||||||||||||||||||||||||||||||   :::|||
      65 GGACGGTTACAAGGTGATCGAGAGCTTCATTAAAGCCGAGCCCACCCTGA 114

     174 hrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGlu 190
           ::::::|||:::|||||||||||||:::|||||||||   |||||||||
     115 AACATGACATGGTGAAGCACCTGGAGCAGTGCGAACATGTGATCATGGAG 164

     191 SerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSe 207
         ||||||||||||   :::|||||||||||||||||||||:::|||||||||
     165 AGTCTTGCATGGAGAGCGGACTCTCCACTGTTTGACCTGCTCAAACAGTC 214

     207 rLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuA 224
         |::::::   |||||||||   ::::::   |||      :::   ||||
     215 TCGCGAG...GAAGGACCCGGTGAACAAGCAGAGCCCCCTGCAACACTCA 261

     224 sn 224
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     262 AC 263
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Date: Feb 13, 2000  5:35 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171029_15735/app_query.fasta.1
 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=seq2.rni
 -GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
 -LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
 -XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
 -YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
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 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
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Search information block:
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Query length: 559
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Database sequences: 214294
Database length: 59861208
Search time (sec): 27.490000


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Sequence                    Strd Orig    ZScore    EScore Len  ! Documentation  ..
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-09-018-628-17 +  102.00  159.95  0.1791    2907  !
/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-751-189-1 +  101.50  144.82  1.25
/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-09-060-836-1 +  101.50  144.82  1.25
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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products a
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


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      34 yrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgVal 50
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 67 nGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuT 84
990 GGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGT 1039
 84 yrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSer 100
1040 ATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1089
101 IleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLe 117
1090 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTT 1139
117 uLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrS 134
1140 ATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACAT 1189
134 erGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsn 150
1190 CTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1239
151 ValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIl 167
1240 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTAT 1289
167 eLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgC 184
1290 CAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGAT 1339
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1340 GTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1389
201 PheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLe 217
1390 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT 1439
217 uGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaA 234
1440 TGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAG 1489
234 laAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThr 250
1490 CAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1539
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seq_documentation_block:
; Sequence 2, Application US/08038760
; Patent No. 5496731
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products an
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


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; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
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US-08-204-329-2

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seq_documentation_block:
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


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; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/470,091
;       FILING DATE:  JUN-16-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
US-08-470-091-2


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; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


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              Ratio:  5.170                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


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;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
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;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10357
;       FILING DATE:  13-SEP-1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/121,108
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  FP-UC 1117
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
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seq_documentation_block:
; Sequence 1, Application US/07708962
; Patent No. 5262321
;  GENERAL INFORMATION:
;    APPLICANT:  Livingston, David M.
;    APPLICANT:  Ewen, Mark E.
;    TITLE OF INVENTION:  Tumor Suppressor
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Choate, Hall & Stewart
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/708,962
;      FILING DATE:  19910531
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kennedy, Bill
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  DFCI 209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-5020
;      TELEFAX:  (617) 227-7566
;      TELEX:  289374
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2808 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-708-962-1

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             Ratio:  1.869                 Gaps:     17
 Percent Similarity:  50.502   Percent Identity: 26.542

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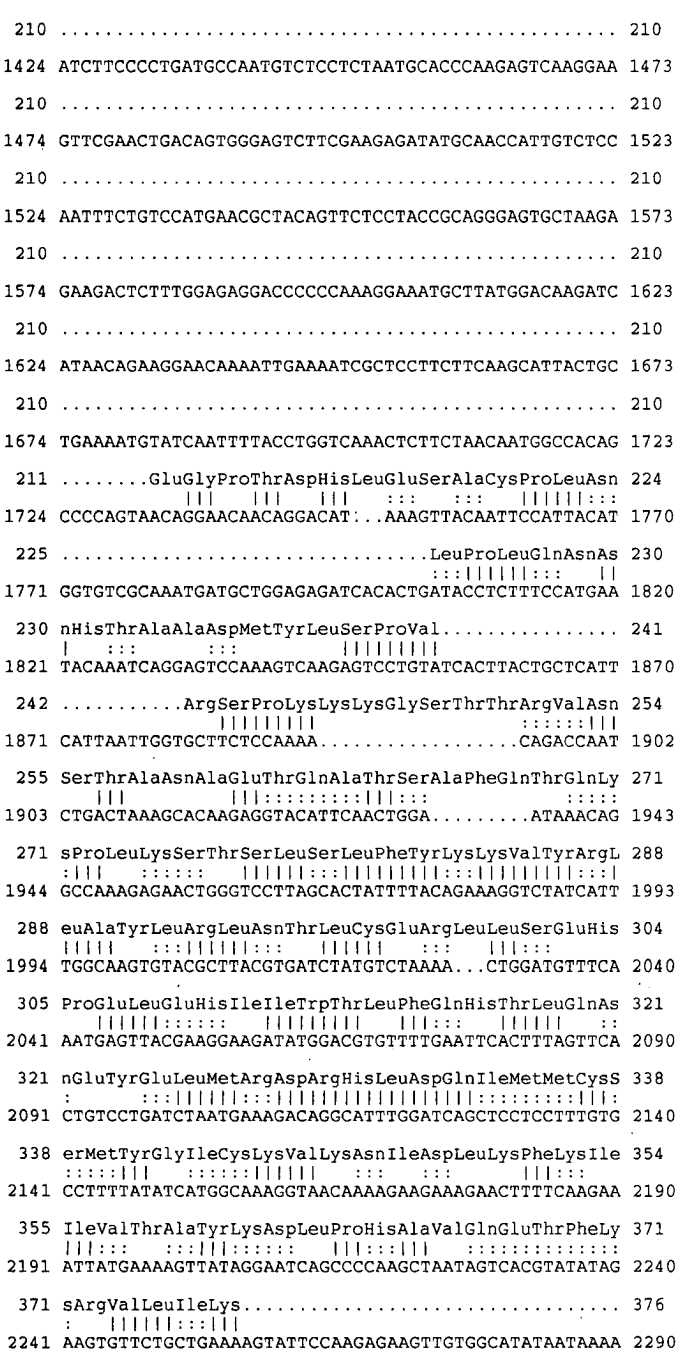
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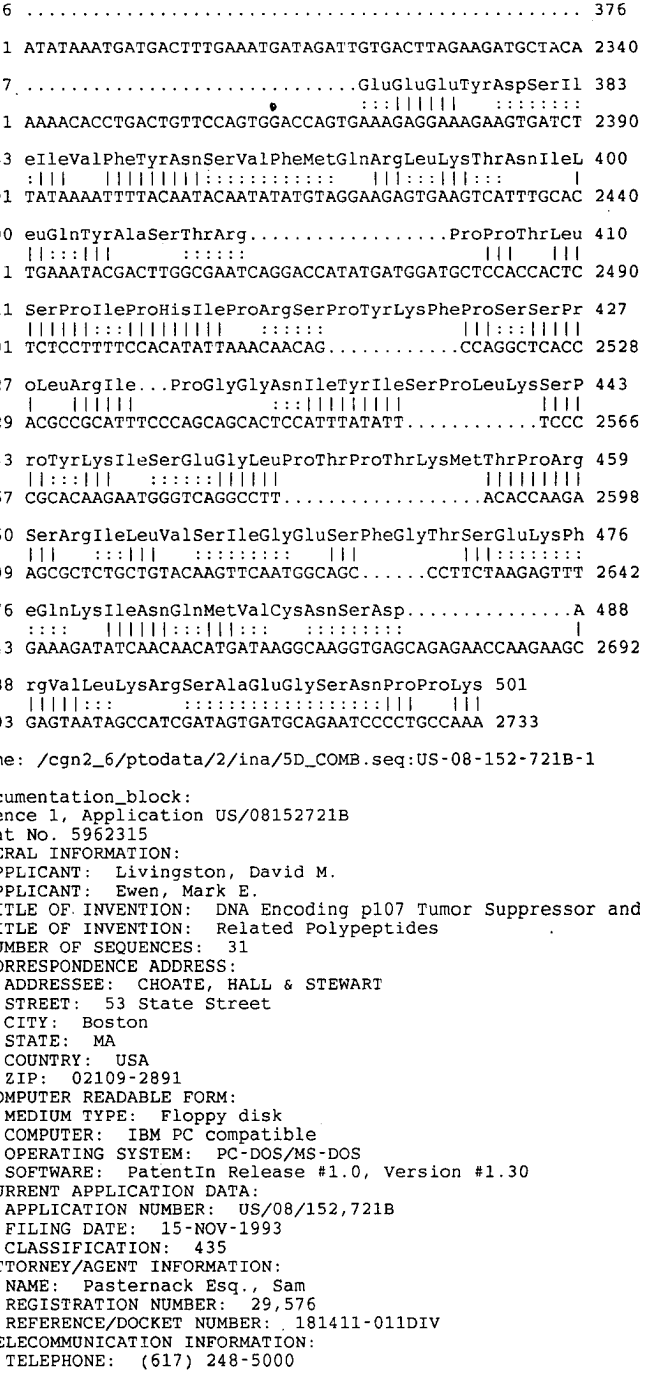
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seq_documentation_block:
; Sequence 1, Application US/08152721B
; Patent No. 5962315
;  GENERAL INFORMATION:
;    APPLICANT:  Livingston, David M.
;    APPLICANT:  Ewen, Mark E.
;    TITLE OF INVENTION:  DNA Encoding p107 Tumor Suppressor and
;    TITLE OF INVENTION:  Related Polypeptides
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHOATE, HALL & STEWART
;      STREET:  53 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2891
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/152,721B
;      FILING DATE:  15-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pasternack Esq., Sam
;      REGISTRATION NUMBER:  29,576
;      REFERENCE/DOCKET NUMBER:  181411-011DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-5000
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;      TELEFAX:  (617) 248-4000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2808 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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;      CLONE:  cDNA encoding p107
US-08-152-721B-1


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    411 SerProIleProHisIleProArgSerProTyrLysPheProSerSerPr 427
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    427 oLeuArgIle...ProGlyGlyAsnIleTyrIleSerProLeuLysSerP 443
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  2529 ACGCCGCATTTCCCAGCAGCACTCCATTTATATT............TCCC 2566

    443 roTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 459
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    460 SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPh 476
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    488 rgValLeuLysArgSerAlaGluGlySerAsnProProLys 501
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seq_documentation_block:
; Sequence 1, Application US/08106493A
; Patent No. 5457049
;  GENERAL INFORMATION:
;    APPLICANT:  Antonio Giordano
;    TITLE OF INVENTION:  "TUMOR SUPPRESSOR PROTEIN PRB2,
;    TITLE OF INVENTION:  RELATED GENE PRODUCTS, AND DNA ENCODING
;    TITLE OF INVENTION:  THEREFOR"
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University-Of The Commonwealth
;      ADDRESSEE:  System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/106,493A
;      FILING DATE:  August 12, 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mullins, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  6056-188
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5457049e
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3249 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  linear
US-08-106-493A-1


alignment_scores:
            Quality:  618.00              Length:    766
              Ratio:  1.648                 Gaps:     22
 Percent Similarity:  48.956   Percent Identity: 24.935

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; Sequence 1, Application US/08429264
; Patent No. 5532340
;  GENERAL INFORMATION:
;    APPLICANT:  Antonio Giordano
;    TITLE OF INVENTION:  "TUMOR SUPPRESSOR PROTEIN
;    TITLE OF INVENTION:  PRB2"
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seidel, Gonda, Lavorgna & Monaco, P.C.
;      STREET:  1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/429,264
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/106,493
;      FILING DATE:  August 12, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, D.A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-188 DI1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5532340e
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3249 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  linear
US-08-429-264-1


alignment_scores:
            Quality:  618.00              Length:    766
              Ratio:  1.648                 Gaps:     22
 Percent Similarity:  48.956   Percent Identity: 24.935

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; Sequence 1, Application US/08832883
; Patent No. 5807681
;  GENERAL INFORMATION:
;    APPLICANT:  Giordano, Antonio
;    APPLICANT:  Baldi, Alphonso
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS AND PROGNOSIS
;    TITLE OF INVENTION:  OF CANCER
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
;      STREET:  Suite 1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,883
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-13 US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4853 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  70..3489
US-08-832-883-1


alignment_scores:
            Quality:  618.00              Length:    766
              Ratio:  1.648                 Gaps:     22
 Percent Similarity:  48.956   Percent Identity: 24.935

alignment_block:
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    3073 AGGGGAGACCTCATTCAGTTCTACAACAACATCTACATCAAACAGATTAA 3122

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    3123 GACATTTGCCATGAAGTACTCACAGGCAAATATGGATGCTCCTCCACTCT 3172

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    3173 CTCCCTATCCATTTGTAAGA..................ACAGGCTCCCCT 3204

     428 LeuArgIle.........ProGlyGlyAsnIleTyrIleSerProLeuLy 441
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     458 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 474
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seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-832-877-1

seq_documentation_block:
; Sequence 1, Application US/08832877
; Patent No. 5840506
;  GENERAL INFORMATION:
;    APPLICANT:  Giordano, Antonio
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  116
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
;      STREET:  Suite 1800 Two Penn Center Plaza
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,877
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  8321-13 US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4853 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  70..3489
US-08-832-877-1


alignment_scores:
            Quality:  618.00              Length:    766
              Ratio:  1.648                 Gaps:     22
 Percent Similarity:  48.956   Percent Identity: 24.935

alignment_block:
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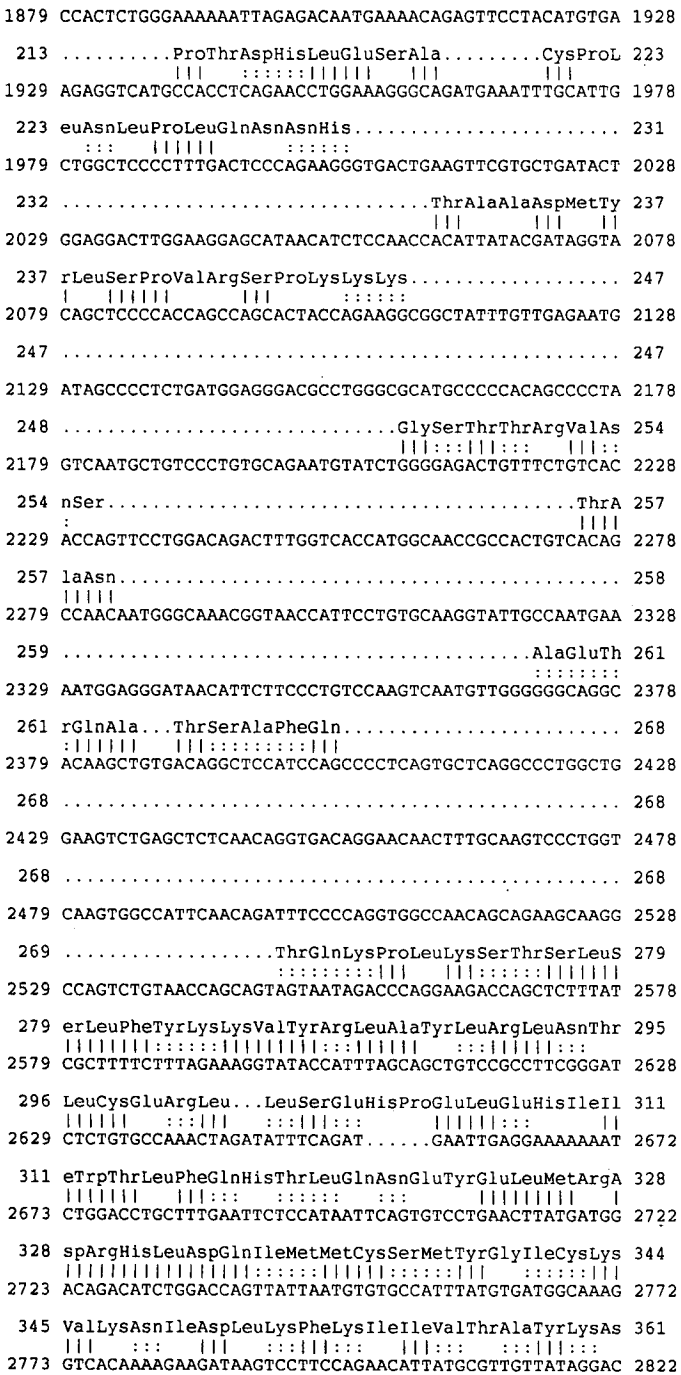
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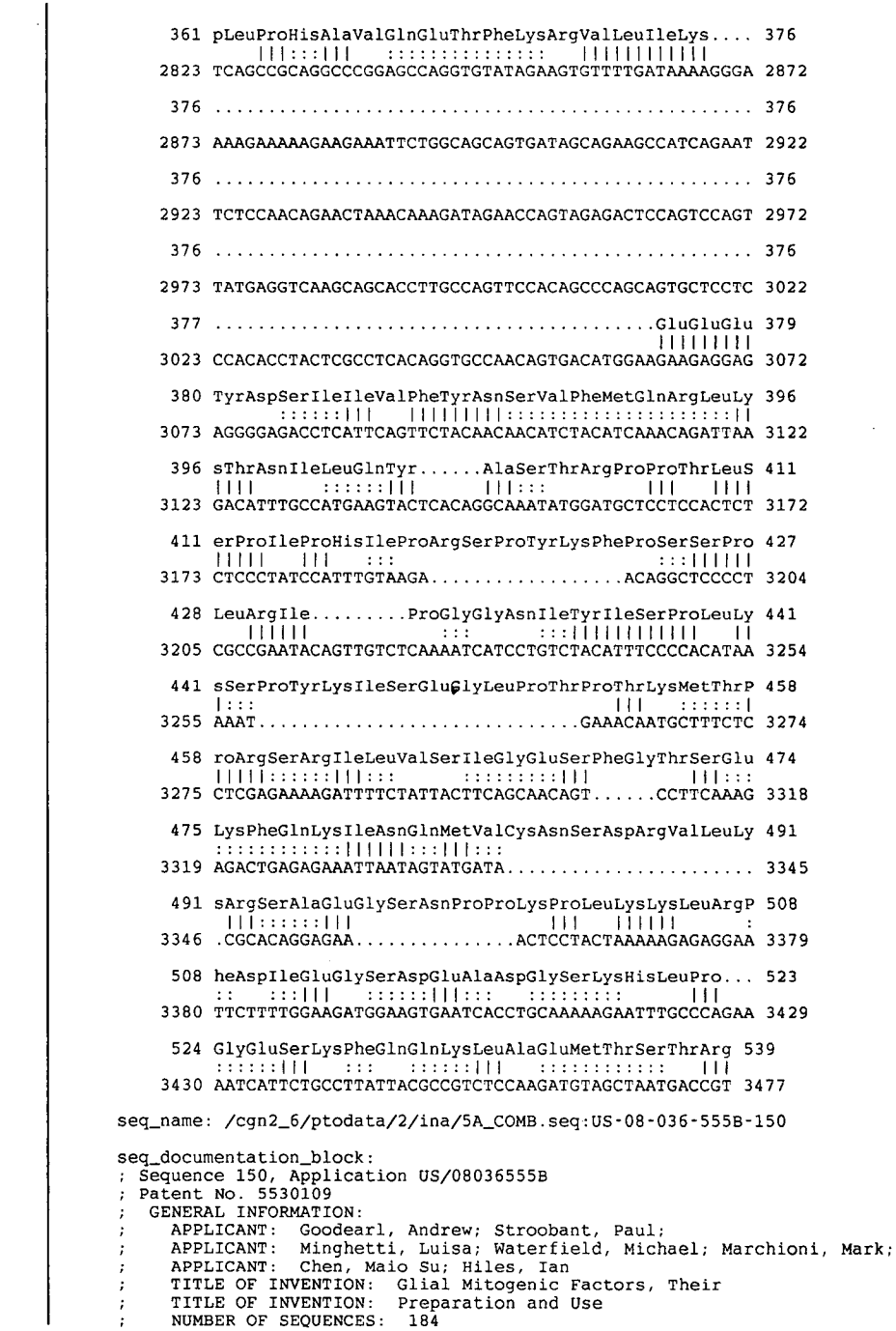
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-036-555B-150

seq_documentation_block:
; Sequence 150, Application US/08036555B
; Patent No. 5530109
;  GENERAL INFORMATION:
;    APPLICANT:  Goodearl, Andrew; Stroobant, Paul;
;    APPLICANT:  Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
;    APPLICANT:  Chen, Maio Su; Hiles, Ian
;    TITLE OF INVENTION:  Glial Mitogenic Factors, Their
;    TITLE OF INVENTION:  Preparation and Use
;    NUMBER OF SEQUENCES:  184
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/036,555B
;      FILING DATE:  24-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  30-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APRIL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.K. 91 07566.3
;      FILING DATE:  10-APRIL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsai, Christine H.
;      REGISTRATION NUMBER:  34,266
;      REFERENCE/DOCKET NUMBER:  LUD 5250.4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1764
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-036-555B-150


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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

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Searched: 214294 seqs, 59861208 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	2493	99.9	2995	4	US-08-959-638-7	Sequence 7, Appli
	3	2493	99.9	2994	4	US-08-482-627-4	Sequence 4, Appli
	4	2460	98.6	3232	1	US-08-038-760-1	Sequence 1, Appli
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	6	2460	98.6	3232	4	US-08-470-091-1	Sequence 1, Appli
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	9	28	1.1	28	4	US-08-859-998-1097	Sequence 1097, Ap
	10	22	0.9	52	1	US-07-826-928A-15	Sequence 15, Appl
	11	22	0.9	52	1	US-07-826-928A-36	Sequence 36, Appl
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	44	16	0.6	9606	1	US-07-741-940-1	Sequence 1, Appli
	45	16	0.6	6924	4	US-08-448-164-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
; GENERAL INFORMATION:
; APPLICANT: SHEPARD, H. M.
; APPLICANT: WEN, SHU F.
; TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
; TITLE OF INVENTION: MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,329
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05866
; FILING DATE: 14-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RENEE A. FITTS
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16930-000400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
US-08-204-329-2

Query Match 99.9%; Score 2493; DB 2; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
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Db    490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549
Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
Db    550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609
Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
Db    610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669
Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
Db    670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729
Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
Db    730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789
Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
Db    790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849
Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
Db    850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909
Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
Db    910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969
Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
Db    970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029
Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
Db   1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089
Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
Db   1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149
Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
Db   1150 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209
Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
Db   1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269
Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
Db   1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329
Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
Db   1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389
Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
Db   1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449
Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
Db   1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509
Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
Db   1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569
Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
Db   1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629
Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
Db   1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689
Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
Db   1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749
Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
Db   1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809
Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
Db   1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869
Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
Db   1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929
Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
Db   1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989
Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
Db   1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049
Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
Db   2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109
Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
Db   2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169
Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
Db   2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229
Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
Db   2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289
Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
Db   2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349
Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
Db   2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409
Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
Db   2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469
Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
Db   2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529
Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
Db   2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589
Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
Db   2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649
Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
Db   2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709
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Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
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Db   2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2769

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   2
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7

  Query Match           99.9%;  Score 2493;  DB 4;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549

Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
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Db    730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

Qy    604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
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Db   1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149

Qy    724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

Qy    1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569

Qy    1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy    1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689

Qy    1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
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Db    1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

Qy    1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

Qy    1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869

Qy    1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929

Qy    1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989

Qy    1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049

Qy    1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

Qy    1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169

Qy    1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

Qy    1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289

Qy    1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349

Qy    1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409

Qy    1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469

Qy    2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

Qy    2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589

Qy    2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649

Qy    2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709

Qy    2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2769

Qy    2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy    2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy    2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
           ||||||||||||||||||||||||||||||||
Db    2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
```

RESULT 3
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
; GENERAL INFORMATION:
; APPLICANT: Lee, Wen-Hwa
; APPLICANT: Lee, Eva Y-H.P
; TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
; TITLE OF INVENTION: and Regulator
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,627
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,947
; FILING DATE: 28-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 1707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 139..2924
US-08-482-627-4

Query Match 99.9%; Score 2493; DB 4; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
Db     430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy      64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
Db     490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549

Qy     124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
Db     550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

Qy     184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
Db     610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy     244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
Db     670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy     304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
Db     730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy     364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
Db     790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy     424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
Db     850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

Qy     484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
Db     910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969

Qy     544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
Db     970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

Qy     604 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
Db    1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089

Qy     664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
Db    1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149

Qy     724 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
Db    1150 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

Qy     784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
Db    1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269

Qy     844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
Db    1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

Qy     904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
Db    1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389

Qy     964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
Db    1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449

Qy    1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
Db    1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

Qy    1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
Db    1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569

Qy    1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
Db    1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy    1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
Db    1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689

Qy    1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
Db    1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

Qy    1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
Db    1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

Qy    1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
Db    1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869

Qy    1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
Db    1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929

Qy    1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
Db    1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989

Qy    1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
Db    1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049

Qy    1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
Db    2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

Qy    1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
Db    2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169

Qy    1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
Db    2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

Qy    1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
Db    2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289

Qy    1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
Db    2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349

Qy    1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
Db    2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409

Qy    1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
Db    2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469

Qy    2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
Db    2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

Qy    2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589

Qy    2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649

Qy    2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709

Qy    2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2769

Qy    2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy    2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy    2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db    2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   4
US-08-038-760-1
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
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US-08-038-760-1

Query Match 98.6%; Score 2460; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy      97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy     157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy     217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy     277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy     337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy     397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy     457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy     517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy     577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy     637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy     697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy     757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy     817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy     877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy     937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy     997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy   1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy   1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy   1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy   1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy   1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy   1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy   1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy   1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy   1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2017 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT   5
US-08-038-760-2/c
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             98.6%;  Score 2460;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
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  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy      97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy     157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy     217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy     277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy     337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy     397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy     457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy     517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy     577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy     637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy     697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy     757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy     817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy     877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy     937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy     997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy    1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy    1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy    1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy    1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy    1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy    1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy    1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy    1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy    1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy    1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy    1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy    1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy    1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy    1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy    1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311

Qy    1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy    2017 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy    2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy    2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071
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Qy   2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT 6
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,091
; FILING DATE: JUN-16-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..2469
US-08-470-091-1

Query Match 98.6%; Score 2460; DB 4; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy     97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy    157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy    217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy    277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy    337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy    397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy    457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy    517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy    577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy    637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy    697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy    757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy    817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy    877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy    937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy    997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy   1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db   1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy   1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy   1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy   1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy   1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy   1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy   1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
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Db   1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy   1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
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Db   1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy   1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2017 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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RESULT 7
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
; GENERAL INFORMATION:
; APPLICANT: Xu, Hong-Ji
; APPLICANT: Hu, Shi-Xue
; APPLICANT: Benedict, William F.
; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,091
; FILING DATE: JUN-16-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,760
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7409-025-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA
US-08-470-091-2

Query Match 98.6%; Score 2460; DB 4; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      37 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC  96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3230 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 3171

Qy      97 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3170 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 3111

Qy     157 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3110 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 3051

Qy     217 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3050 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 2991

Qy     277 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2990 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

Qy     337 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 2871

Qy     397 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2870 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 2811

Qy     457 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 516
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Db    2810 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 2751

Qy     517 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2750 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 2691

Qy     577 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 636
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Db    2690 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

Qy     637 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 696
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Db    2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 2571

Qy     697 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 756
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Db    2570 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 2511

Qy     757 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 816
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Db    2510 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 2451

Qy     817 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 876
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Db    2450 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 2391

Qy     877 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 936
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Db    2390 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 2331

Qy     937 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2330 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 2271

Qy     997 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2270 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 2211

Qy    1057 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2210 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 2151

Qy    1117 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2150 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 2091

Qy    1177 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1236
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Db    2090 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 2031

Qy    1237 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2030 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1971

Qy    1297 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1970 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1911

Qy    1357 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1910 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1851

Qy    1417 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1850 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1791

Qy    1477 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1790 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy    1537 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1671

Qy    1597 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1670 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1611

Qy    1657 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1716
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1610 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1551

Qy    1717 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1776
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1550 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1491

Qy    1777 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1490 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1431

Qy    1837 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1430 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1371

Qy    1897 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1370 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1311

Qy    1957 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2016
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1310 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1251

Qy    2017 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2076
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Db    1250 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 1191

Qy    2077 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1190 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

Qy    2137 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 1071

Qy    2197 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2256
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Db   1070 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 1011

Qy   2257 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2316
Db   1010 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 951

Qy   2317 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2376
Db    950 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 891

Qy   2377 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2436
Db    890 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 831

Qy   2437 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
Db    830 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 771
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RESULT   8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;     APPLICANT:  The Regents of the University of California
;     APPLICANT:  and Canji, Inc.
;     TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;     TITLE OF INVENTION:  Susceptibility Gene Product
;     NUMBER OF SEQUENCES:  3
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Campbell and Flores
;       STREET:  4370 La Jolla Village Drive
;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10357
;       FILING DATE:  13-SEP-1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/121,108
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  FP-UC 1117
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2923
PCT-US94-10357-1
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  Query Match             97.8%;  Score 2442;  DB 6;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2492;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63
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Db    430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 489

Qy     64 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 123
Db    490 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 549

Qy    124 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 183
Db    550 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

Qy    184 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 243
Db    610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 669

Qy    244 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 303
Db    670 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

Qy    304 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 363
Db    730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 789

Qy    364 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 423
Db    790 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 849

Qy    424 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 483
Db    850 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

Qy    484 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 543
Db    910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 969

Qy    544 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 603
Db    970 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

Qy    604 CCTTTTATGAATTCTGTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 663
Db   1030 CCTTTTATGAATTCTGTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 1089

Qy    664 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 723
Db   1090 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 1149

Qy    724 GATCATGATAAAACTGTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 783
Db   1150 GATCATGATAAAACTGTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

Qy    784 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 843
Db   1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1269

Qy    844 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 903
Db   1270 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

Qy    904 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 963
Db   1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1389

Qy    964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1023
Db   1390 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1449

Qy   1024 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1083
Db   1450 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

Qy   1084 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1143
Db   1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1569
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Qy   1144 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

Qy   1204 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1689

Qy   1264 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1749

Qy   1324 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

Qy   1384 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1869

Qy   1444 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929

Qy   1504 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1989

Qy   1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 2049

Qy   1624 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

Qy   1684 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 2169

Qy   1744 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

Qy   1804 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2289

Qy   1864 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2349

Qy   1924 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2409

Qy   1984 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2469

Qy   2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

Qy   2104 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2589

Qy   2164 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2649
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Qy   2224 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2709

Qy   2284 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCAGTGAAAAAACTACGCTTT 2769

Qy   2344 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

Qy   2404 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2889

Qy   2464 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2496
          ||||||||||||||||||||||||||||||||
Db   2890 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.1%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00027;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy   2413 CTGGCAGAAATGACTTCTACTCGAACAC 2440
          ||||||||||||||||||||||||||||
Db      1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    871 ATGATTTTAAATTCAGCAAGTG 892
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  11
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    871 ATGATTTTAAATTCAGCAAGTG 892
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  12
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2171 CAACACCAACAAAAATGACTCC 2192
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Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  13
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2171 CAACACCAACAAAAATGACTCC 2192
          ||||||||||||||||||||||
Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  14
PCT-US95-08604-22/c
; Sequence 22, Application PC/TUS9508604
;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  HSC Reasearch and Development Limitied Partnership
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  125
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08604
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/271,942
;      FILING DATE:  08-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
PCT-US95-08604-22


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  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 22, Application PC/TUS9508606
;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Capatos, Denis
;    APPLICANT:  Matthews, David E.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08606
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:  US 08/271,946
;      APPLICATION NUMBER:  08-JUL-1994
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
PCT-US95-08606-22


  Query Match             0.9%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Job time: 8846 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
692.685 Million cell updates/sec

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Scoring table: OLIGO_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	2343	100.0	2994	2	US-08-204-329-2	Sequence 2, Appli
	4	2343	100.0	3232	4	US-08-470-091-1	Sequence 1, Appli
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	6	2343	100.0	2995	4	US-08-959-638-7	Sequence 7, Appli
	7	2343	100.0	2994	4	US-08-482-627-4	Sequence 4, Appli
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	9	28	1.2	28	4	US-08-859-998-1097	Sequence 1097, Ap
	10	22	0.9	52	1	US-07-826-928A-15	Sequence 15, Appl
	11	22	0.9	52	1	US-07-826-928A-36	Sequence 36, Appl
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c	17	20	0.9	44	2	US-08-625-209A-22	Sequence 22, Appl
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c	21	17	0.7	28	1	US-07-941-523-12	Sequence 12, Appl
	22	17	0.7	90	1	US-08-123-702-17	Sequence 17, Appl
c	23	17	0.7	469	1	US-08-318-905-20	Sequence 20, Appl
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	25	17	0.7	2628	1	US-08-143-219-1	Sequence 1, Appli
	26	17	0.7	450	2	US-08-213-452-1	Sequence 1, Appli
c	27	17	0.7	469	2	US-08-483-140-20	Sequence 20, Appl
c	28	17	0.7	8082	2	US-08-306-691B-41	Sequence 41, Appl
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	30	17	0.7	4080	2	US-08-570-311-7	Sequence 7, Appli
	31	17	0.7	6241	2	US-08-570-311-25	Sequence 25, Appl
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	35	17	0.7	2562	3	US-08-434-998-8	Sequence 8, Appli
	36	17	0.7	2562	3	US-08-487-797-8	Sequence 8, Appli
c	37	17	0.7	469	4	US-08-910-041-20	Sequence 20, Appl
c	38	17	0.7	8082	6	PCT-US93-06251-28	Sequence 28, Appl
	39	17	0.7	2562	6	PCT-US95-02058-8	Sequence 8, Appli
c	40	16	0.7	3771	1	US-07-876-280-5	Sequence 5, Appli
	41	16	0.7	9606	1	US-07-741-940-1	Sequence 1, Appli
	42	16	0.7	2693	1	US-07-872-644-50	Sequence 50, Appl
	43	16	0.7	2077	1	US-07-872-644-52	Sequence 52, Appl
	44	16	0.7	7859	1	US-07-854-596B-4	Sequence 4, Appli
	45	16	0.7	6924	4	US-08-448-164-2	Sequence 2, Appli

ALIGNMENTS

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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


  Query Match           100.0%;  Score 2343;  DB 1;  Length 3232;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

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Db   1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263

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Qy   2341 AAA 2343
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Db   2464 AAA 2466


RESULT   2
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; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


  Query Match             100.0%;  Score 2343;  DB 1;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3113 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 3054

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3053 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 2994

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2993 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 2934

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2933 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 2874

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2873 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 2814

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2813 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 2754

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2753 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 2694

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 2634

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 2574

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 2514

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 2454

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 2394

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 2334

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2333 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 2274

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 2214

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2213 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 2154

Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2153 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 2094

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2093 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 2034

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2033 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1974

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1973 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1914

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1913 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
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Db   1853 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1794

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1793 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1733 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1674

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1673 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1614

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1613 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1554

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1494

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1434

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1374

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1314

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1254

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1194

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1134

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 1074

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 1014

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 954

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 894

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 834

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 774

Qy   2341 AAA 2343
          |||

Db    773 AAA 771


RESULT   3
US-08-204-329-2
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


  Query Match           100.0%;  Score 2343;  DB 2;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCGATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCGATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879
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Qy    301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
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Db    880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy    361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy    421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
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Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy   2341 AAA 2343
          |||
Db   2920 AAA 2922
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RESULT 4
US-08-470-091-1
; Sequence 1, Application US/08470091
; Patent No. 5912236
; GENERAL INFORMATION:

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;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


  Query Match             100.0%;  Score 2343;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 183

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 243

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 303

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 363

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 423

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 483

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 543

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 603

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 663

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     664 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 723

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     724 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 783

Qy     661 GTAATTCCTCCACACAGTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     784 GTAATTCCTCCACACAGTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 843

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     844 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 903

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     904 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 963

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     964 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1023

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1083

Qy     961 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1084 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1143

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1144 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1203

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1204 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1263

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1264 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1383

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1384 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1443

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1444 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1503

Qy    1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1504 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1563
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Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1683

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1743

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1803

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1863

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1923

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1983

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2043

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2103

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2163

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2283

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2343

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2403

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2463

Qy   2341 AAA 2343
          |||
Db   2464 AAA 2466


RESULT   5
US-08-470-091-2/c
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2

  Query Match             100.0%;  Score 2343;  DB 4;  Length 3232;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3113 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 3054

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3053 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 2994

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2993 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 2934

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2933 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 2874

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2873 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 2814

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2813 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 2754

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2753 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 2694

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
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Db   2693 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 2634

Qy    481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540

Db   2633 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 2574

Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600

Db   2573 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 2514

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660

Db   2513 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 2454

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720

Db   2453 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 2394

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780

Db   2393 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 2334

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840

Db   2333 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 2274

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900

Db   2273 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 2214

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960

Db   2213 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 2154

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020

Db   2153 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 2094

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080

Db   2093 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 2034

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140

Db   2033 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1974

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200

Db   1973 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1914

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260

Db   1913 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1854

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320

Db   1853 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1794

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380

Db   1793 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440

Db   1733 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1674

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Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560

Db   1613 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1554

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620

Db   1553 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1494

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680

Db   1493 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1434

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740

Db   1433 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1374

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800

Db   1373 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1314

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860

Db   1313 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1254

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920

Db   1253 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1194

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980

Db   1193 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1134

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040

Db   1133 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 1074

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100

Db   1073 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 1014

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160

Db   1013 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 954

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220

Db    953 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 894

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280

Db    893 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 834

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Db    833 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 774

Qy   2341 AAA 2343

Db    773 AAA 771
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RESULT 6
US-08-959-638-7
; Sequence 7, Application US/08959638
; Patent No. 5932210
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wills, Ken N.
; APPLICANT: Maneval, Daniel C.
; TITLE OF INVENTION: Recombinant Adenoviral Vector and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700

```
;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/959,638
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/328,673
;       FILING DATE:  25-OCT-1994
;       APPLICATION NUMBER:  US 08/233,777
;       FILING DATE:  19-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/142,669
;       FILING DATE:  25-OCT-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  P-CJ 1192
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2995 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2922
US-08-959-638-7

  Query Match             100.0%;  Score 2343;  DB 4;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy     661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
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Db    1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
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Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
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Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy    1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy    1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy    1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy    1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy    1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy    2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy    2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy    2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy    2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy    2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
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Db    2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy    2341 AAA 2343
           |||
Db    2920 AAA 2922


RESULT   7
US-08-482-627-4
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


  Query Match           100.0%;  Score 2343;  DB 4;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2343;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119
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Qy    541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy    601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

Qy    661 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy    721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy    781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy    841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy    901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy    961 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy   1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy   1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy   1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
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Db   1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy   1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy   1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy   1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy   1381 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy   1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
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Db   2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy   1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
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Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy   1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
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Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy   1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
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Db   2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy   1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 2319

Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
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Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy   2341 AAA 2343
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Db   2920 AAA 2922
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RESULT   8
PCT-US94-10357-1
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


  Query Match             97.8%;  Score 2292;  DB 6;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2342;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG 639

Qy      61 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 ACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCT 699

Qy     121 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

Qy     181 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 240
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Db     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy     241 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

Qy     301 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTA 939

Qy     361 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAG 999

Qy     421 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 480
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Db    1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

Qy     481 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 1119

Qy     541 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

Qy     601 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT 1239

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 GTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATG 1299

Qy     721 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 ATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

Qy     781 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1419

Qy     841 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

Qy     901 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGA 1539

Qy     961 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 TTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG 1599

Qy    1021 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

Qy    1081 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1140
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Db    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1719

Qy    1141 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

Qy    1201 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCA 1839

Qy    1261 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA 1899

Qy    1321 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

Qy    1381 TCTCCTGTAAGATCTGCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 2019

Qy    1441 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1500
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Db    2020 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

Qy    1501 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 1560
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Db    2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAA 2139

Qy    1561 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACC 2199

Qy    1621 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1680
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Db    2200 CTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

Qy    1681 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1740
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Qy   1741 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1800
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Db   2320 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

Qy   1801 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 1860
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Db   2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   1861 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 1920
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Db   2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   1921 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 AGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2559

Qy   1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100
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Db   2620 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy   2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2160
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Db   2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   2161 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2220
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2740 CCTCCTAAACCAGTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGA 2799

Qy   2221 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2280
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Db   2800 AGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

Qy   2281 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2919

Qy   2341 AAA 2343
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Db   2920 AAA 2922
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RESULT   9
US-08-859-998-1097
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


  Query Match             1.2%;  Score 28;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2260 CTGGCAGAAATGACTTCTACTCGAACAC 2287
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Db      1 CTGGCAGAAATGACTTCTACTCGAACAC 28


RESULT  10
US-07-826-928A-15
; Sequence 15, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-15


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    718 ATGATTTTAAATTCAGCAAGTG 739
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RESULT  11
US-07-826-928A-36
; Sequence 36, Application US/07826928A
; Patent No. 5439829
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Leslie D.
;    APPLICANT:  Cook, James A.
;    APPLICANT:  David, Gary S.
;    APPLICANT:  Hochschwender, Susan M.
;    APPLICANT:  Kasher, Mary S.
;    APPLICANT:  Smith, Michele C.
;    APPLICANT:  Stemmer, Willem P.
;    TITLE OF INVENTION:  METHOD OF IMMOBILIZING AND CROSS LINKING
;    TITLE OF INVENTION:  PROTEINS AND OTHER MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lilly Corporate Center
;      CITY:  Indianapolis
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/826,928A
;      FILING DATE:  19920124
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Richard B.
;      REGISTRATION NUMBER:  35,296
;      REFERENCE/DOCKET NUMBER:  X8180A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3589
;      TELEFAX:  317-276-1294
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  52 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-826-928A-36


  Query Match             0.9%;  Score 22;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    718 ATGATTTTAAATTCAGCAAGTG 739
          ||||||||||||||||||||||
Db     31 ATGATTTTAAATTCAGCAAGTG 52


RESULT  12
US-08-271-946A-22/c
; Sequence 22, Application US/08271946A
; Patent No. 5545527
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,946A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-002-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-946A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2018 CAACACCAACAAAAATGACTCC 2039
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Db     22 CAACACCAACAAAAATGACTCC 1


RESULT  13
US-08-271-942A-22/c
; Sequence 22, Application US/08271942A
; Patent No. 5550020
;  GENERAL INFORMATION:
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  123
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,942A
;      FILING DATE:  08-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
US-08-271-942A-22


  Query Match             0.9%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2018 CAACACCAACAAAAATGACTCC 2039
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Db      22 CAACACCAACAAAAATGACTCC 1


RESULT  14
PCT-US95-08604-22/c
; Sequence 22, Application PC/TUS9508604
;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  HSC Reasearch and Development Limitied Partnership
;    APPLICANT:  Gallie, Brenda L.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Stevens, John K.
;    TITLE OF INVENTION:  Method, Reagents and Kit for Diagnosis
;    TITLE OF INVENTION:  and Targeted Screening for Retinoblastoma
;    NUMBER OF SEQUENCES:  125
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08604
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/271,942
;      FILING DATE:  08-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marina T. Larson
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-003-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:
;      NAME/KEY:  primer for exon 23 of human RB1 gene
PCT-US95-08604-22


  Query Match             0.9%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2018 CAACACCAACAAAAATGACTCC 2039
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Db      22 CAACACCAACAAAAATGACTCC 1


RESULT  15
PCT-US95-08606-22/c
; Sequence 22, Application PC/TUS9508606
;  GENERAL INFORMATION:
;    APPLICANT:  Visible Genetics Inc.
;    APPLICANT:  Stevens, John K.
;    APPLICANT:  Dunn, James M.
;    APPLICANT:  Capatos, Denis
;    APPLICANT:  Matthews, David E.
;    TITLE OF INVENTION:  Method for Testing for Mutations in DNA
;    TITLE OF INVENTION:  from a Patient Sample
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street, Suite 309
;      CITY:  Yorktown Heights
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10598-4412
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS 5.0
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08606
;      FILING DATE:
;      CLASSIFICATION:
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;     PRIOR APPLICATION DATA:  US 08/271,946
;      APPLICATION NUMBER:  08-JUL-1994
;      FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Marina T. Larson
;       REGISTRATION NUMBER:  32,038
;       REFERENCE/DOCKET NUMBER:  VGEN.P-002-WO
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (914) 245-3252
;       TELEFAX:  (914) 962-4330
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  22
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  genomic DNA
;     HYPOTHETICAL:  no
;     ANTI-SENSE:  no
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  human
;     FEATURE:
;       NAME/KEY:  primer for exon 23 of human RB1 gene
PCT-US95-08606-22


  Query Match             0.9%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2018 CAACACCAACAAAAATGACTCC 2039
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Db      22 CAACACCAACAAAAATGACTCC 1


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Date: Feb 13, 2000  3:53 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.rni
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 -XGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
 -YGAPEXT=60.000 -DELOP=6.000 -DELEXT=7.000 -START=1
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 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US09026459 -NCPU=6
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Search information block:
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Query length: 851
Database: Issued_Patents_NA:*
Database sequences: 214294
Database length: 59861208
Search time (sec): 316.800000

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WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-604-913B-12 +     7.00    90.77  1.3e+03   2293
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seq_documentation_block:
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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 Percent Similarity: 100.000   Percent Identity: 100.000

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seq_documentation_block:
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


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; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4

alignment_scores:
          Quality:  850.00              Length:    850
            Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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       2 GluLysValSerSerValAspGlyValLeuGlyGlyTyrIleGlnLysLy 18
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     373 GAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAA 422

      18 sLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspG 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     423 AAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATG 472

      35 luMetSerPheThrPheThrGlnLeuGlnLysAsnIleGluIleServal 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     473 AGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

      52 HisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAs 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGA 572

      68 pAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuP 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     573 TAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCT 622

      85 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     623 TCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGC 672

     102 SerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTr 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     673 AGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTG 722

     118 pIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspL 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     723 GATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATC 772

     135 euValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys 151
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     773 TGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

     152 LeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIlePr 168
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     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACC 872

     168 oIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaA 185
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     873 CATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCAC 922

     185 rgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCys 201
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     923 GGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGT 972

     202 LysGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAs 218
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     973 AAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAA 1022

     218 nPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuP 235
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    1023 TTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTC 1072

     235 roGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsn 251
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    1073 CAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

     252 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 268
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1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGAC 1172

 268 rAspSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnL 285
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1173 TGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACC 1222

 285 euAspGluGluValAsnValIleProProHisThrProValArgThrVal 301
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1223 TTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTT 1272

 302 MetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGl 318
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1273 ATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCA 1322

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1323 ACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAA 1372

 335 ysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGlu 351
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 368 gTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuL 385
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 418 tAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspL 435
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1623 GGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATT 1672

 435 euSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPhe 451
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1673 TGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

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 485 laTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAsp 501
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1923 TCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGAT 1972

 535 erProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 551
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 585 euAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHis 601
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2123 TAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACAT 2172

 602 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 618
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2173 ATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCAT 2222

 618 tArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleC 635
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2223 GAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATAT 2272

 635 ysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyr 651
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 668 sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG 685
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2373 AGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGC 2422

 685 lnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThr 701
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2423 AGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACC 2472

 702 LeuSerProIleProHisIleProArgSerProTyrLysPheProSerSe 718
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2473 TTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTC 2522

 718 rProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerP 735
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2523 ACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTC 2572

 735 roTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 751
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 785 erAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAsp 801
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 802 IleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSe 818
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-038-760-1

seq_documentation_block:
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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


alignment_scores:
            Quality:  820.00            Length:    820
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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 Align seg 1/1  to: US-08-038-760-1  from: 1  to: 3232

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      48 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 65
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      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

      65 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 81
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     107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

      82 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 98
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     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

      98 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 115
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

     115 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 131
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

     132 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 148
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     148 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 165
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     357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

     165 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 181
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     407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

     182 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 198
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     457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

     198 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 215
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     507 AGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTT 556

     215 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 231
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     232 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 248
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     248 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 265
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     657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

     265 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 281
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     707 CTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGA 756

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     315 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 331
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     857 CAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

     332 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 348
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     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACAT 956

     348 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 365
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     957 CTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTG 1006

     365 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 381
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1007 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 1056

     382 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 398
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    1057 TCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAA 1106

     398 sLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuG 415
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1107 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 1156

 415 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 431
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 432 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 448
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 448 aPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnL 465
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 465 euThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 481
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1307 TGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATG 1356

 482 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGl 498
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1357 GAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACA 1406

 498 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 515
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1407 ATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTC 1456

 515 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 531
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1457 TTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

 532 ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerTh 548
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
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;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


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            Quality:  820.00              Length:    820
              Ratio:  1.000                 Gaps:      0
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; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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132 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 148
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; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


alignment_scores:
            Quality:  820.00              Length:    820
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1180 TTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 1131

 732 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 748
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1130 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAAT 1081

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 765 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 781
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 782 LeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysLe 798
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; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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     573 TAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCT 622

      85 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 101
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     168 oIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaA 185
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     185 rgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCys 201
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    1073 CAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

     252 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 268
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1373 AAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

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1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCG 1472

 368 gTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuL 385
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1473 ATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTA 1522

 385 ysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsn 401
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1523 AATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAAT 1572

 402 AspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMe 418
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2123 TAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACAT 2172

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; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


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              Ratio:  1.000                Gaps:      0
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-878-960-1

seq_documentation_block:
; Sequence 1, Application US/07878960
; Patent No. 5444164
;  GENERAL INFORMATION:
;    APPLICANT:  Purchio, Anthony F.
;    APPLICANT:  Skonier, John
;    APPLICANT:  Neubauer, Michael G.
;    TITLE OF INVENTION:  TGF-BETA INDUCED GENE AND PROTEIN
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/878,960
;      FILING DATE:  05-MAY-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/833,835
;      FILING DATE:  05-FEB-1992
;      NAME:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sorrentino, Joseph M.
;      REGISTRATION NUMBER:  32,598
;      REFERENCE/DOCKET NUMBER:  ON0092-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206/728-4800
;      TELEFAX:  206/727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2691 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  LUNG
;      CELL TYPE:  ADENOCARCINOMA
;      CELL LINE:  A549
US-07-878-960-1


alignment_scores:
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seq_documentation_block:
; Sequence 11, Application US/07891942G
; Patent No. 5679511
;  GENERAL INFORMATION:
;    APPLICANT:  Kwon, Byoung Se
;    TITLE OF INVENTION:  cDNA CLONES FOR HUMAN TYROSINASE AND FOR
;    TITLE OF INVENTION:  A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christopher A. Michaels, Barnard, Brown &
;      ADDRESSEE:  Michaels
;      STREET:  306 East State Street; Suite 220
;      CITY:  Ithaca
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  14850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/891,942G
;      FILING DATE:  01-JUN-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/915,753
;      FILING DATE:  06-OCT-1986
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/362,847
;      FILING DATE:  07-JUN-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michaels, Christopher A
;      REGISTRATION NUMBER:  34,390
;      REFERENCE/DOCKET NUMBER:  IND1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  607-273-1711
;      TELEFAX:  607-273-2609
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2397 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-891-942G-11


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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-675-211-1

seq_documentation_block:
; Sequence 1, Application US/07675211
; Patent No. 5219737
;  GENERAL INFORMATION:
;    APPLICANT:  KAJIYAMA, NAOKI
;    APPLICANT:  NAKANO, EIICHI
;    TITLE OF INVENTION:  MUTANT LUCIFERASE OF A FIREFLY, MUTANT
;    TITLE OF INVENTION:  LUCIFERASE GENES, NOVEL RECOMBINANT DNAS CONTAINING THE
;    TITLE OF INVENTION:  GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  N.Y.
;      COUNTRY:  U.S.A
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/675,211
;      FILING DATE:  19910326
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MISROCK, S. LESLIE
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-026-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1644 base pairs
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US-07-675-211-1


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; Patent No. 5229285
;  GENERAL INFORMATION:
;    APPLICANT:  Kajiyama, Naoki
;    APPLICANT:  Nakano, Eiichi
;    TITLE OF INVENTION:  Thermostable Luciferase Of Firefly,
;    TITLE OF INVENTION:  Thermostable Luciferase Gene Of Firefly, No. 5229285el Reco
;    TITLE OF INVENTION:  DNA, And Process For The Preparation Of Thermostable
;    TITLE OF INVENTION:  Luciferase Of Firefly
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;    CURRENT APPLICATION DATA:
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;      FILING DATE:  19920623
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-048
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1644 base pairs
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US-07-903-047-1


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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-767-135-1
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; Patent No. 5234811
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    APPLICANT:  Sorge, Joseph A
;    TITLE OF INVENTION:  An Assay for a New Gaucher Disease
;    TITLE OF INVENTION:  Mutation
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  3366 No. 5234811th Torrey Pines Court, Suite 240
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/767,135
;      FILING DATE:  19910927
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0422P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
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;      LOCATION:  3564..4116
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;      LOCATION:  4117..4354
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;    FEATURE:
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;      LOCATION:  4355..5227
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;      NAME/KEY:  exon
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;      LOCATION:  5853..6016
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US-07-767-135-1


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alignment_block:
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 Align seq 1/1  to reverse of: US-07-767-135-1  from: 1  to: 7620

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; Patent No. 5266459
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    TITLE OF INVENTION:  GAUCHER'S DISEASE: DETECTION OF A NEW
;    TITLE OF INVENTION:  MUTATION IN INTRON 2 OF THE GLUCOCEREBROSIDASE GENE
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5266459th Torrey Pines Road, TPC 8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/841,652
;      FILING DATE:  19920224
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0670P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7620 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
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US-07-841-652-1


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Date: Feb 13, 2000  3:55 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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seq_documentation_block:
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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seq_documentation_block:
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
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;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:  19930325
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
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; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;  MOLECULE TYPE:  DNA
US-08-038-760-2


alignment_scores:
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; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1


alignment_scores:
            Quality:  820.00              Length:    820
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x US-08-470-091-1   ..

 Align seg 1/1  to: US-08-470-091-1  from: 1  to: 3232

      13 AspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIleGl 29
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       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGA 56

      29 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 46
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

      46 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

      63 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 79
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

      79 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 96
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

      96 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 112
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257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

113 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 129
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307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 356

129 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 146
    ||||||||||||||||||||||||||||||||||||||||||||||||||
357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

146 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 162
    ||||||||||||||||||||||||||||||||||||||||||||||||||
407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

163 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 179
    ||||||||||||||||||||||||||||||||||||||||||||||||||
457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

179 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 196
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507 AGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTT 556

196 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 212
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557 ATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

213 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 229
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607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 656

229 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 246
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657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

246 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 262
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707 CTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGA 756

263 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVa 279
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757 AAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGT 806

279 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 296
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807 TAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAG 856

296 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 312
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857 CAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

313 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 329
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907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACAT 956

329 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 346
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957 CTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTG 1006

346 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 362
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1007 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 1056

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1107 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 1156

396 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 412
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1157 AGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

413 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 429
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1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGC 1256

429 aPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnL 446
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1257 CTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACT 1306

446 euThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 462
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1307 TGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATG 1356

463 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGl 479
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1357 GAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACA 1406

479 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 496
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1407 ATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTC 1456

496 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 512
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1557 TGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCAT 1606

546 euLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 562
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563 TyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGl 579
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1657 TATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGA 1706

579 uLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluT 596
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613 TyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleVa 629
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1857 AACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTG 1906

646 alLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSer 662
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1907 TTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCG 1956

663 ValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrAr 679
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1957 GTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAG 2006

679 gProProThrLeuSerProIleProHisIleProArgSerProTyrLysP 696
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2007 GCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGT 2056

696 heProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 712
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2057 TTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106
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     713 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 729
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     729 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 746
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    2157 GACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTT 2206

     746 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 762
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     763 LeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysLe 779
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seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-470-091-2

seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


alignment_scores:
            Quality:  820.00              Length:    820
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x US-08-470-091-2/rev   ..

 Align seg 1/1  to reverse of: US-08-470-091-2  from: 1  to: 3232

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      29 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 46
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      46 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 62
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    3030 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 2981

      96 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 112
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    2980 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

     113 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 129
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    2930 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 2881

     129 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 146
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    2880 TTTTATTAAACTCTCACGTCCCATGTTGCTCAAAGAACCATATAAAACAG 2831

     146 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 162
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    2830 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 2781

     163 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 179
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    2780 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 2731

     179 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 196
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    2730 AGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTT 2681

     196 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 212
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    2680 ATTTCAAAAATTTTATAGCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

     213 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 229
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2630 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 2581

     229 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 246
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 279 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 296
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 329 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 346
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 346 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 362
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2230 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 2181

 363 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 379
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2180 TCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAA 2131

 379 sLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuG 396
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2130 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 2081

 396 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 412
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 413 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 429
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 429 aPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnL 446
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1980 CTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACT 1931

 446 euThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 462
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 463 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGl 479
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1880 GAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACA 1831

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1830 ATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTC 1781

 496 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 512
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1780 TTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

 513 ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerTh 529
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1730 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTAC 1681

 529 rAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProL 546
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; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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              Ratio:  1.000                Gaps:      0
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; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
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US-08-859-998-1097


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seq_documentation_block:
; Sequence 1, Application US/07878960
; Patent No. 5444164
;  GENERAL INFORMATION:
;    APPLICANT:  Purchio, Anthony F.
;    APPLICANT:  Skonier, John
;    APPLICANT:  Neubauer, Michael G.
;    TITLE OF INVENTION:  TGF-BETA INDUCED GENE AND PROTEIN
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/878,960
;      FILING DATE:  05-MAY-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/833,835
;      FILING DATE:  05-FEB-1992
;      NAME:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sorrentino, Joseph M.
;      REGISTRATION NUMBER:  32,598
;      REFERENCE/DOCKET NUMBER:  ON0092-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206/728-4800
;      TELEFAX:  206/727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2691 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  LUNG
;      CELL TYPE:  ADENOCARCINOMA
;      CELL LINE:  A549
US-07-878-960-1


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seq_documentation_block:
; Sequence 11, Application US/07891942G
; Patent No. 5679511
;  GENERAL INFORMATION:
;    APPLICANT:  Kwon, Byoung Se
;    TITLE OF INVENTION:  cDNA CLONES FOR HUMAN TYROSINASE AND FOR
;    TITLE OF INVENTION:  A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christopher A. Michaels, Barnard, Brown &
;      ADDRESSEE:  Michaels
;      STREET:  306 East State Street; Suite 220
;      CITY:  Ithaca
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  14850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/891,942G
;      FILING DATE:  01-JUN-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/915,753
;      FILING DATE:  06-OCT-1986
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/362,847
;      FILING DATE:  07-JUN-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michaels, Christopher A
;      REGISTRATION NUMBER:  34,390
;      REFERENCE/DOCKET NUMBER:  IND1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  607-273-1711
;      TELEFAX:  607-273-2609
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
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;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-891-942G-11


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seq_documentation_block:
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; Patent No. 5219737
;  GENERAL INFORMATION:
;    APPLICANT:  KAJIYAMA, NAOKI
;    APPLICANT:  NAKANO, EIICHI
;    TITLE OF INVENTION:  MUTANT LUCIFERASE OF A FIREFLY, MUTANT
;    TITLE OF INVENTION:  LUCIFERASE GENES, NOVEL RECOMBINANT DNAS CONTAINING THE
;    TITLE OF INVENTION:  GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 AVENUE OF THE AMERICAS
;      CITY:  NEW YORK
;      STATE:  N.Y.
;      COUNTRY:  U.S.A
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/675,211
;      FILING DATE:  19910326
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MISROCK, S. LESLIE
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-026-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
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US-07-675-211-1


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seq_documentation_block:
; Sequence 1, Application US/07903047
; Patent No. 5229285
;  GENERAL INFORMATION:
;    APPLICANT:  Kajiyama, Naoki
;    APPLICANT:  Nakano, Eiichi
;    TITLE OF INVENTION:  Thermostable Luciferase Of Firefly,
;    TITLE OF INVENTION:  Thermostable Luciferase Gene Of Firefly, No. 5229285el Reco
;    TITLE OF INVENTION:  DNA, And Process For The Preparation Of Thermostable
;    TITLE OF INVENTION:  Luciferase Of Firefly
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/903,047
;      FILING DATE:  19920623
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-048
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1644 base pairs
;      TYPE:  NUCLEIC ACID
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US-07-903-047-1


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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-767-135-1

seq_documentation_block:
; Sequence 1, Application US/07767135
; Patent No. 5234811
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    APPLICANT:  Sorge, Joseph A
;    TITLE OF INVENTION:  An Assay for a New Gaucher Disease
;    TITLE OF INVENTION:  Mutation
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  3366 No. 5234811th Torrey Pines Court, Suite 240
;      CITY:  La Jolla
;      STATE:  CA
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;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/767,135
;      FILING DATE:  19910927
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0422P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7620 base pairs
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;      LOCATION:  4355..5227
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;      LOCATION:  5853..6016
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US-07-767-135-1


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            Quality:    7.00              Length:      7
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alignment_block:
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 Align seg 1/1  to reverse of: US-07-767-135-1  from: 1  to: 7620

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-841-652-1

seq_documentation_block:
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; Patent No. 5266459
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    TITLE OF INVENTION:  GAUCHER'S DISEASE: DETECTION OF A NEW
;    TITLE OF INVENTION:  MUTATION IN INTRON 2 OF THE GLUCOCEREBROSIDASE GENE
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5266459th Torrey Pines Road, TPC 8
;      CITY:  La Jolla
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;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/841,652
;      FILING DATE:  19920224
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0670P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7620 base pairs
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
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;    ANTI-SENSE:  NO
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US-07-841-652-1


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              Ratio:  1.000                Gaps:      0
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 Align seg 1/1  to reverse of: US-07-841-652-1  from: 1  to: 7620

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Date: Feb 13, 2000  3:57 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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Query length: 781
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Database sequences: 214294
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
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;      LOCATION:  19..2469
US-08-038-760-1


alignment_scores:
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seq_documentation_block:
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


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           Quality:  781.00              Length:    781
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; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
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;       CITY:  SAN FRANCISCO
;       STATE:  CALIFORNIA
;       COUNTRY:  U.S.A.
;       ZIP:  94111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/204,329
;       FILING DATE:  15-AUG-1994
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US92/05866
;       FILING DATE:  14-JUL-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  RENEE A. FITTS
;       REGISTRATION NUMBER:  35,136
;       REFERENCE/DOCKET NUMBER:  16930-000400US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
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US-08-470-091-1


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seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


alignment_scores:
            Quality:  781.00              Length:    781
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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seq_documentation_block:
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


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            Quality:  781.00              Length:    781
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; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;     APPLICANT:  The Regents of the University of California
;     APPLICANT:  and Canji, Inc.
;     TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;     TITLE OF INVENTION:  Susceptibility Gene Product
;     NUMBER OF SEQUENCES:  3
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Campbell and Flores
;       STREET:  4370 La Jolla Village Drive
;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10357
;       FILING DATE:  13-SEP-1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/121,108
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  FP-UC 1117
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2923
PCT-US94-10357-1


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seq_documentation_block:
; Sequence 1097, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1097:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1097


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seq_documentation_block:
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; Patent No. 5444164
;  GENERAL INFORMATION:
;    APPLICANT:  Purchio, Anthony F.
;    APPLICANT:  Skonier, John
;    APPLICANT:  Neubauer, Michael G.
;    TITLE OF INVENTION:  TGF-BETA INDUCED GENE AND PROTEIN
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bristol-Myers Squibb Company
;      STREET:  3005 First Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/878,960
;      FILING DATE:  05-MAY-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/833,835
;      FILING DATE:  05-FEB-1992
;      NAME:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sorrentino, Joseph M.
;      REGISTRATION NUMBER:  32,598
;      REFERENCE/DOCKET NUMBER:  ON0092-
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206/728-4800
;      TELEFAX:  206/727-3601
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2691 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  LUNG
;      CELL TYPE:  ADENOCARCINOMA
;      CELL LINE:  A549
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seq_documentation_block:
; Sequence 11, Application US/07891942G
; Patent No. 5679511
;  GENERAL INFORMATION:
;    APPLICANT:  Kwon, Byoung Se
;    TITLE OF INVENTION:  cDNA CLONES FOR HUMAN TYROSINASE AND FOR
;    TITLE OF INVENTION:  A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
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;       ADDRESSEE:  Christopher A. Michaels, Barnard, Brown &
;       ADDRESSEE:  Michaels
;       STREET:  306 East State Street; Suite 220
;       CITY:  Ithaca
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  14850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/891,942G
;       FILING DATE:  01-JUN-1992
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  06/915,753
;       FILING DATE:  06-OCT-1986
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/362,847
;       FILING DATE:  07-JUN-1989
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Michaels, Christopher A
;       REGISTRATION NUMBER:  34,390
;       REFERENCE/DOCKET NUMBER:  IND1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  607-273-1711
;       TELEFAX:  607-273-2609
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2397 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-07-891-942G-11


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seq_documentation_block:
; Sequence 1, Application US/07675211
; Patent No. 5219737
;  GENERAL INFORMATION:
;     APPLICANT:  KAJIYAMA, NAOKI
;     APPLICANT:  NAKANO, EIICHI
;     TITLE OF INVENTION:  MUTANT LUCIFERASE OF A FIREFLY, MUTANT
;     TITLE OF INVENTION:  LUCIFERASE GENES, NOVEL RECOMBINANT DNAS CONTAINING THE
;     TITLE OF INVENTION:  GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  PENNIE & EDMONDS
;       STREET:  1155 AVENUE OF THE AMERICAS
;       CITY:  NEW YORK
;       STATE:  N.Y.
;       COUNTRY:  U.S.A
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/675,211
;       FILING DATE:  19910926
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MISROCK, S. LESLIE
;       REGISTRATION NUMBER:  18,872
;       REFERENCE/DOCKET NUMBER:  7005-026-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-9741
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
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US-07-675-211-1


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seq_documentation_block:
; Sequence 1, Application US/07903047
; Patent No. 5229285
;  GENERAL INFORMATION:
;     APPLICANT:  Kajiyama, Naoki
;     APPLICANT:  Nakano, Eiichi
;     TITLE OF INVENTION:  Thermostable Luciferase Of Firefly,
;     TITLE OF INVENTION:  Thermostable Luciferase Gene Of Firefly, No. 5229285el Reco
;     TITLE OF INVENTION:  DNA, And Process For The Preparation Of Thermostable
;     TITLE OF INVENTION:  Luciferase Of Firefly
;     NUMBER OF SEQUENCES:  11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Pennie & Edmonds
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
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;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/903,047
;       FILING DATE:  19920623
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;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-048
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1644 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
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US-07-903-047-1


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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-767-135-1

seq_documentation_block:
; Sequence 1, Application US/07767135
; Patent No. 5234811
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    APPLICANT:  Sorge, Joseph A
;    TITLE OF INVENTION:  An Assay for a New Gaucher Disease
;    TITLE OF INVENTION:  Mutation
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  3366 No. 5234811th Torrey Pines Court, Suite 240
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/767,135
;      FILING DATE:  19910927
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0422P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7620 base pairs
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;    ANTI-SENSE:  NO
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;      LOCATION:  4355..5227
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US-07-767-135-1


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alignment_block:
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 Align seg 1/1  to reverse of: US-07-767-135-1  from: 1  to: 7620

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seq_documentation_block:
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; Patent No. 5266459
;  GENERAL INFORMATION:
;    APPLICANT:  Beutler, Ernest
;    TITLE OF INVENTION:  GAUCHER'S DISEASE: DETECTION OF A NEW
;    TITLE OF INVENTION:  MUTATION IN INTRON 2 OF THE GLUCOCEREBROSIDASE GENE
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5266459th Torrey Pines Road, TPC 8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/841,652
;      FILING DATE:  19920224
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bingham, Douglas A
;      REGISTRATION NUMBER:  32,457
;      REFERENCE/DOCKET NUMBER:  SCR0670P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7620 base pairs
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;      TOPOLOGY:  linear
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;       OTHER INFORMATION:  /function= "Intron 9"
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;       LOCATION:  6386..6502
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US-07-841-652-1


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              Ratio:  1.000                Gaps:       0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to reverse of: US-07-841-652-1  from: 1  to: 7620

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Date: Feb 13, 2000  3:39 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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Query length: 928
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Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

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gb_est3:R57845        +   29.00  442.29  7.2e-16   152  ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529     -   29.00  434.44  2.0e-15   462  ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097     +   29.00  431.42  2.9e-15   709  ! AI646097 vw54h07.x1 Soares mous
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gb_est36:AI931087     +   11.00  158.83  4.42      267  ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:D15138        +   10.00  141.64  40.07     338  ! D15138 RICC0141A Rice callus Or
gb_est1:D38851        +   10.00  140.79  44.66     381  ! D38851 RICC1624A Rice callus Or
gb_est1:D38980        +   10.00  139.99  49.52     427  ! D38980 RICR0089A Rice root Oryz
gb_est1:D40024        -   10.00  141.27  42.00     356  ! D40024 RICS1743A Rice shoot Ory
gb_est2:D47372        -   10.00  141.62  40.18     339  ! D47372 RICS12716A Rice green sh
gb_est2:D48004        -   10.00  141.12  42.85     364  ! D48004 RICS13911A Rice green
gb_est7:W29241        -   10.00  134.35  102.00    948  ! W29241 mb96e12.r1 Soares mou
gb_est7:W29419        -   10.00  133.47  114.30   1075  ! W29419 mb98h11.r1 Soares mo
gb_est7:W29461        -   10.00  134.12  105.11    980  ! W29461 mb99b11.r1 Soares mou
gb_est7:W29564        -   10.00  133.22  117.96   1113  ! W29564 mc03d11.r1 Soares mo
gb_gss15:AQ650463     -   10.00  141.23  42.21     358  ! AQ650463 Sheared DNA-18F2.TF

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00              Length:    159
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     490 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 506
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     506 uAspSerGlyThrAspLeuSerProTrpIleLeuAsnValLeuAsnL 523
         ||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     523 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 539
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     540 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 556
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     556 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 573
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     573 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 589
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     590 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 606
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     606 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 623
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     623 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 639
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     640 LysProLeuLysSerThrSerLeuSer 648
         |||||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
           Quality:  117.00              Length:    117
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AI745644/rev    ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     714 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 730
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     730 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 747
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     747 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 763
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     764 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     780 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 797
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCGTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     797 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 813
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     814 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 830
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     830 g 830
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
```

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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


alignment_scores:
            Quality:  116.00              Length:    116
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     715 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 731
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     731 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 748
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     748 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 764
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     765 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 781
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     781 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 798
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     798 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 814
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     815 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 830
         ||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a      63 c      52 g      83 t
ORIGIN


alignment_scores:
            Quality:   85.00              Length:     85
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     645 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 661
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     661 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 678
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     678 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 694
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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    102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

    695 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 711
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

    711 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 728
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

    728 yrLys 729
        |||||
    252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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US-09-026-459A-51 x AA072780   ..

Align seg 1/1  to: AA072780  from: 1  to: 522

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        ||||||||||||||||||||||||||||||||||||||||||||||||||
    258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

    810 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 827
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

    827 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 843
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

    844 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 860
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

    860 s 860
        |
    458 A 458

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
```

```
ORIGIN


alignment_scores:
            Quality:   60.00              Length:     60
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

      29 ProGluGluAspProGluGlnAspSerGlyProGluAspLeuProLeuVa 45
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGT 319

      45 lArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeuCysG 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     318 CAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTC 269

      62 lnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeuThrTrp 78
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 AGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGG 219

      79 GluLysValSerSerValAspGlyValLeu 88
         |||||||||||||||||||||||||||||||
     218 GAGAAAGTTTCATCTGTGGATGGAGTATTG 189

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


alignment_scores:
            Quality:   53.00              Length:     53
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     513 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 529
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     529 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     546 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 562
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     563 TrpLeuSer 565
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
```

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 80 c 90 g 133 t 3 others
ORIGIN

alignment_scores:
Quality: 52.00 Length: 52
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-51 x AA210875 ..

Align seg 1/1 to: AA210875 from: 1 to: 456

```
    877 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 893
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

    893 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 910
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

    910 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 926
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

    927 GluLys 928
        ||||||
    175 GAGAAA 180
```

seq_name: gb_est13:AA361277

seq_documentation_block:

LOCUS AA361277 304 bp mRNA EST 21-APR-1997
DEFINITION EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION AA361277
VERSION AA361277.1 GI:2013596
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 304)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., , Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 12140200

COMMENT On Sep 12, 1996 this sequence version replaced gi:1407493.
Other_ESTs: THC168922
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers
source 1. .304
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165411"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 94 a 79 c 43 g 86 t 2 others
ORIGIN

alignment_scores:
Quality: 49.00 Length: 49
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-51 x AA361277 ..

Align seg 1/1 to: AA361277 from: 1 to: 304

```
    581 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 597
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

    597 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 614
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    100 GAATAATCACACTGCAGGAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

    614 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 629
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196
```

seq_name: gb_est19:AA765882

seq_documentation_block:

LOCUS AA765882 171 bp mRNA EST 08-FEB-1998
DEFINITION oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA765882
VERSION AA765882.1 GI:2817120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044576.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

```
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Insert Length: 2415   Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00             Length:     43
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     445 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 461
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     461 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 478
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     478 snAspAsnIlePheHisMetSerLeuLeu 487
         |||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS       AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION  ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AI020392
VERSION     AI020392.1  GI:3234728
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00             Length:     42
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     824 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     840 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 857
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     857 rgValLeuLysArgSerAlaGluGly 865
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     463 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 479
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     479 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 496
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     496 laThrTyrSerArgSerThr 502
         ||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     862 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 878
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     878 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 895
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     895 erLysPheGlnGln 899
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    101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

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     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     557 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 574
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     574 ysGlnSerLysAsp 578
         ||||||||||||||
     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
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                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

857 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 874
    ||||||||||||||||||||||||||||||||||||||||||||||||||
268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

874 ysLeuArgPhe 877
    ||||||||||
318 AACTACGCTTT 328
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OM of: US-09-026-459A-39 to: GenEmbl:*   out_format : pfs

Date: Feb 13, 2000  8:13 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
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 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
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Search information block:
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gb_pat:A01444         +  286.00 5153.40  5.0e-279  4580  ! A01444 H.sapiens DNA for 4.6 k
gb_pr3:AF043224       +   93.00 1664.81  1.0e-84    426  ! AF043224 Homo sapiens retinobla
gb_pat:E12560         +   72.00 1266.27  1.6e-62   4591  ! E12560 cDNA encoding Rb (retin
gb_ro:MUSPP105RB      +   72.00 1266.27  1.6e-62   4591  ! M26391 Mouse retinoblastoma su
gb_pr1:HUMRBSY79      +   68.00 1209.85  2.3e-59    480  ! M19701 Human mutated retinoblas
gb_pr2:HUMRB1501V     +   66.00 1176.00  1.8e-57    340  ! L49220 Homo sapiens retinoblast
gb_pat:I09384         +   65.00 1152.72  3.5e-56    693  ! I09384 Sequence 17 from Patent
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gb_pr1:HUMRETBLAS     +   65.00 1112.73  5.9e-54  180388  ! L11910 Human retinoblastoma
gb_ro:RATRP           +   59.00 1030.39  2.3e-49   4432  ! D25233 Rat mRNA for retinoblas
gb_pat:I09389         +   55.00  968.93  6.0e-46    935  ! I09389 Sequence 22 from Patent
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gb_pat:I09377         +   48.00  844.86  4.9e-39    609  ! I09377 Sequence 10 from Patent
gb_pat:I09386         +   48.00  844.39  5.2e-39    650  ! I09386 Sequence 19 from Patent
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gb_pr1:HUMRBS17       +   48.00  844.39  5.2e-39    650  ! M27860 Human retinoblastoma sus
gb_pr2:HUMRB08EX      +   48.00  849.58  2.7e-39    316  ! L41896 Homo sapiens retinoblast
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gb_pr2:HUMRB1610K     +   43.00  761.23  2.2e-34    224  ! L49223 Homo sapiens retinoblast
gb_pr2:HUMRB17MUT     +   43.00  758.73  3.1e-34    317  ! L41999 Homo sapiens retinoblast
gb_pat:I09373         +   41.00  718.19  5.6e-32    570  ! I09373 Sequence 6 from Paten
gb_pr1:HUMRBS04       +   41.00  718.19  5.6e-32    570  ! M27848 Human retinoblastoma
gb_pr2:HUMRB04MUT     +   41.00  719.98  4.4e-32    444  ! L41892 Homo sapiens retinobl
gb_pr2:HUMRB19MUT     +   41.00  719.38  4.8e-32    483  ! L41906 Homo sapiens retinobl
gb_pr2:HUMRB20MUU     +   41.00  721.69  3.6e-32    350  ! L41996 Homo sapiens retinobl
gb_pat:I09385         +   40.00  699.79  5.9e-31    589  ! I09385 Sequence 18 from Pate

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seq_documentation_block:
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DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
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ORIGIN


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     322 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 371

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
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     372 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 421

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
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     422 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 471

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     472 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 521

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     522 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 571

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     572 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 621

     131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     622 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 671

     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
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     672 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 721

     164 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 180
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 181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
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 772 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 821

 197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 822 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 871

 214 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 230
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 872 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 921

 231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 922 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 971

 247 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 264
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 972 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 1021

 264 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 280
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1022 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1071

 281 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 297
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1122 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 1171

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1222 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1271

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DEFINITION  Sequence 2 from patent US 5710255.
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VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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ORIGIN


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      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and
            mutations.
ACCESSION   L41870
VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
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  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
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            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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VERSION     M28419.1  GI:190962
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
            Bookstein,R. and Lee,E.Y.
  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


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alignment_block:
 US-09-026-459A-39 x HUMRBSA   ..

 Align seg 1/1  to: HUMRBSA  from: 1  to: 2994

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1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1909

 514 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 530
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1910 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

 531 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 547
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1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 2009

 547 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 564
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2010 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 2059

 564 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 580
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2060 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 2109

 581 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 597
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2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

 597 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 614
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2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 2209

 614 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 630
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2210 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

 631 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 647
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 647 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 664
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 681 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 697
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 697 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 714
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 714 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 730
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   731 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 747
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   747 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 764
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   764 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
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   781 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 797
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   797 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 814
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   814 euProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 830
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   831 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 847
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seq_name: gb_pat:I18496

seq_documentation_block:
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DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


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           Quality:  820.00            Length:    820
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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 Align seg 1/1  to: I18496  from: 1  to: 3232

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       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGA 56

      48 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 65
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

      65 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 81
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

      82 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 98
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

      98 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 115
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

     115 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 131
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     132 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 148
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 356

     148 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 165
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     165 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 181
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     182 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 198
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     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 656

     248 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 265
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

     265 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 281
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
     757 AAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGT 806

     298 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 315
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     807 TAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAG 856

     315 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 331
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     857 CAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

     332 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 348
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1007 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 1056

 382 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 398
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
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 565 euLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 581
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 582 TyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGl 598
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 598 uLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluT 615
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 682 ValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrAr 698
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1957 GTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAG 2006

 698 gProProThrLeuSerProIleProHisIleProArgSerProTyrLysP 715
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DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
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     65 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 81
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   3130 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 3081

     82 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 98
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   3080 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 3031

     98 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 115
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    115 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 131
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    132 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 148
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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    148 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 165
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   2680 ATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 2631

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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
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            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
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  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
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ORIGIN


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   2348 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2397

    728 yrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThr 744
        |||||||||||||||||||||||||||||||||||||||||||||||||||
   2398 ATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2447

    745 ProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSe 761
        |||||||||||||||||||||||||||||||||||||||||||||||||||
   2448 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2497

    761 rPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnS 778
        |||||||||||||||||||||||||||||||||||||||||||||||||||
   2498 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACA 2547

    778 erAspArgValLeu 782
        |||||||||||||
   2548 GCGACCGTGTGCTC 2561

seq_name: gb_pr3:AF043224

seq_documentation_block:
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
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SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
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                     /gene="RB1"
                     /number=5
     CDS             <1. .137
                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
                     "
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                     /gene="RB1"
                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
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     exon            351. .418
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     exon            419. .>426
                     /gene="RB1"
                     /number=7
BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN


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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AF043224   ..

 Align seg 1/1  to: AF043224  from: 1  to: 426

      31 ValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIl 47
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     133 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 182

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     183 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 232

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     233 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 282

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     283 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 332

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     333 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 382

     114 euLysValSerTrpIleThrPheLeuLeu 123
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     383 TAAAAGTTTCTTGGATCACATTTTTATTA 411
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seq_name: gb_pat:E12560

seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .4591
            FT                   /organism='Mus musculus'
            FT                   /cell_type='B-cell precursor' FT
                /cell_line='70Z-3'
            FT   5'UTR           1. .98
            FT   CDS             99. .2864
            FT                   /product='Rb protein'
            FT   3'UTR           2865. .4591.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN


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            Quality:   72.00            Length:     72
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 US-09-026-459A-39 x E12560   ..

 Align seg 1/1  to: E12560  from: 1  to: 4591

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     733 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     750 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 766
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     767 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     783 sArgSerAlaGluGly 788
         ||||||||||||||||
    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
     source          1. .4591
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                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
     CDS             99. .2864
                     /codon_start=1
                     /product="pp105 Rb protein"
                     /protein_id="AAA39964.1"
                     /db_xref="GI:200453"
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                     EIEEPEFIALCQKLKVPDHVRERAWLTWEKVSSVDGILEGYIQKKKELWGICIFIAAV
                     DLDEMPFTFTELQKSIETSVYKFFDLLKEIDTSTKVDNAMSRLLKKYNVLCALYSKLE
                     RTCELIYLTQPSSALSTEINSMLVLKISWITFLLAKGEVLQMEDDLVISFQLMLCVVD
                     YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
                     CNIDEVKNVYFKNFIPFINSLGIVSSNGLPEVESLSKRYEEVYLKNKDLDARLFLDHD
                     KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
                     NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
                     MESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTLQHLDSGTDLSF
                     PWILNVLNLKAFDFYKVIESFIKVEANLTREMIKHLERCEHRIMESLAWLSDSPLFDL
                     IKQSKDGEGPDNLEPACPLSLPLQGNHTAADMYLSPLRSPKKRTSTTRVNSAANTETQ
                     AASAFHTQKPLKSTSLALFYKKVYRLAYLRLNTLCARLLSDHPELEHIIWTLFQHTLQ
                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                     EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
                     ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
                     EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
                     VSNKEEK"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x MUSPP105RB   ..

 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     733 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     750 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 766
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     767 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     783 sArgSerAlaGluGly 788
         ||||||||||||||||
    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_pri:HUMRBSY79

seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
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                     /db_xref="taxon:9606"
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     gene            139. .300
                     /gene="RB1"
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                     /note="mutated retinoblastoma protein"
                     /codon_start=1
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     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x HUMRBSY79   ..

 Align seg 1/1  to: HUMRBSY79  from: 1  to: 480

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     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     142 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 159
         |||||||||||||||||||||||||||||||||||||||||||||||||
     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     159 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 175
         |||||||||||||||||||||||||||||||||||||||||||||||||
     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     176 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 192
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     192 nAsp 193
         ||||
     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
     source          1. .340
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                     /map="13q14.2"
     gene            1. .340
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                     /gene="RB1"
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                     /number=16
     exon            65. .260
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
     CDS             <65. .120
                     /gene="RB1"
                     /note="exon 17"
                     /codon_start=3
                     /db_xref="GDB:G00-118-734"
                     /product="retinoblastoma suspectibility protein"
                     /protein_id="AAA82549.1"
                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
                     /gene="RB1"
                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
     intron          261. .>340
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN


alignment_scores:
            Quality:   66.00             Length:     66
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x HUMRB1501V   ..

 Align seg 1/1  to: HUMRB1501V  from: 1  to: 340

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     439 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 456
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     456 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 472
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     473 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 488
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260
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OM of: US-09-026-459A-37 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
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 -THREADS=1

Search information block:
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Query length: 781
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


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gb_est32:AI745644   -  117.00 2164.20  8.8e-112  415  ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643   -  116.00 2145.56  9.6e-111  411  ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103   +   85.00 1568.20  1.4e-78   285  ! AA382103 EST95270 Activated T-c
gb_est9:AA072780    +   67.00 1226.82  1.4e-59   522  ! AA072780 mm76a05.r1 Stratagene
gb_est17:AA664676   -   53.00  968.30  3.6e-45   329  ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875   +   52.00  947.13  5.5e-44   456  ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277   +   49.00  894.04  4.9e-41   304  ! AA361277 EST70529 T-cell lympho
gb_est19:AA765882   -   43.00  786.08  5.1e-35   171  ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392   +   42.00  761.86  1.1e-33   356  ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411   -   40.00  717.35  3.4e-31   914  ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402      +   38.00  686.40  1.8e-29   386  ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485   -   38.00  680.29  4.0e-29   871  ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391      +   37.00  666.42  2.4e-28   457  ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845      +   29.00  524.98  1.8e-20   152  ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529   -   29.00  516.63  5.2e-20   462  ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097   +   29.00  513.41  7.9e-20   709  ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255   +   27.00  478.24  7.1e-18   525  ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628   +   25.00  442.37  7.1e-16   427  ! AA709628 vv41c11.r1 Soares 2NbM
gb_est42:AV302462   +   23.00  411.68  3.6e-14   174  ! AV302462 AV302462 RIKEN full-le
gb_est14:AA396353   -   17.00  291.60  1.8e-07   492  ! AA396353 vb27g08.r1 Soares mous
gb_est30:AI646038   +   17.00  287.65  3.0e-07   832  ! AI646038 vw54a10.x1 Soares mous
gb_est33:AV111279   +   16.00  277.01  1.2e-06   284  ! AV111279 AV111279 Mus musculus
gb_est21:AA959709   +   15.00  253.62  2.3e-05   529  ! AA959709 vw54a04.s1 Soares mous
gb_est21:AA959836   +   15.00  252.49  2.7e-05   615  ! AA959836 vw54h01.s1 Soares mous
gb_est30:AI662832   +   15.00  253.00  2.5e-05   575  ! AI662832 vb27g08.x1 Soares mous
gb_est32:C82304     +   14.00  231.81  0.0004    799  ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300    +   14.00  230.24  0.0005    986  ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est36:AI931087   +   11.00  183.91  0.1773    267  ! AI931087 fc77c03.y1 Zebrafish W
gb_est20:AA861150   -   10.00  162.06  2.92      405  ! AA861150 ak36a12.s1 Soares_test
gb_est16:AA558448   -    9.00  141.20  42.37     539  ! AA558448 nk39a08.s1 NCI_CGAP_GC
gb_est20:AA868515   -    9.00  138.71  58.32     751  ! AA868515 ak43c04.s1 Soares_test
gb_est41:AV280802   +    9.00  147.50  18.89     233  ! AV280802 AV280802 RIKEN full-le
gb_est41:AV316571   +    9.00  147.03  20.06     248  ! AV316571 AV316571 RIKEN full-le
gb_est44:AW182968   -    9.00  139.31  54.05     694  ! AW182968 xj65f07.x1 Soares_NFL_
gb_est44:AW207606   +    9.00  144.36  28.27     354  ! AW207606 UI-H-BI1-afk-h-06-0-UI
gb_gss1:CNS00WI4    +    9.00  139.03  56.00     720  ! AL093610 Arabidopsis thaliana g
gb_gss3:B67798      +    9.00  141.50  40.78     518  ! B67798 T24H12TR TAMU Arabidopsi
gb_gss5:AQ821350    +    9.00  140.08  48.94     626  ! AQ821350 HS_5216_B1_F12_T7A RPD
gb_gss10:AQ231238   -    9.00  142.64  35.23     445  ! AQ231238 HS_2058_A1_A04_T7 C
gb_gss11:AQ305493   -    9.00  141.63  40.10     509  ! AQ305493 HS_2041_B2_G10_T7 C
gb_gss11:AQ333161   -    9.00  141.75  39.49     501  ! AQ333161 HS_5004_B2_D05_SP6E
gb_gss14:AQ571705   -    9.00  141.83  39.11     496  ! AQ571705 HS_2119_A1_D03_T7C
gb_est1:D11916      -    8.00  120.50  603.32    703  ! D11916 HUM000S105 Liver HepG
gb_gss15:AQ661549   -    8.00  122.77  450.42    519  ! AQ661549 HS_5192_A2_A02_SP6E

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00             Length:    159
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     343 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 359
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     359 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 376
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     376 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 392
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     393 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 409
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     409 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 426
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     426 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 442
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     443 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 459
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     459 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 476
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     476 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 492
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     493 LysProLeuLysSerThrSerLeuSer 501
         |||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
            Quality:  117.00              Length:    117
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     567 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 583
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     583 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     600 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 616
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     617 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 633
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     633 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 650
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     650 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 666
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     667 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 683
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     683 g 683
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
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          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         www-bio.llnl.gov/bbrp/image/image.html

         Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
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                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
            Quality:  116.00              Length:    116
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     568 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 584
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     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     584 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 601
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     601 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 617
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     618 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 634
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     634 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 651
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     651 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 667
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     668 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 683
         |||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
            Quality:   85.00              Length:     85
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

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       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     514 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 531
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     531 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 547
         |||||||||||||||||||||||||||||||||||||||||||||||||
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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     548 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 564
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     564 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 581
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     581 yrLys 582
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     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:

 US-09-026-459A-37 x AA072780   ..

 Align seg 1/1  to: AA072780  from: 1  to: 522

     647 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 663
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     663 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 680
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     680 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 696
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     697 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 713
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     713 s 713
         |
     458 A 458

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN
```

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alignment_scores:
           Quality:   53.00              Length:     53
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     366 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 382
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     382 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 399
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     399 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 415
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     416 TrpLeuSer 418
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


alignment_scores:
           Quality:   52.00              Length:     52
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AA210875   ..

 Align seg 1/1  to: AA210875  from: 1  to: 456

     730 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 746
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     746 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 763
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     763 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 779
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     780 GluLys 781
         ||||||
     175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
```

```
           9712 Medical Center Drive, Rockville, MD 20850 USA
           Tel: 3018699056
           Fax: 3018699423
           Email: arkerlav@tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please check the TIGR Human Gene
           Index (http://www.tigr.org/tdb/hgi/hgi.html)
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


alignment_scores:
            Quality:   49.00            Length:     49
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     434 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 450
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     450 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 467
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     467 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 482
         ||||||||||||||||||||||||||||||||||||||||||||||||
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS        AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION   oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
             similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
             mRNA sequence.
ACCESSION    AA765882
VERSION      AA765882.1  GI:2817120
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 171)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044576.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Trace considered overall poor quality
             Insert Length: 2415   Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00            Length:     43
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     298 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 314
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     314 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 331
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAAGGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     331 snAspAsnIlePheHisMetSerLeuLeu 340
         ||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS        AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION   ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
             clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
             susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION    AI020392
VERSION      AI020392.1  GI:3234728
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 356)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
```

```
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00            Length:     42
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     677 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 693
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     693 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 710
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     710 rgValLeuLysArgSerAlaGluGly 718
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00            Length:     40
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     316 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 332
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     332 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 349
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     349 laThrTyrSerArgSerThr 355
         |||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     715 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 731
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     731 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 748
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     748 erLysPheGlnGln 752
         ||||||||||||||
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
```

```
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     394 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 410
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     410 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 427
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     427 ysGlnSerLysAsp 431
```

```
          ||||||||||||||
     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
            Quality:   37.00            Length:     37
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x N41391    ..

 Align seg 1/1  to: N41391  from: 1  to: 457

     694 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspAr 710
         ||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
     218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

     710 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 727
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

     727 ysLeuArgPhe 730
         ||||||||||
     318 AACTACGCTTT 328

seq_name: gb_est3:R57845

seq_documentation_block:
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


alignment_scores:
            Quality:   29.00            Length:     29
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x R57845    ..

 Align seg 1/1  to: R57845  from: 1  to: 152

     639 ProArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGl 655
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 CCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGG 52

     655 yAsnIleTyrIleSerProLeuLysSerProTyrLys 667
```

```
                                     ||||||||||||||||||||||||||||||||||||
53 GAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 89
```

```
OM of: US-09-026-459A-35 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15917/app_query.fasta.1
 -DB=EST -QFMT=fastap -SUFFIX=oligo.rst -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-35
Query length: 832
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence          Strd Orig    ZScore   EScore Len  ! Documentation  ..
gb_est38:AL120941   +  159.00 2956.70  6.3e-156  572  ! AL120941 DKFZp762D143_r1 762 (s
gb_est32:AI745644   -  117.00 2170.65  3.9e-112  415  ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643   -  116.00 2151.95  4.2e-111  411  ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103   +   85.00 1572.73  7.8e-79   285  ! AA382103 EST95270 Activated T-c
gb_est9:AA072780    +   67.00 1230.33  9.2e-60   522  ! AA072780 mm76a05.r1 Stratagene
gb_est17:AA664676   -   53.00  970.95  2.6e-45   329  ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875   +   52.00  949.75  3.9e-44   456  ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277   +   49.00  896.45  3.6e-41   304  ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882   -   43.00  788.10  3.9e-35   171  ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392   +   42.00  763.87  8.8e-34   356  ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411   -   40.00  719.31  2.7e-31   914  ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402      +   38.00  688.18  1.4e-29   386  ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485   -   38.00  682.12  3.1e-29   871  ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391      +   37.00  668.15  1.9e-28   457  ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845      +   29.00  526.16  1.5e-20   152  ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529   -   29.00  517.89  4.4e-20   462  ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097   +   29.00  514.70  6.7e-20   709  ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255   +   27.00  479.39  6.2e-18   525  ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628   +   25.00  443.38  6.2e-16   427  ! AA709628 vv41c11.r1 Soares 2NbM
gb_est42:AV302462   +   23.00  412.52  3.3e-14   174  ! AV302462 RIKEN full-le
gb_est21:AA959709   +   22.00  385.47  1.1e-12   529  ! AA959709 vw54a04.s1 Soares mous
gb_est21:AA959836   +   22.00  384.35  1.2e-12   615  ! AA959836 vw54h01.s1 Soares mous
gb_est30:AI646038   +   22.00  382.10  1.6e-12   832  ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832   +   22.00  384.85  1.1e-12   575  ! AI662832 vb27g08.x1 Soares mous
gb_est14:AA396353   -   17.00  292.15  1.7e-07   492  ! AA396353 vb27g08.r1 Soares mous
gb_est27:AA955457   +   16.00  273.69  1.8e-06   472  ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est33:AV111279   +   16.00  277.47  1.1e-06   284  ! AV111279 AV111279 Mus musculus
gb_est32:C82304     +   14.00  232.22  0.0004    799  ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300    +   14.00  230.66  0.0004    986  ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est36:AI931087   +   11.00  184.06  0.1737    267  ! AI931087 fc77c03.y1 Zebrafish W
gb_est20:AA861150   -   10.00  162.19  2.87      405  ! AA861150 ak36a12.s1 Soares_test
gb_est16:AA558448   -    9.00  141.29  41.90     539  ! AA558448 nk39a08.s1 NCI_CGAP_GC
gb_est20:AA868515   -    9.00  138.82  57.50     751  ! AA868515 ak43c04.s1 Soares_test
gb_est41:AV280802   +    9.00  147.53  18.82     233  ! AV280802 AV280802 RIKEN full-le
gb_est41:AV316571   +    9.00  147.07  19.97     248  ! AV316571 AV316571 RIKEN full-le
gb_est44:AW182968   -    9.00  139.41  53.33     694  ! AW182968 xj65f07.x1 Soares_NFL_
gb_est44:AW207606   +    9.00  144.42  28.05     354  ! AW207606 UI-H-BI1-afk-h-06-0-UI
gb_gss1:CNS00WI4    +    9.00  139.14  55.23     720  ! AL093610 Arabidopsis thaliana g
gb_gss3:B67798      +    9.00  141.59  40.34     518  ! B67798 T24H12TR TAMU Arabidopsi
gb_gss5:AQ821350    +    9.00  140.18  48.33     626  ! AQ821350 HS_5216_B1_F12_T7A
gb_gss10:AQ231238   -    9.00  142.72  34.90     445  ! AQ231238 HS_2058_A1_A04_T7 C
gb_gss11:AQ305493   -    9.00  141.72  39.67     509  ! AQ305493 HS_2041_B2_G10_T7 C
gb_gss11:AQ333161   -    9.00  141.84  39.07     501  ! AQ333161 HS_5004_B2_D05_SP6E
gb_gss14:AQ571705   -    9.00  141.91  38.70     496  ! AQ571705 HS_2119_A1_D03_T7C
gb_gss15:AQ661549   -    8.00  122.80  448.90    519  ! AQ661549 HS_5192_A2_A02_SP6E

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer;K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00             Length:    159
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     394 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 410
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     410 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 427
         |||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     427 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 443
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
```

```
     444 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 460
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     460 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 477
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     477 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 493
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     494 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 510
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     510 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 527
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     527 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 543
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     544 LysProLeuLysSerThrSerLeuSer 552
         |||||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477
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seq_name: gb_est32:AI745644

seq_documentation_block:

LOCUS AI745644 415 bp mRNA EST 21-JUN-1999
DEFINITION tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI745644
VERSION AI745644.1 GI:5113932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137189.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers
source 1. .415
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2219219"
/clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"

BASE COUNT 118 a 75 c 87 g 135 t
ORIGIN

alignment_scores:
Quality: 117.00 Length: 117
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-35 x AI745644/rev ..

Align seg 1/1 to reverse of: AI745644 from: 1 to: 415

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     618 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 634
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     634 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 651
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     651 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 667
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     668 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 684
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     684 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 701
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     701 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 717
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     718 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 734
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     734 g 734
         |
      63 G 63
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seq_name: gb_est32:AI745643

seq_documentation_block:

LOCUS AI745643 411 bp mRNA EST 21-JUN-1999
DEFINITION tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI745643
VERSION AI745643.1 GI:5113931
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137188.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
            Quality:  116.00             Length:    116
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     619 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 635
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     635 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 652
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     652 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 668
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     669 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 685
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     685 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 702
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     702 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 718
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     719 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 734
         ||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
            Quality:   85.00             Length:     85
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     549 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 565
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     565 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 582
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     582 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 598
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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```
     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     599 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 615
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     615 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 632
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     632 yrLys 633
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 US-09-026-459A-35 x AA072780   ..

 Align seg 1/1  to: AA072780  from: 1  to: 522

     698 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 714
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     714 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 731
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     731 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 747
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     748 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 764
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     764 s 764
         |
     458 A 458

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN
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alignment_scores:
            Quality:   53.00              Length:     53
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     417 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 433
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     433 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 450
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     450 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 466
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     467 TrpLeuSer 469
         !!!!!!!!!
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


alignment_scores:
            Quality:   52.00              Length:     52
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AA210875   ..

 Align seg 1/1  to: AA210875  from: 1  to: 456

     781 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 797
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     797 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 814
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     814 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 830
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     831 GluLys 832
         ||||||
     175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
```

```
           9712 Medical Center Drive, Rockville, MD 20850 USA
           Tel: 3018699056
           Fax: 3018699423
           Email: arkerlav@tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please check the TIGR Human Gene
           Index (http://www.tigr.org/tdb/hgi/hgi.html)
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


alignment_scores:
            Quality:   49.00             Length:     49
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     485 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 501
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     501 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 518
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     518 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 533
         ||||||||||||||||||||||||||||||||||||||||||||||
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS        AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION   oal4a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
             similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
             mRNA sequence.
ACCESSION    AA765882
VERSION      AA765882.1  GI:2817120
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 171)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044576.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Trace considered overall poor quality
             Insert Length: 2415   Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00             Length:     43
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     349 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 365
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     365 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 382
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     382 snAspAsnIlePheHisMetSerLeuLeu 391
         |||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS        AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION   ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
             clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
             susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION    AI020392
VERSION      AI020392.1  GI:3234728
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 356)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
```

```
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE.COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00             Length:     42
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     728 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 744
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     744 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 761
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     761 rgValLeuLysArgSerAlaGluGly 769
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00             Length:     40
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     367 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 383
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     383 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     400 laThrTyrSerArgSerThr 406
         |||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00             Length:     38
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     766 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 782
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     782 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 799
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     799 erLysPheGlnGln 803
         |||||||||||||||
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
```

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LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00             Length:     38
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     445 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 461
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     461 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 478
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     478 ysGlnSerLysAsp 482
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```
        ||||||||||||||
    207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
            Quality:   37.00            Length:     37
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x N41391   ..

 Align seg 1/1  to: N41391  from: 1  to: 457

     745 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspAr 761
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

     761 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 778
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

     778 ysLeuArgPhe 781
         ||||||||||
     318 AACTACGCTTT 328

seq_name: gb_est3:R57845

seq_documentation_block:
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


alignment_scores:
            Quality:   29.00            Length:     29
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x R57845   ..

 Align seg 1/1  to: R57845  from: 1  to: 152

     690 ProArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGl 706
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
       3 CCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGG 52

     706 yAsnIleTyrIleSerProLeuLysSerProTyrLys 718
```

```
                                    ||||||||||||||||||||||||||||||||||||
53 GAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 89
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```
OM of: US-09-026-459A-33 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15917/app_query.fasta.1
 -DB=EST -QFMT=fastap -SUFFIX=oligo.rst -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-33
Query length: 851
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence            Strd Orig    ZScore    EScore Len   ! Documentation  ..
gb_est38:AL120941     +  159.00 2951.66  1.2e-155  572   ! AL120941 DKFZp762D143_r1 762 (s
gb_est32:AI745644     -  117.00 2166.91  6.2e-112  415   ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643     -  116.00 2148.24  6.8e-111  411   ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103     +   85.00 1569.98  1.1e-78   285   ! AA382103 EST95270 Activated T-c
gb_est9:AA072780      +   67.00 1228.13  1.2e-59   522   ! AA072780 mm76a05.r1 Stratagene
gb_est17:AA664676     -   53.00  969.19  3.2e-45   329   ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875     +   52.00  948.01  4.9e-44   456   ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277     +   49.00  894.81  4.5e-41   304   ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882     -   43.00  786.64  4.7e-35   171   ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392     +   42.00  762.44  1.1e-33   356   ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411     -   40.00  717.94  3.2e-31   914   ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402        +   38.00  686.87  1.7e-29   386   ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485     -   38.00  680.82  3.7e-29   871   ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391        +   37.00  666.88  2.2e-28   457   ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845        +   29.00  525.14  1.7e-20   152   ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529     -   29.00  516.86  5.0e-20   462   ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097     +   29.00  513.68  7.6e-20   709   ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255     +   27.00  478.43  7.0e-18   525   ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628     +   25.00  442.49  7.0e-16   427   ! AA709628 vv41c11.r1 Soares 2NbM
gb_est21:AA959836     +   24.00  421.03  1.1e-14   615   ! AA959836 vw54h01.s1 Soares mous
gb_est27:AA955457     +   24.00  423.00  8.5e-15   472   ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est30:AI646038     +   24.00  418.78  1.5e-14   832   ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832     +   24.00  421.53  1.0e-14   575   ! AI662832 vb27g08.x1 Soares mous
gb_est21:AA959709     +   23.00  403.41  1.1e-13   529   ! AA959709 vw54a04.s1 Soares mous
gb_est42:AV302462     +   23.00  411.68  3.6e-14   174   ! AV302462 AV302462 RIKEN full-le
gb_est14:AA396353     -   17.00  291.50  1.8e-07   492   ! AA396353 vb27g08.r1 Soares mous
gb_est33:AV111279     +   16.00  276.85  1.2e-06   284   ! AV111279 AV111279 Mus musculus
gb_est32:C82304       +   14.00  231.67  0.0004    799   ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300      +   14.00  230.10  0.0005    986   ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est36:AI931087     +   11.00  183.60  0.1844    267   ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:T24020        -   10.00  162.87  2.63      349   ! T24020 seq2177 3HFLSK20 Homo sa
gb_est20:AA861150     -   10.00  161.76  3.04      405   ! AA861150 ak36a12.s1 Soares_test
gb_est22:AI074792     -   10.00  159.20  4.21      571   ! AI074792 oy03a06.s1 Soares_sene
gb_est16:AA558448     -    9.00  140.89  44.12     539   ! AA558448 nk39a08.s1 NCI_CGAP_GC
gb_est20:AA868515     -    9.00  138.42  60.55     751   ! AA868515 ak43c04.s1 Soares_test
gb_est41:AV280802     +    9.00  147.13  19.82     233   ! AV280802 AV280802 RIKEN full-le
gb_est41:AV316571     +    9.00  146.67  21.03     248   ! AV316571 AV316571 RIKEN full-le
gb_est44:AW182968     -    9.00  139.01  56.16     694   ! AW182968 xj65f07.x1 Soares_NFL_
gb_est44:AW207606     +    9.00  144.02  29.54     354   ! AW207606 UI-H-BI1-afk-h-06-0-UI
gb_gss1:CNS00WI4      +    9.00  138.74  58.16     720   ! AL093610 Arabidopsis thalian
gb_gss3:B67798        +    9.00  141.19  42.48     518   ! B67798 T24H12TR TAMU Arabido
gb_gss5:AQ821350      +    9.00  139.78  50.89     626   ! AQ821350 HS_5216_B1_F12_T7A
gb_gss10:AQ231238     -    9.00  142.32  36.75     445   ! AQ231238 HS_2058_A1_A04_T7 C
gb_gss11:AQ305493     -    9.00  141.32  41.77     509   ! AQ305493 HS_2041_B2_G10_T7 C
gb_gss14:AQ571705     -    9.00  141.51  40.75     496   ! AQ571705 HS_2119_A1_D03_T7C

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES              Location/Qualifiers
     source           1. .572
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="DKFZp762D143"
                      /clone_lib="762 (synonym: hmel2)"
                      /tissue_type="melanoma (MeWo cell line)"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00              Length:    159
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     413 AlaLeuGluValValMetAlaTrTyrSerArgSerThrSerGlnAsnLe 429
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     429 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     446 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 462
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
```

```
     463 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 479
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     479 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 496
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     496 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 512
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     513 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 529
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     529 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 546
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     546 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 562
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     563 LysProLeuLysSerThrSerLeuSer 571
         ||||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
           Quality:  117.00              Length:    117
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     637 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 653
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     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     653 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 670
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     670 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 686
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     687 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 703
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     703 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     720 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 736
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     737 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 753
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     753 g 753
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
```

```
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
           Quality:  116.00             Length:    116
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     638 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 654
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     654 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 671
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     671 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 687
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     688 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 704
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     704 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 721
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     721 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 737
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     738 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 753
         |||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
           Quality:   85.00             Length:     85
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     568 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 584
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     584 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 601
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     601 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 617
         |||||||||||||||||||||||||||||||||||||||||||||||||
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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     618 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 634
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     634 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 651
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     651 yrLys 652
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:

 US-09-026-459A-33 x AA072780   ..

 Align seg 1/1  to: AA072780  from: 1  to: 522

     717 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 733
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     733 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     750 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 766
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     767 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     783 s 783
         |
     458 A 458

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN
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alignment_scores:
           Quality:   53.00            Length:     53
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     436 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 452
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     452 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 469
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     469 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 485
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     486 TrpLeuSer 488
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


alignment_scores:
           Quality:   52.00            Length:     52
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AA210875   ..

 Align seg 1/1  to: AA210875  from: 1  to: 456

     800 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 816
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     816 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 833
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     833 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 849
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     850 GluLys 851
         ||||||
     175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
```

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           9712 Medical Center Drive, Rockville, MD 20850 USA
           Tel: 3018699056
           Fax: 3018699423
           Email: arkerlav@tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please check the TIGR Human Gene
           Index (http://www.tigr.org/tdb/hgi/hgi.html)
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


alignment_scores:
            Quality:   49.00             Length:     49
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     504 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     520 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 537
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     537 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 552
         ||||||||||||||||||||||||||||||||||||||||||||||
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS        AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION   oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
           ' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
             mRNA sequence.
ACCESSION    AA765882
VERSION      AA765882.1  GI:2817120
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 171)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044576.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Trace considered overall poor quality
             Insert Length: 2415   Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00             Length:     43
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     368 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 384
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     384 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 401
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     401 snAspAsnIlePheHisMetSerLeuLeu 410
         ||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS        AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION   ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
             clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
             susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION    AI020392
VERSION      AI020392.1  GI:3234728
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 356)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
```

```
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00             Length:     42
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     747 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 763
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     763 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     780 rgValLeuLysArgSerAlaGluGly 788
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00             Length:     40
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     386 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 402
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     402 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 419
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     419 laThrTyrSerArgSerThr 425
         ||||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     785 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 801
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     801 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 818
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     818 erLysPheGlnGln 822
         |||||||||||||||
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
```

```
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     464 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     480 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 497
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     497 ysGlnSerLysAsp 501
```

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          ||||||||||||||
      207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391         457 bp    mRNA            EST      24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
            Quality:   37.00             Length:     37
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x N41391   ..

 Align seg 1/1  to: N41391  from: 1  to: 457

     764 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspAr 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

     780 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 797
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

     797 ysLeuArgPhe 800
         ||||||||||
     318 AACTACGCTTT 328

seq_name: gb_est3:R57845

seq_documentation_block:
LOCUS       R57845         152 bp    mRNA            EST      02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
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            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="F6142"
                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


alignment_scores:
            Quality:   29.00             Length:     29
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x R57845   ..

 Align seg 1/1  to: R57845  from: 1  to: 152

     709 ProArgSerProTyrLysPheProSerSerProLeuArgIleProGlyGl 725
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 CCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGG 52

     725 yAsnIleTyrIleSerProLeuLysSerProTyrLys 737
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    ||||||||||||||||||||||||||||||||||||
53  GAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 89
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OM of: US-09-026-459A-31 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15917/app_query.fasta.1
 -DB=EST -QFMT=fastap -SUFFIX=oligo.rst -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-31
Query length: 874
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


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gb_est38:AL120941    +  159.00 2961.48   3.4e-156  572  ! AL120941 DKFZp762D143_r1 762 (s
gb_est32:AI745644    -  117.00 2174.04   2.5e-112  415  ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643    -  116.00 2155.30   2.8e-111  411  ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103    +   85.00 1575.06   5.8e-79   285  ! AA382103 EST95270 Activated T-c
gb_est9:AA072780     +   67.00 1232.03   7.4e-60   522  ! AA072780 mm76a05.r1 Stratagene
gb_est17:AA664676    -   53.00  972.20   2.2e-45   329  ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875    +   52.00  950.95   3.3e-44   456  ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277    +   49.00  897.57   3.1e-41   304  ! AA361277 EST70529 T-cell lympho
gb_est19:AA765882    -   43.00  789.03   3.5e-35   171  ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392    +   42.00  764.75   7.9e-34   356  ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411    -   40.00  720.09   2.4e-31   914  ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402       +   38.00  688.92   1.3e-29   386  ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485    -   38.00  682.84   2.9e-29   871  ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391       +   37.00  668.85   1.7e-28   457  ! N41391 yw70g06.r1 Soares_placen
gb_est22:AI074792    -   33.00  591.96   3.3e-24   571  ! AI074792 oy03a06.s1 Soares_sene
gb_est3:R57845       +   29.00  526.63   1.4e-20   152  ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529    -   29.00  518.32   4.2e-20   462  ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097    +   29.00  515.12   6.3e-20   709  ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255    +   27.00  479.76   5.9e-18   525  ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628    +   25.00  443.69   6.0e-16   427  ! AA709628 vv41c11.r1 Soares 2NbM
gb_est21:AA959836    +   24.00  422.16   9.5e-15   615  ! AA959836 vw54h01.s1 Soares mous
gb_est27:AA955457    +   24.00  424.13   7.4e-15   472  ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est30:AI646038    +   24.00  419.90   1.3e-14   832  ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832    +   24.00  422.66   8.9e-15   575  ! AI662832 vb27g08.x1 Soares mous
gb_est21:AA959709    +   23.00  404.48   9.2e-14   529  ! AA959709 vw54a04.s1 Soares mous
gb_est42:AV302462    +   23.00  412.78   3.2e-14   174  ! AV302462 AV302462 RIKEN full-le
gb_est1:T24020       -   17.00  294.75   1.2e-07   349  ! T24020 seq2177 3HFLSK20 Homo sa
gb_est14:AA396353    -   17.00  292.18   1.6e-07   492  ! AA396353 vb27g08.r1 Soares mous
gb_est33:AV111279    +   16.00  277.48   1.1e-06   284  ! AV111279 AV111279 Mus musculus
gb_est32:C82304      +   14.00  232.14   0.0004    799  ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300     +   14.00  230.57   0.0004    986  ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est36:AI931087    +   11.00  183.92   0.1770    267  ! AI931087 fc77c03.y1 Zebrafish W
gb_est20:AA861150    -   10.00  162.00   2.94      405  ! AA861150 ak36a12.s1 Soares_test
gb_est16:AA558448    -    9.00  141.06   43.19     539  ! AA558448 nk39a08.s1 NCI_CGAP_GC
gb_est20:AA868515    -    9.00  138.58   59.35     751  ! AA868515 ak43c04.s1 Soares_test
gb_est41:AV280802    +    9.00  147.32   19.34     233  ! AV280802 AV280802 RIKEN full-le
gb_est41:AV316571    +    9.00  146.86   20.53     248  ! AV316571 AV316571 RIKEN full-le
gb_est44:AW182968    -    9.00  139.17   55.02     694  ! AW182968 xj65f07.x1 Soares_NFL_
gb_est44:AW207606    +    9.00  144.20   28.87     354  ! AW207606 UI-H-BI1-afk-h-06-0-UI
gb_gss1:CNS00WI4     +    9.00  138.89   57.00     720  ! AL093610 Arabidopsis thalian
gb_gss3:B67798       +    9.00  141.35   41.57     518  ! B67798 T24H12TR TAMU Arabido
gb_gss5:AQ821350     +    9.00  139.94   49.85     626  ! AQ821350 HS_5216_B1_F12_T7A
gb_gss10:AQ231238    -    9.00  142.49   35.94     445  ! AQ231238 HS_2058_A1_A04_T7 C
gb_gss11:AQ305493    -    9.00  141.48   40.88     509  ! AQ305493 HS_2041_B2_G10_T7 C
gb_gss14:AQ571705    -    9.00  141.68   39.88     496  ! AQ571705 HS_2119_A1_D03_T7C

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
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             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     436 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 452
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       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     452 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 469
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     469 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 485
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     486 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 502
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     502 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 519
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     519 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 535
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     536 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 552
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     552 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 569
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     569 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 585
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     586 LysProLeuLysSerThrSerLeuSer 594
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     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .415
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2219219"
                      /clone_lib="NCI_CGAP_Ov23"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
            Quality:  117.00              Length:    117
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

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     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     676 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 693
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     693 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 709
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     710 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 726
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     726 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 743
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     743 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 759
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     760 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 776
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     776 g 776
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
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DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a      74 c      87 g     133 t
ORIGIN


alignment_scores:
            Quality:  116.00              Length:    116
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     677 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 694
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     694 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 710
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     711 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 727
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     727 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 744
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     744 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 760
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     761 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 776
         ||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
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                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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BASE COUNT       87 a      63 c      52 g      83 t
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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     607 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 624
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     624 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 640
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     657 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 674
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     674 yrLys 675
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     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
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DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
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                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
           Quality:   67.00            Length:     67
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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US-09-026-459A-31 x AA072780   ..

Align seg 1/1  to: AA072780  from: 1  to: 522

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     258 AGTTCACCCTTACGGATCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     756 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 773
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     773 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 789
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     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     790 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 806
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     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

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seq_name: gb_est17:AA664676

seq_documentation_block:
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DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
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                     (1996) Cancer Research 56:5380-5383."
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ORIGIN
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Date: Feb 13, 2000  4:05 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.rni
 -GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
 -LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000
 -XGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
 -YGAPEXT=60.000 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=oligo -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US09026459 -NCPU=6
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Search information block:
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Query length: 928
Database: Issued_Patents_NA:*
Database sequences: 214294
Database length: 59861208
Search time (sec): 316.800000

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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


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alignment_block:
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      19 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 68

     129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
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      69 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 118
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146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
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119 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 168

163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
169 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 218

179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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219 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 268

196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
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269 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 318

213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
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319 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 368

229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
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369 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 418

246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
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263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
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seq_documentation_block:
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


alignment_scores:
            Quality:  816.00              Length:    816
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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seq_documentation_block:
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
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;      LOCATION:  19..2469
US-08-470-091-1


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            Quality:  816.00              Length:    816
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seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


alignment_scores:
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seq_documentation_block:
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


alignment_scores:
            Quality:  816.00              Length:    816
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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    525 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 574

    146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
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    575 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 624

    163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
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    179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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    196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
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    213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
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seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-482-627-4

seq_documentation_block:
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


alignment_scores:
            Quality:  816.00              Length:    816
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000    Percent Identity: 100.000

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 Align seg 1/1  to: US-08-482-627-4  from: 1  to: 2994

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;  GENERAL INFORMATION:
;     APPLICANT:  The Regents of the University of California
;     APPLICANT:  and Canji, Inc.
;     TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;     TITLE OF INVENTION:  Susceptibility Gene Product
;     NUMBER OF SEQUENCES:  3
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Campbell and Flores
;       STREET:  4370 La Jolla Village Drive
;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10357
;       FILING DATE:  13-SEP-1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/121,108
;       FILING DATE:  13-SEP-1993
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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seq_documentation_block:
; Sequence 1, Application US/07915246
; Patent No. 5401836
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris L.
;    APPLICANT:  Fallis, Lynne
;    APPLICANT:  Bellmare, Guy
;    APPLICANT:  Boivin, Rodolphe
;    TITLE OF INVENTION:  A BRASSICA REGULATORY SEQUENCE FOR
;    TITLE OF INVENTION:  ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held, and Malloy
;      STREET:  500 W. Madison St. 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/915,246
;      FILING DATE:  19920716
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien, Donald J.
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  91 P 1125
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312 707-8889
;      TELEFAX:  312 707-9155
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1505 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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;      ORGANISM:  Brassica napus
;      STRAIN:  Westar
;      DEVELOPMENTAL STAGE:  Somatic
;      TISSUE TYPE:  Root
US-07-915-246-1


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seq_documentation_block:
; Sequence 1, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
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;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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US-08-234-783-1


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            Quality:   10.00              Length:     10
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seq_documentation_block:
; Sequence 3, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
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;      LENGTH:  1680 base pairs
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;      STRANDEDNESS:  double
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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
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;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
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;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
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;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
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; Patent No. 5686288
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/246,982A
;      FILING DATE:  May 20, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Jorge, A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  0609.3880002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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; Patent No. 5693757
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,265
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0609.3880003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
;      TYPE:  nucleic acid
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  TITLE     Human DNA in the diagnosis of retinoblastoma
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1187 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1236

 413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
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1237 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1286

 429 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 446
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 446 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 462
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1337 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1386

 463 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 479
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1387 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1436

 479 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 496
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1437 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1486

 496 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 512
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1537 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1586

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 546 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 562
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 596 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 612
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1837 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1886

 629 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 646
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1887 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1936

 646 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 662
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seq_name: gb_pat:I18496

seq_documentation_block:
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DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


alignment_scores:
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              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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     129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      69 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 118

     146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     119 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 168

     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     169 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 218

     179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     219 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 268

     196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     269 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 318

     213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     319 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 368

     229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
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     369 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 418

     246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     419 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 468

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     279 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 296
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     619 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 668

     329 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 346
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     669 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 718

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     396 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 412
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     413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
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     919 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 968

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    1019 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1068

     463 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 479
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1519 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1568

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 763 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 779
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DEFINITION  Sequence 2 from patent US 5496731.
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VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


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    3118 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 3069

     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
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DEFINITION  Sequence 2 from patent US 5710255.
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VERSION     I81465.1  GI:3209762
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SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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BASE COUNT      974 a    618 c    593 g    809 t
ORIGIN


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SOURCE      Homo sapiens cDNA to mRNA.
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
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  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
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  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
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  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
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COMMENT     Mutation data provided by Dr. B.L.Gallie,
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            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4600)
  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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            [published erratum appears in Proc Natl Acad Sci U S A 1988
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
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  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
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  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
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  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


alignment_scores:
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alignment_block:
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seq_documentation_block:
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DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
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BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


alignment_scores:
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  389 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 405
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2498 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACA 2547

 855 erAspArgValLeu 859
     |||||||||||||
2548 GCGACCGTGTGCTC 2561
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seq_name: gb_pr3:AF043224

seq_documentation_block:
LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /tissue_type="osteosarcoma cells xenotransplanted to nude
                     mice"
     gene            <1. .426
                     /gene="RB1"
     exon            <1. .7
                     /gene="RB1"
                     /number=5
     CDS             <1. .137
                     /gene="RB1"
                     /note="tandem duplication of exons 3-6; frameshift causes
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                     a premature stop codon relative to the wild type protein"
                     /codon_start=3
                     /product="retinoblastoma susceptibility protein"
                     /protein_id="AAC26845.1"
                     /db_xref="GI:2865464"
                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
                     "
     exon            8. .76
                     /gene="RB1"
                     /number=6
     exon            77. .192
                     /gene="RB1"
                     /number=3
     exon            193. .312
                     /gene="RB1"
                     /number=4
     exon            313. .350
                     /gene="RB1"
                     /number=5
     exon            351. .418
                     /gene="RB1"
                     /number=6
     exon            419. .>426
                     /gene="RB1"
                     /number=7
BASE COUNT      145 a     61 c     82 g    138 t
ORIGIN


alignment_scores:
            Quality:   88.00             Length:     88
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x AF043224   ..

 Align seg 1/1  to: AF043224  from: 1  to: 426

     113 MetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHi 129
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     148 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 197

     129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     198 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 247

     146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     248 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 297

     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     298 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 347

     179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     348 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 397

     196 leThrPheLeuLeu 200
         |||||||||||||||
     398 TCACATTTTTATTA 411

seq_name: gb_pat:E12560

seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .4591
            FT                   /organism='Mus musculus'
            FT                   /cell_type='B-cell precursor' FT
                /cell_line='70Z-3'
            FT   5'UTR           1. .98
            FT   CDS             99. .2864
            FT                   /product='Rb protein'
            FT   3'UTR           2865. .4591.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN


alignment_scores:
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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x E12560   ..

 Align seg 1/1  to: E12560  from: 1  to: 4591

     794 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 810
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     810 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 827
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     827 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 843
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     844 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 860
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     860 sArgSerAlaGluGly 865
         |||||||||||||||
    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
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```
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
     CDS             99. .2864
                     /codon_start=1
                     /product="pp105 Rb protein"
                     /protein_id="AAA39964.1"
                     /db_xref="GI:200453"
                     /translation="MPPKAPRRAAAAEPPPPPPPPPREDDPAQDSGPEELPLARLEFE
                     EIEEPEFIALCQKLKVPDHVRERAWLTWEKVSSVDGILEGYIQKKKELWGICIFIAAV
                     DLDEMPFTFTELQKSIETSVYKFFDLLKEIDTSTKVDNAMSRLLKKYNVLCALYSKLE
                     RTCELIYLTQPSSALSTEINSMLVLKISWITFLLAKGEVLQMEDDLVISFQLMLCVVD
                     YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
                     CNIDEVKNVYFKNFIPFINSLGIVSSNGLPEVESLSKRYEEVYLKNKDLDARLFLDHD
                     KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
                     NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
                     MESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTLQHLDSGTDLSF
                     PWILNVLNLKAFDFYKVIESFIKVEANLTREMIKHLERCEHRIMESLAWLSDSPLFDL
                     IKQSKDGEGPDNLEPACPLSLPLQGNHTAADMYLSPLRSPKKRTSTTRVNSAANTETQ
                     AASAFHTQKPLKSTSLALFYKKVYRLAYLRLNTLCARLLSDHPELEHIIWTLFQHTLQ
                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                     EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
                     ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
                     EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
                     VSNKEEK"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


alignment_scores:
            Quality:   72.00            Length:     72
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x MUSPP105RB   ..

 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

     794 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 810
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     810 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 827
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     827 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 843
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     844 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     860 sArgSerAlaGluGly 865
         |||||||||||||||||
    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_pr1:HUMRBSY79

seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
                     /note="mutated retinoblastoma protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x HUMRBSY79   ..

 Align seg 1/1  to: HUMRBSY79  from: 1  to: 480

     203 GlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMe 219
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     219 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 236
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     236 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     253 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 269
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     269 nAsp 270
         ||||
     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /isolate="Patient G364"
                     /db_xref="taxon:9606"
                     /cell_type="leukocyte"
                     /map="13q14.2"
     gene            1. .340
                     /gene="RB1"
     intron          <1. .64
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=16
     exon            65. .260
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
     CDS             <65. .120
                     /gene="RB1"
                     /note="exon 17"
                     /codon_start=3
                     /db_xref="GDB:G00-118-734"
                     /product="retinoblastoma suspectibility protein"
                     /protein_id="AAA82549.1"
                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
                     /gene="RB1"
                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
     intron          261. .>340
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN


alignment_scores:
            Quality:   66.00            Length:     66
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:
 US-09-026-459A-51 x HUMRB1501V   ..

 Align seg 1/1  to: HUMRB1501V  from: 1  to: 340

     500 ArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTr 516
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     516 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 533
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     533 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 549
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     550 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 565
         ||||||||||||||||||||||||||||||||||||||||||||||||
     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260
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OM of: US-09-026-459A-49 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:39 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
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 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
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 -THREADS=1

Search information block:
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Query length: 871
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence            Strd Orig    ZScore    EScore Len  ! Documentation  ..
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gb_est32:AI745644     -  117.00 1795.65  3.0e-91   415  ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643     -  116.00 1780.25  2.1e-90   411  ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103     +   85.00 1303.18  8.0e-64   285  ! AA382103 EST95270 Activated T-c
gb_est9:AA072780      +   67.00 1020.39  4.5e-48   522  ! AA072780 mm76a05.r1 Stratagene
gb_est22:AI074792     -   60.00  911.44  5.3e-42   571  ! AI074792 oy03a06.s1 Soares_sene
gb_est17:AA664676     -   53.00  807.04  3.5e-36   329  ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875     +   52.00  789.25  3.4e-35   456  ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277     +   49.00  745.70  9.0e-33   304  ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882     -   43.00  656.94  7.9e-28   171  ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392     +   42.00  636.28  1.1e-26   356  ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411     -   40.00  598.66  1.4e-24   914  ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402        +   38.00  573.81  3.4e-23   386  ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485     -   38.00  568.05  7.1e-23   871  ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391        +   37.00  557.15  2.9e-22   457  ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845        +   29.00  441.15  8.3e-16   152  ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529     -   29.00  433.29  2.3e-15   462  ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097     +   29.00  430.25  3.4e-15   709  ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255     +   27.00  401.44  1.4e-13   525  ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628     +   25.00  371.95  5.9e-12   427  ! AA709628 vv41c11.r1 Soares 2NbM
gb_est21:AA959836     +   24.00  353.90  6.0e-11   615  ! AA959836 vw54h01.s1 Soares mous
gb_est27:AA955457     +   24.00  355.77  4.7e-11   472  ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est30:AI646038     +   24.00  351.76  7.9e-11   832  ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832     +   24.00  354.37  5.7e-11   575  ! AI662832 vb27g08.x1 Soares mous
gb_est21:AA959709     +   23.00  339.49  3.8e-10   529  ! AA959709 vw54a04.s1 Soares mous
gb_est42:AV302462     +   23.00  347.36  1.4e-10   174  ! AV302462 AV302462 RIKEN full-le
gb_est1:T24020        -   17.00  249.60  3.9e-05   349  ! T24020 seq2177 3HFLSK20 Homo sa
gb_est14:AA396353     -   17.00  247.17  5.3e-05   492  ! AA396353 vb27g08.r1 Soares mous
gb_est3:R70325        +   16.00  233.21  0.0003    397  ! R70325 yj81b10.r1 Soares breast
gb_est33:AV111279     +   16.00  235.58  0.0002    284  ! AV111279 AV111279 Mus musculus
gb_est32:C82304       +   14.00  197.32  0.0317    799  ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300      +   14.00  195.83  0.0384    986  ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est34:AV147820     +   11.00  158.95  4.35      256  ! AV147820 AV147820 Mus musculus
gb_est36:AI931087     +   11.00  158.66  4.52      267  ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:D15138        +   10.00  141.51  40.72     338  ! D15138 RICC0141A Rice callus Or
gb_est1:D38851        +   10.00  140.67  45.40     381  ! D38851 RICC1624A Rice callus Or
gb_est1:D38980        +   10.00  139.86  50.35     427  ! D38980 RICR0089A Rice root Oryz
gb_est1:D40024        -   10.00  141.15  42.68     356  ! D40024 RICS1743A Rice shoot Ory
gb_est2:D47372        -   10.00  141.49  40.83     339  ! D47372 RICS12716A Rice green sh
gb_est2:D48004        -   10.00  140.99  43.55     364  ! D48004 RICS13911A Rice green
gb_est7:W29241        -   10.00  134.21  103.85    948  ! W29241 mb96e12.r1 Soares mou
gb_est7:W29419        -   10.00  133.32  116.41   1075  ! W29419 mb98h11.r1 Soares mo
gb_est7:W29461        -   10.00  133.98  107.03    980  ! W29461 mb99b11.r1 Soares mou
gb_est7:W29564        -   10.00  133.08  120.13   1113  ! W29564 mc03d11.r1 Soares mo
gb_gss15:AQ650463     -   10.00  141.11  42.90     358  ! AQ650463 Sheared DNA-18F2.TF

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00              Length:    159
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     433 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 449
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     449 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 466
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     466 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 482
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
```

```
     483 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 499
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     499 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 516
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     516 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 532
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     533 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 549
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     549 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 566
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     566 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 582
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     583 LysProLeuLysSerThrSerLeuSer 591
         |||||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
           Quality:  117.00              Length:    117
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     657 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 673
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     673 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 690
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     690 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 706
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     707 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 723
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     723 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 740
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTGCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     740 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 756
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     757 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 773
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     773 g 773
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
```

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alignment_scores:
           Quality:   53.00              Length:     53
             Ratio:  1.000               Gaps:        0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     459 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 475
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     475 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 492
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     492 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 508
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     509 TrpLeuSer 511
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28ml3 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


alignment_scores:
           Quality:   52.00              Length:     52
             Ratio:  1.000               Gaps:        0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AA210875   ..

 Align seg 1/1  to: AA210875  from: 1  to: 456

     823 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 839
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     839 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 856
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     856 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 872
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     873 GluLys 874
         ||||||
     175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
```

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           9712 Medical Center Drive, Rockville, MD 20850 USA
           Tel: 3018699056
           Fax: 3018699423
           Email: arkerlav@tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please check the TIGR Human Gene
           Index (http://www.tigr.org/tdb/hgi/hgi.html)
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


alignment_scores:
            Quality:   49.00             Length:     49
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     527 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 543
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      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     543 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 560
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     560 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 575
         ||||||||||||||||||||||||||||||||||||||||||||||
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS        AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION   oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
             similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
             mRNA sequence.
ACCESSION    AA765882
VERSION      AA765882.1  GI:2817120
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 171)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044576.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Trace considered overall poor quality
             Insert Length: 2415   Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00             Length:     43
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     391 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 407
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     407 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 424
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     424 snAspAsnIlePheHisMetSerLeuLeu 433
         |||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS        AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION   ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
             clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
             susceptibility protein (MOUSE);; mRNA sequence.
ACCESSION    AI020392
VERSION      AI020392.1  GI:3234728
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 356)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
```

```
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00             Length:     42
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     770 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 786
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     786 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 803
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     803 rgValLeuLysArgSerAlaGluGly 811
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00             Length:     40
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     409 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 425
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     425 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 442
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     442 laThrTyrSerArgSerThr 448
         ||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402        386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00              Length:     38
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     808 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 824
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     824 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 841
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     841 erLysPheGlnGln 845
         ||||||||||||||
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
```

```
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00              Length:     38
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     487 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 503
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     503 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 520
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     520 ysGlnSerLysAsp 524
```

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          ||||||||||||||
     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
            Quality:   37.00            Length:     37
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x N41391   ..

 Align seg 1/1  to: N41391  from: 1  to: 457

     787 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspAr 803
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

     803 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 820
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

     820 ysLeuArgPhe 823
         ||||||||||
     318 AACTACGCTTT 328

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


alignment_scores:
            Quality:   33.00            Length:     33
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

       2 AspPheThrAlaLeuCysGlnLysLeuLysIleProAspHisValArgGl 18
```

```
    ||||||||||||||||||||||||||||||||||||||||||||||||||
287 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGA 238

 18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeu 34
    ||||||||||||||||||||||||||||||||||||||||||||||||||
237 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTG 189
```

```
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
           Quality:  116.00             Length:    116
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     658 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 674
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     674 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 691
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     691 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 707
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     708 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 724
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     724 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 741
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     741 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 757
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     758 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 773
         |||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
           Quality:   85.00             Length:     85
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     588 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 604
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     604 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 621
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     621 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 637
         |||||||||||||||||||||||||||||||||||||||||||||||||
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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     638 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 654
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     654 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 671
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     671 yrLys 672
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
```

```
 US-09-026-459A-49 x AA072780   ..

 Align seg 1/1  to: AA072780  from: 1  to: 522

     737 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 753
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     753 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 770
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     770 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 786
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     787 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 803
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     803 s 803
         |
     458 A 458

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTAGCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
```

```
ORIGIN


alignment_scores:
            Quality:   60.00             Length:     60
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

      29 ProGluGluAspProGluGlnAspSerGlyProGluAspLeuProLeuVa 45
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGT 319

      45 lArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeuCysG 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     318 CAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTC 269

      62 lnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeuThrTrp 78
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 AGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGG 219

      79 GluLysValSerSerValAspGlyValLeu 88
         |||||||||||||||||||||||||||||||
     218 GAGAAAGTTTCATCTGTGGATGGAGTATTG 189

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


alignment_scores:
            Quality:   53.00             Length:     53
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     456 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 472
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     472 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 489
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     489 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 505
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     506 TrpLeuSer 508
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
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(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 80 c 90 g 133 t 3 others
ORIGIN

alignment_scores:
Quality: 52.00 Length: 52
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-49 x AA210875 ..

Align seg 1/1 to: AA210875 from: 1 to: 456

```
     820 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 836
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     836 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 853
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     853 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 869
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     870 GluLys 871
         ||||||
     175 GAGAAA 180
```

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS AA361277 304 bp mRNA EST 21-APR-1997
DEFINITION EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION AA361277
VERSION AA361277.1 GI:2013596
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 304)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., , Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 12140200

COMMENT On Sep 12, 1996 this sequence version replaced gi:1407493.
Other_ESTs: THC168922
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .304
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165411"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 94 a 79 c 43 g 86 t 2 others
ORIGIN

alignment_scores:
Quality: 49.00 Length: 49
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-49 x AA361277 ..

Align seg 1/1 to: AA361277 from: 1 to: 304

```
     524 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     540 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 557
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     557 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 572
         ||||||||||||||||||||||||||||||||||||||||||||||||
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196
```

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS AA765882 171 bp mRNA EST 08-FEB-1998
DEFINITION oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA765882
VERSION AA765882.1 GI:2817120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044576.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

```
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Insert Length: 2415    Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00            Length:     43
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     388 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 404
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     404 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 421
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     421 snAspAsnIlePheHisMetSerLeuLeu 430
         ||||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS        AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION   ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
             clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
             susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION    AI020392
VERSION      AI020392.1  GI:3234728
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 356)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
             Waterston,R.
  TITLE      The WashU-HHMI Mouse EST Project
  JOURNAL    Unpublished (1996)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044708.
             Contact: Marra M/Mouse EST Project
             WashU-HHMI Mouse EST Project
             Washington University School of MedicineP
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:900436
             Seq primer: -28m13 rev1 ET from Amersham
             High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00            Length:     42
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     767 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     783 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 800
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     800 rgValLeuLysArgSerAlaGluGly 808
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS        AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION   vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
             IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
             PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
             protein (MOUSE);, mRNA sequence.
ACCESSION    AA763411
VERSION      AA763411.1  GI:2813158
KEYWORDS     EST.
SOURCE       house mouse.
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00            Length:     40
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     406 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 422
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     422 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 439
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     439 laThrTyrSerArgSerThr 445
         ||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     805 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 821
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     821 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 838
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     838 erLysPheGlnGln 842
         ||||||||||||||
```

```
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     484 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     500 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 517
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     517 ysGlnSerLysAsp 521
         ||||||||||||||
     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
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Date: Feb 13, 2000  4:04 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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Search information block:
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Query length: 871
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WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


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seq_documentation_block:
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


alignment_scores:
            Quality:  628.00              Length:    628
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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seq_documentation_block:
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/470,091
;       FILING DATE:  JUN-16-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  19..2469
US-08-470-091-1


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     244 AsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLe 260
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     583 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 632

     260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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     633 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 682

     277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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     683 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 732

     294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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     783 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAAC 832

     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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     833 AATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 882

     344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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     883 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 932

     360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
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     933 AAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTG 982

     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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     983 TGGGACAGGGTTGTGTGGAAATTGGATCACAGCGATACAAACTTGGAGTT 1032

     394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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     410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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     427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
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     577 erAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPhe 593
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     644 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIl 660
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    1883 CTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGAT 1932

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    1933 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 1982

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    1983 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 2032

     727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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     744 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGl 760
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    2083 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGA 2132

     760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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    2133 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2182

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    2183 CAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAG 2232

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     844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
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     860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to reverse of: US-08-470-091-2  from: 1  to: 3232

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     277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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    2554 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 2505

     294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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    2504 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 2455

     310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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    2354 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 2305

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     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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     394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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2104 TGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 2055

 444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerProProTrpIl 460
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2054 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 2005

 460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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 477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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1954 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 1905

 494 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSe 510
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1904 GAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTC 1855

 510 rProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrA 527
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 544 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGl 560
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1654 CAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTT 1605

 594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
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1604 TATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA 1555

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1104 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 1055

 777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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seq_documentation_block:
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
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;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


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seq_documentation_block:
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949

;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
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;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
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 260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
1089 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 1138

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 294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
1189 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1238

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1289 AATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

 344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 1388

 360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
1389 AAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTG 1438

 377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
1439 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 1488

 394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
1489 CGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1538

 410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
1539 ATTATCCATTCAAAATTTAGCAAACTTCTGAATGACAACATTTTTCATA 1588

 427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
1589 TGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

 444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 460
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 494 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSe 510
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 510 rProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrA 527
1839 ACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTG 1888

 527 spHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 543
1889 ATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

 544 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGl 560
1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGG 1988

 560 ySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrS 577
1989 TTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCT 2038

 577 erAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPhe 593
2039 CAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTT 2088

 594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
2089 TATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA 2138

 610 uArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuP 627
2139 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTT 2188

 627 heGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 643
2189 TCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2238

 644 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIl 660
2239 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATAT 2288

 660 eAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisA 677
2289 AGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATG 2338

 677 laValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAsp 693
2339 CTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGAT 2388

 694 SerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAs 710
2389 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2438

 710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
2439 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 2488

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2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGA 2588

 760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
2589 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2638

 777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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 794 MetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAs 810
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-915-246-1

seq_documentation_block:
; Sequence 1, Application US/07915246
; Patent No. 5401836
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris L.
;    APPLICANT:  Fallis, Lynne
;    APPLICANT:  Bellmare, Guy
;    APPLICANT:  Boivin, Rodolphe
;    TITLE OF INVENTION:  A BRASSICA REGULATORY SEQUENCE FOR
;    TITLE OF INVENTION:  ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held, and Malloy
;      STREET:  500 W. Madison St. 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/915,246
;      FILING DATE:  19920716
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien, Donald J.
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  91 P 1125
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312 707-8889
;      TELEFAX:  312 707-9155
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1505 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Brassica napus
;      STRAIN:  Westar
;      DEVELOPMENTAL STAGE:  Somatic
;      TISSUE TYPE:  Root
US-07-915-246-1


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seq_documentation_block:
; Sequence 1, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
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US-08-234-783-1


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seq_documentation_block:
; Sequence 3, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
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;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
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;      TOPOLOGY:  unknown
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US-08-234-783-3


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seq_documentation_block:
; Sequence 1, Application US/08456907
; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;       APPLICATION NUMBER:  US/08/456,907
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/234,783
;       FILING DATE:  28-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST48AUSA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9200
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1680 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
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US-08-456-907-3


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; Sequence 5, Application US/08246982A
; Patent No. 5686288
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/246,982A
;      FILING DATE:  May 20, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Jorge, A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  0609.3880002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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 Align seg 1/1  to: US-08-246-982A-5  from: 1  to: 10366

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; Sequence 5, Application US/08453265
; Patent No. 5693757
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,265
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0609.3880003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
;      TYPE:  nucleic acid
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;      TOPOLOGY:  linear
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About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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 -DB=EST -QFMT=fastap -SUFFIX=oligo.rst -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-47
Query length: 869
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence           Strd Orig    ZScore    EScore Len  ! Documentation  ..
gb_est38:AL120941    +  159.00 2430.24  1.3e-126  572  ! AL120941 DKFZp762D143_r1 762 (s
gb_est32:AI745644    -  117.00 1786.23  1.0e-90   415  ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643    -  116.00 1770.91  7.1e-90   411  ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103    +   85.00 1296.49  1.9e-63   285  ! AA382103 EST95270 Activated T-c
gb_est9:AA072780     +   67.00 1015.25  8.8e-48   522  ! AA072780 mm76a05.r1 Stratagene
gb_est22:AI074792    -   60.00  906.90  9.5e-42   571  ! AI074792 oy03a06.s1 Soares_sene
gb_est17:AA664676    -   53.00  803.08  5.8e-36   329  ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875    +   52.00  785.39  5.6e-35   456  ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277    +   49.00  742.09  1.4e-32   304  ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882    -   43.00  653.82  1.2e-27   171  ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392    +   42.00  633.26  1.7e-26   356  ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411    -   40.00  595.84  2.0e-24   914  ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402       +   38.00  571.14  4.8e-23   386  ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485    -   38.00  565.40  1.0e-22   871  ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391       +   37.00  554.56  4.0e-22   457  ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845       +   29.00  439.23  1.1e-15   152  ! R57845 F6142 Fetal heart Homo s
gb_est11:AA258255    +   27.00  399.71  1.7e-13   525  ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628    +   25.00  370.40  7.3e-12   427  ! AA709628 vv41c11.r1 Soares 2NbM
gb_est21:AA959836    +   24.00  352.44  7.3e-11   615  ! AA959836 vw54h01.s1 Soares mous
gb_est27:AA955457    +   24.00  354.30  5.7e-11   472  ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est29:AI606529    -   24.00  354.45  5.6e-11   462  ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646038    +   24.00  350.30  9.6e-11   832  ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI646097    +   24.00  351.43  8.3e-11   709  ! AI646097 vw54h07.x1 Soares mous
gb_est30:AI662832    +   24.00  352.91  6.8e-11   575  ! AI662832 vb27g08.x1 Soares mous
gb_est21:AA959709    +   23.00  338.11  4.6e-10   529  ! AA959709 vw54a04.s1 Soares mous
gb_est42:AV302462    +   23.00  345.95  1.7e-10   174  ! AV302462 AV302462 RIKEN full-le
gb_est1:T24020       -   17.00  248.72  4.3e-05   349  ! T24020 seq2177 3HFLSK20 Homo sa
gb_est14:AA396353    -   17.00  246.30  5.9e-05   492  ! AA396353 vb27g08.r1 Soares mous
gb_est3:R70325       +   16.00  232.42  0.0004    397  ! R70325 yj81b10.r1 Soares breast
gb_est33:AV111279    +   16.00  234.79  0.0003    284  ! AV111279 AV111279 Mus musculus
gb_est32:C82304      +   14.00  196.72  0.0343    799  ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300     +   14.00  195.23  0.0415    986  ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est34:AV147820    +   11.00  158.58  4.56      256  ! AV147820 AV147820 Mus musculus
gb_est36:AI931087    +   11.00  158.28  4.74      267  ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:D15138       +   10.00  141.23  42.21     338  ! D15138 RICC0141A Rice callus Or
gb_est1:D38851       +   10.00  140.39  47.04     381  ! D38851 RICC1624A Rice callus Or
gb_est1:D38980       +   10.00  139.59  52.15     427  ! D38980 RICR0089A Rice root Oryz
gb_est1:D40024       -   10.00  140.87  44.24     356  ! D40024 RICS1743A Rice shoot Ory
gb_est2:D47372       -   10.00  141.21  42.32     339  ! D47372 RICS12716A Rice green sh
gb_est2:D48004       -   10.00  140.71  45.14     364  ! D48004 RICS13911A Rice green
gb_est7:W29241       -   10.00  133.96  107.28    948  ! W29241 mb96e12.r1 Soares mou
gb_est7:W29419       -   10.00  133.07  120.21   1075  ! W29419 mb98h11.r1 Soares mo
gb_est7:W29461       -   10.00  133.73  110.55    980  ! W29461 mb99b11.r1 Soares mou
gb_est7:W29564       -   10.00  132.83  124.04   1113  ! W29564 mc03d11.r1 Soares mo
gb_gss15:AQ650463    -   10.00  140.83  44.46     358  ! AQ650463 Sheared DNA-18F2.TF

seq_name: gb_est38:AL120941

seq_documentation_block:
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DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES              Location/Qualifiers
     source           1. .572
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="DKFZp762D143"
                      /clone_lib="762 (synonym: hmel2)"
                      /tissue_type="melanoma (MeWo cell line)"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00              Length:    159
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     431 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 447
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     447 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 464
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     464 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     481 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 497
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     497 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 514
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     514 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 530
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     531 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 547
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     547 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 564
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     564 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 580
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     581 LysProLeuLysSerThrSerLeuSer 589
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     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
           Quality:  117.00              Length:    117
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     655 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 671
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     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     671 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 688
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     688 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 704
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     705 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 721
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     721 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 738
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTGCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     738 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 754
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     755 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 771
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAAGACCAACAAAAATGACTCCAAGATCAAG 64

     771 g 771
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
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                     /db_xref="taxon:9606"
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                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
           Quality:  116.00             Length:    116
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     656 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 672
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     672 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 689
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     689 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 705
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     706 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 722
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     722 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 739
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     739 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 755
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     756 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 771
         |||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
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                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
           Quality:   85.00             Length:     85
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     586 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 602
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     602 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 619
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     619 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 635
         |||||||||||||||||||||||||||||||||||||||||||||||||
```

```
     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     636 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 652
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     652 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 669
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     669 yrLys 670
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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```
 US-09-026-459A-47 x AA072780   ..

 Align seg 1/1  to: AA072780  from: 1  to: 522

     735 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 751
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     751 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 768
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     768 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     785 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 801
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     801 s 801
         |
     458 A 458

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
```

```
ORIGIN


alignment_scores:
            Quality:   60.00             Length:     60
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

      29 ProGluGluAspProGluGlnAspSerGlyProGluAspLeuProLeuVa 45
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGT 319

      45 lArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeuCysG 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     318 CAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTC 269

      62 lnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeuThrTrp 78
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     268 AGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGG 219

      79 GluLysValSerSerValAspGlyValLeu 88
         |||||||||||||||||||||||||||||||
     218 GAGAAAGTTTCATCTGTGGATGGAGTATTG 189

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


alignment_scores:
            Quality:   53.00             Length:     53
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     454 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 470
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     470 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 487
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     487 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 503
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     504 TrpLeuSer 506
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
```

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 80 c 90 g 133 t 3 others
ORIGIN

alignment_scores:
Quality: 52.00 Length: 52
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-47 x AA210875 ..

Align seg 1/1 to: AA210875 from: 1 to: 456

818 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 834
25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

834 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 851
75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

851 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 867
125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

868 GluLys 869
175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS AA361277 304 bp mRNA EST 21-APR-1997
DEFINITION EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION AA361277
VERSION AA361277.1 GI:2013596
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 304)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., , Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 12140200

COMMENT On Sep 12, 1996 this sequence version replaced gi:1407493.
Other_ESTs: THC168922
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .304
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165411"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 94 a 79 c 43 g 86 t 2 others
ORIGIN

alignment_scores:
Quality: 49.00 Length: 49
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-47 x AA361277 ..

Align seg 1/1 to: AA361277 from: 1 to: 304

522 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 538
50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

538 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 555
100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

555 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 570
150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS AA765882 171 bp mRNA EST 08-FEB-1998
DEFINITION oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA765882
VERSION AA765882.1 GI:2817120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044576.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

```
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Insert Length: 2415   Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
           Quality:   43.00            Length:     43
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     386 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 402
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     402 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 419
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     419 snAspAsnIlePheHisMetSerLeuLeu 428
         |||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS       AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION  ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AI020392
VERSION     AI020392.1  GI:3234728
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
           Quality:   42.00            Length:     42
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     765 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 781
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     781 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 798
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     798 rgValLeuLysArgSerAlaGluGly 806
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
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  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     404 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 420
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     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     420 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 437
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     437 laThrTyrSerArgSerThr 443
         ||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     803 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 819
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       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     819 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 836
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     836 erLysPheGlnGln 840
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     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AA763485/rev   ..

 Align seq 1/1  to reverse of: AA763485  from: 1  to: 871

     482 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 498
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     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     498 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 515
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     515 ysGlnSerLysAsp 519
         ||||||||||||||
     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo.".
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
            Quality:   37.00            Length:     37
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x N41391   ..
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Align seg 1/1  to: N41391  from: 1  to: 457

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    218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

    798 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 815
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

    815 ysLeuArgPhe 818
        ||||||||||
    318 AACTACGCTTT 328
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OM of: US-09-026-459A-49 to: GenEmbl:*   out_format : pfs

Date: Feb 13, 2000  8:20 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-49
Query length: 871
Database: GenEmbl:*
Database sequences: 821193
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Search time (sec): 10867.920000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
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Sequence              Strd Orig    ZScore    EScore Len   ! Documentation  ..
gb_pat:I05311           +  628.00 11739.39  0.0       4597  ! I05311 Sequence 1 from Patent
gb_pat:I18496           +  628.00 11742.03  0.0       3232  ! I18496 Sequence 1 from patent
gb_pat:I18497           -  628.00 11742.03  0.0       3232  ! I18497 Sequence 2 from patent
gb_pat:I81465           +  628.00 11742.60  0.0       2994  ! I81465 Sequence 2 from patent
gb_pr2:HUMRB1MRNA       +  628.00 11739.00  0.0       4839  ! L41870 Homo sapiens retinobla
gb_pr2:HUMRBA1RA        +  628.00 11739.38  0.0       4600  ! M33647 Human retinoblastoma a
gb_pr2:HUMRBSA          +  628.00 11742.60  0.0       2994  ! M28419 Human retinoblastoma s
gb_pat:I09369           +  577.00 10782.44  0.0       4597  ! I09369 Sequence 1 from Patent
gb_pr2:HUMRBS           +  560.00 10463.23  0.0       4740  ! M15400 Human retinoblastoma s
gb_pat:A01444           +  286.00 5322.26   2.0e-288  4580  ! A01444 H.sapiens DNA for 4.6 k
gb_pr3:AF043224         +  112.00 2075.22   1.4e-107  426   ! AF043224 Homo sapiens retinobla
gb_pat:E12560           +   72.00 1306.84   9.1e-65   4591  ! E12560 cDNA encoding Rb (retin
gb_ro:MUSPP105RB        +   72.00 1306.84   9.1e-65   4591  ! M26391 Mouse retinoblastoma su
gb_pr2:HUMRB1501V       +   66.00 1213.79   1.4e-59   340   ! L49220 Homo sapiens retinoblast
gb_pat:I09384           +   65.00 1189.68   3.0e-58   693   ! I09384 Sequence 17 from Patent
gb_pr1:HUMRBS15         +   65.00 1189.68   3.0e-58   693   ! M27858 Human retinoblastoma sus
gb_pr1:HUMRETBLAS       +   65.00 1147.94   6.4e-56   180388  ! L11910 Human retinoblastoma
gb_ro:RATRP             +   59.00 1063.17   3.4e-51   4432  ! D25233 Rat mRNA for retinoblas
gb_pat:I09389           +   55.00  999.80   1.1e-47   935   ! I09389 Sequence 22 from Patent
gb_pr1:HUMRBS20         +   55.00  999.80   1.1e-47   935   ! M27863 Human retinoblastoma sus
gb_pr2:HUMRB23EX        +   55.00 1005.80   5.3e-48   420   ! L41910 Homo sapiens retinoblast
gb_pr2:HUMRB4MU2        +   55.00 1003.71   6.9e-48   555   ! L41904 Homo sapiens retinoblast
gb_pr2:HUMRB1777L       +   54.00  990.87   3.6e-47   252   ! L49230 Homo sapiens retinoblast
gb_ro:RATRTNBLST        +   52.00  937.43   3.4e-44   2102  ! L07126 Rattus norvegicus retin
gb_pr2:HUMRB17MU2       +   51.00  928.66   1.1e-43   555   ! L41924 Homo sapiens retinoblast
gb_pat:I09387           +   49.00  889.21   1.7e-41   717   ! I09387 Sequence 20 from Patent
gb_pr1:HUMRBS18         +   49.00  889.21   1.7e-41   717   ! L35147 Human retinoblastoma sus
gb_pr2:HUMRB1SDDL       +   49.00  897.94   5.4e-42   224   ! L49225 Homo sapiens retinoblast
gb_un:M27861            +   49.00  889.21   1.7e-41   717   ! M27861 Figure 2. Retinoblastoma
gb_pat:I09386           +   48.00  871.18   1.7e-40   650   ! I09386 Sequence 19 from Patent
gb_pr1:HUMRBS17         +   48.00  871.18   1.7e-40   650   ! M27860 Human retinoblastoma sus
gb_pr1:HUMRBS22         +   47.00  847.16   3.6e-39   1310  ! M27865 Human retinoblastoma su
gb_pr2:HUMRB25EX        +   47.00  852.71   1.8e-39   625   ! L41912 Homo sapiens retinoblast
gb_pat:I09370           +   46.00  830.36   3.1e-38   1008  ! I09370 Sequence 3 from Patent
gb_pr1:HSRB1G           +   46.00  830.05   3.3e-38   1050  ! X16439 Human retinoblastoma ge
gb_pr1:HUMRBS01         +   46.00  830.13   3.2e-38   1040  ! M27845 Human retinoblastoma su
gb_pr1:HUMRBSY79        +   46.00  835.93   1.5e-38   480   ! M19701 Human mutated retinoblas
gb_pr2:HUMRB01MUT       +   46.00  839.19   1.0e-38   311   ! L41889 Homo sapiens retinoblast
gb_pat:I09371           +   43.00  776.76   3.0e-35   704   ! I09371 Sequence 4 from Patent W
gb_pr1:HUMRBS02         +   43.00  776.76   3.0e-35   704   ! M27846 Human retinoblastoma
gb_pr2:HUMRB02EX        +   43.00  780.82   1.8e-35   410   ! L41890 Homo sapiens retinobl
gb_pr2:HUMRB1610K       +   43.00  785.36   1.0e-35   224   ! L49223 Homo sapiens retinobl
gb_pr2:HUMRB17MUT       +   43.00  782.75   1.4e-35   317   ! L41999 Homo sapiens retinobl
gb_pat:I09373           +   41.00  740.82   3.1e-33   570   ! I09373 Sequence 6 from Paten
gb_pr1:HUMRBS04         +   41.00  740.82   3.1e-33   570   ! M27848 Human retinoblastoma

seq_name: gb_pat:I05311

seq_documentation_block:
LOCUS       I05311       4597 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN


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             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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seq_name: gb_pat:I18496

seq_documentation_block:
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


alignment_scores:
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     294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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seq_documentation_block:
LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


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             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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  ORGANISM  Unknown.
            Unclassified.
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  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
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  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT M5G 1X8
            Canada
            Ph:  416 813-5868
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VERSION     M33647.1  GI:190945
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  AUTHORS   Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,E.,
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  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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            [published erratum appears in Proc Natl Acad Sci U S A 1988
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VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
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  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
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  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
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LOCUS       AF043224      426 bp    mRNA            PRI       21-JUL-1998
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
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            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
     source          1. .426
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                     /tissue_type="osteosarcoma cells xenotransplanted to nude
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                     /number=5
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                     /codon_start=3
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                     /translation="SSISTEINSALVLKVSWITFLLAKGRLYSKEKGTVGNLYLYCSS
                     "
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     exon            193. .312
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     105 eAlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnL 122
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     126 TGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGA 175

     122 ysAsnIleGluIleSerValHisLysPheAsnLeuLeuLysGluIle 138
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     176 AAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATT 225

     139 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTy 155
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     226 GATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTA 275

     155 rAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuI 172
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     276 TGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTA 325

     172 leTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAla 188
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     326 TATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 375

     189 LeuValLeuLysValSerTrpIleThrPheLeuLeu 200
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seq_name: gb_pat:E12560

seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
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            FT   source          1. .4591
            FT                   /organism='Mus musculus'
            FT                   /cell_type='B-cell precursor' FT
                /cell_line='70Z-3'
            FT   5'UTR           1. .98
            FT   CDS             99. .2864
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
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ORIGIN


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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     753 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 770
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     770 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 786
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    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     787 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 803
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     803 sArgSerAlaGluGly 808
         |||||||||||||||||
    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
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                     /sub_species="domesticus"
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     CDS             99. .2864
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BASE COUNT     1395 a   969 c    898 g   1329 t
ORIGIN      Chromosome 14.


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     753 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 770
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    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

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    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     787 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 803
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    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
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                     /map="13q14.2"
     gene            1. .340
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                     /translation="VHLRILILEQICLSHGF"
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     459 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 476
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     476 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 492
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     493 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 508
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     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260

seq_name: gb_pat:I09384

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LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
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ORIGIN


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     252 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 301

     460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     302 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 351

     477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     352 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 401

     494 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 508
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     402 GAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 446
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About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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seq_documentation_block:
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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seq_documentation_block:
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
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;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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US-08-470-091-1


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; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


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seq_documentation_block:
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
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US-08-959-638-7


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seq_documentation_block:
; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
```

```
;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  United States
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/482,627
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/951,947
;       FILING DATE:  28-SEP-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  P-UC 1707
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  139..2924
US-08-482-627-4


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            Quality:  687.00              Length:    687
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;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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; Patent No. 5401836
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris L.
;    APPLICANT:  Fallis, Lynne
;    APPLICANT:  Bellmare, Guy
;    APPLICANT:  Boivin, Rodolphe
;    TITLE OF INVENTION:  A BRASSICA REGULATORY SEQUENCE FOR
;    TITLE OF INVENTION:  ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held, and Malloy
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;       STREET:  500 W. Madison St. 34th Floor
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/915,246
;       FILING DATE:  19920716
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pochopien, Donald J.
;       REGISTRATION NUMBER:  32,167
;       REFERENCE/DOCKET NUMBER:  91 P 1125
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312 707-8889
;       TELEFAX:  312 707-9155
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1505 base pairs
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;       TOPOLOGY:  linear
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;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
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;       ORGANISM:  Brassica napus
;       STRAIN:  Westar
;       DEVELOPMENTAL STAGE:  Somatic
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US-07-915-246-1


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; Sequence 1, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;     APPLICANT:  Herlyn, Meenhard
;     APPLICANT:  Morris, Jennifer
;     APPLICANT:  Rauscher III, Frank J.
;     APPLICANT:  Rodeck, Ulrich
;     TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;     TITLE OF INVENTION:  Use Therefor
;     NUMBER OF SEQUENCES:  7
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Howson and Howson
;       STREET:  Spring House Corporate Cntr, PO Box 457
;       CITY:  Spring House
;       STATE:  Pennsylvania
;       COUNTRY:  USA
;       ZIP:  19477
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/234,783
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST48USA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9200
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  633 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
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;  GENERAL INFORMATION:
;     APPLICANT:  Herlyn, Meenhard
;     APPLICANT:  Morris, Jennifer
;     APPLICANT:  Rauscher III, Frank J.
;     APPLICANT:  Rodeck, Ulrich
;     TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;     TITLE OF INVENTION:  Use Therefor
;     NUMBER OF SEQUENCES:  7
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Howson and Howson
;       STREET:  Spring House Corporate Cntr, PO Box 457
;       CITY:  Spring House
;       STATE:  Pennsylvania
;       COUNTRY:  USA
;       ZIP:  19477
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/234,783
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
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;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST48USA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9200
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1680 base pairs
;       TYPE:  nucleic acid
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US-08-234-783-3


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; Patent No. 5633142
;  GENERAL INFORMATION:
;     APPLICANT:  Herlyn, Meenhard
;     APPLICANT:  Morris, Jennifer
;     APPLICANT:  Rauscher III, Frank J.
;     APPLICANT:  Rodeck, Ulrich
;     TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;     TITLE OF INVENTION:  Use Therefor
;     NUMBER OF SEQUENCES:  7
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Howson and Howson
;       STREET:  Spring House Corporate Cntr, PO Box 457
;       CITY:  Spring House
;       STATE:  Pennsylvania
;       COUNTRY:  USA
;       ZIP:  19477
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
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;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/456,907
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/234,783
;       FILING DATE:  28-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST48AUSA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9200
;       TELEFAX:  215-540-5818
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;       LENGTH:  633 base pairs
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;     APPLICANT:  Morris, Jennifer
;     APPLICANT:  Rauscher III, Frank J.
;     APPLICANT:  Rodeck, Ulrich
;     TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;     TITLE OF INVENTION:  Use Therefor
;     NUMBER OF SEQUENCES:  7
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Howson and Howson
;       STREET:  Spring House Corporate Cntr, PO Box 457
;       CITY:  Spring House
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;       MEDIUM TYPE:  Floppy disk
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;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/456,907
;       FILING DATE:
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;       APPLICATION NUMBER:  US 08/234,783
;       FILING DATE:  28-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST48AUSA
;     TELECOMMUNICATION INFORMATION:
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; Sequence 5, Application US/08246982A
; Patent No. 5686288
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/246,982A
;      FILING DATE:  May 20, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Jorge, A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  0609.3880002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      NAME/KEY:  CDS
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US-08-246-982A-5


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; Patent No. 5693757
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,265
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0609.3880003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
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Date: Feb 13, 2000  8:18 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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            Unclassified.
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  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
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 Percent Similarity: 100.000   Percent Identity: 100.000

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REFERENCE   1  (bases 1 to 3232)
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  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
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  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
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    199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
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    216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
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    506 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 555

    233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
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    249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
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    299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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    333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
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    399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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VERSION     I81465.1  GI:3209762
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2994)
  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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ORIGIN


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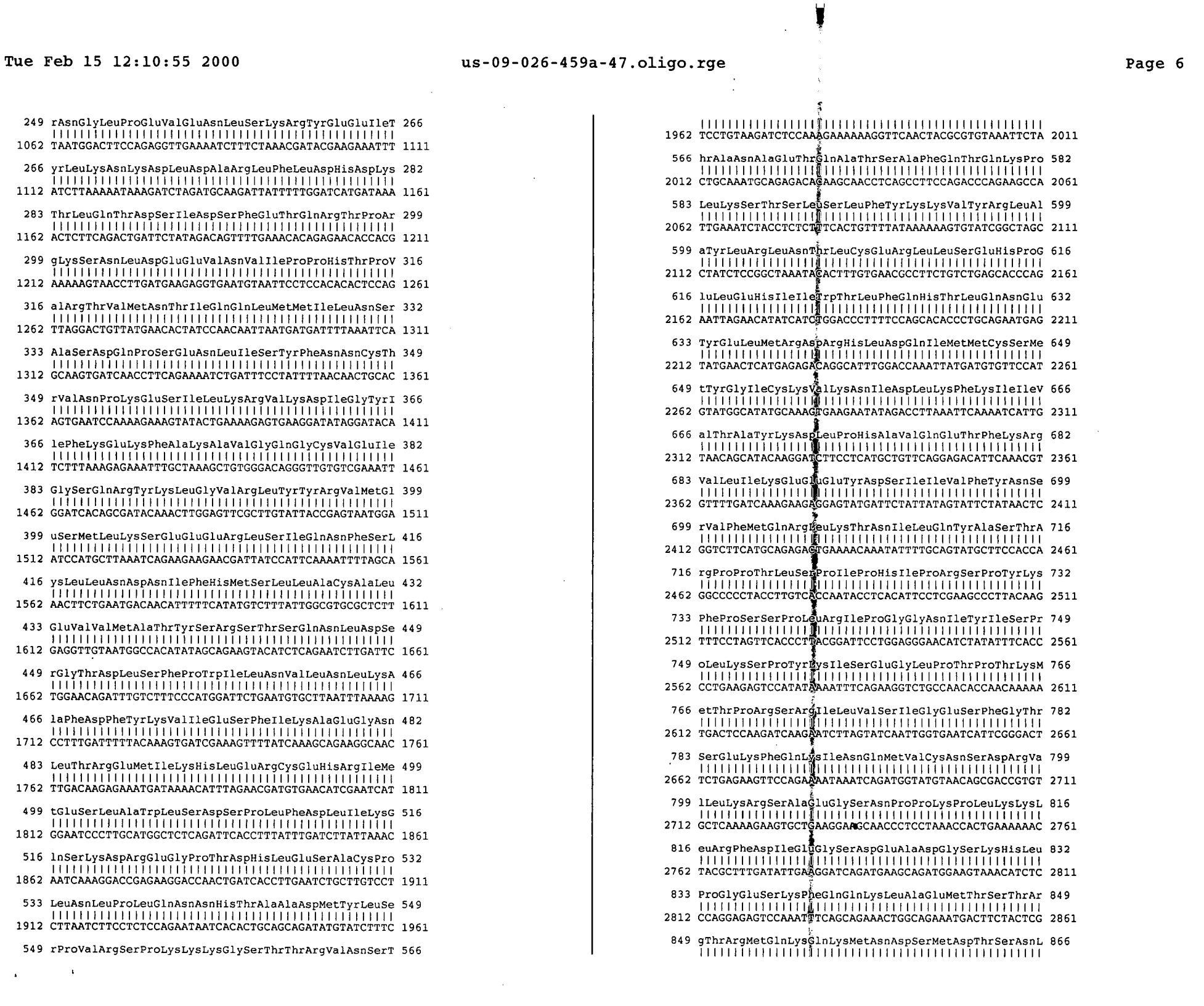
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VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
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  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
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  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
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            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
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            E-mail: brenda@hafiz.eric.on.ca.
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  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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SOURCE      Unknown.
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  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
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  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
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  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


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           Quality:  560.00              Length:    560
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x HUMRBS    ..

 Align seg 1/1  to: HUMRBS  from: 1  to: 4740

    310 IleProProHisThrProValArgThrValMetAsnThrIleGlnGlnLe 326
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   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATT 1292

    326 uMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleS 343
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1293 AATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTT 1342

    343 erTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysArg 359
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1343 CCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGA 1392

    360 ValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGl 376
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    376 yGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgL 393
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1443 ACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCT 1492

    393 euTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgLeu 409
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    410 SerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSe 426
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    426 rLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSerT 443
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 526 sLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrA 543
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1893 CCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTG 1942

 543 laAlaAspMetTyrLeuSerProValArgSerProLysLysLysGlySer 559
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1943 CAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCA 1992

 560 ThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAl 576
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1993 ACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGC 2042

 576 aPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrL 593
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 593 ysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArg 609
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 626 nHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspG 643
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 643 lnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAsp 659
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 676 lGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerI 693
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 693 leIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIle 709
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 710 LeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIl 726
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2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACAT 2492

 726 eProArgSerProTyrLysPheProSerSerProLeuArgIleProGlyG 743
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 760 LeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIl 776
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 776 eGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetV 793
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 793 alCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnPro 809
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 810 ProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAl 826
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 826 aAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuA 843
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2793 AGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGG 2842

 843 laGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAsp 859
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2843 CAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGAT 2892

 860 SerMetAspThrSerAsnLysGluGluLys 869
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2893 AGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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seq_name: gb_pat:A01444

seq_documentation_block:
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DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
FEATURES             Location/Qualifiers
     source          1. .4580
                     /organism="Homo sapiens"
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BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


alignment_scores:
           Quality:  286.00            Length:    522
             Ratio:  0.550              Gaps:      1
 Percent Similarity:  99.617   Percent Identity: 99.617

alignment_block:
 US-09-026-459A-47 x A01444   ..

 Align seg 1/1  to: A01444  from: 1  to: 4580

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    1001 CATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAG 1050

     296 gThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProH 313
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1051 AACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCAC 1100

     313 isThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIle 329
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1101 ACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1150

     330 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 346
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    1151 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAA 1200
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 346 nAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspI 363
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1201 CAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATA 1250

 363 leGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCys 379
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1251 TAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT.GGACAGGGTTGT 1299

 380 ValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrAr 396
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1300 GTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCG 1349

 396 gValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnA 413
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1350 AGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAA 1399

 413 snPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla 429
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 446 nLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuA 463
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 463 snLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAla 479
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 480 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHi 496
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1600 GAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACA 1649

 496 sArgIleMetGluSerLeu.AlaTrpLeuSerAspSerProLeuPheAsp 512
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1650 TCGAATCATGGAATC.CTTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1698

 513 LeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSe 529
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1699 CTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1748

 529 rAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspM 546
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1749 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATA 1798

 546 etTyrLeuSerProValArgSerProLysLysLysGlySerThrThrArg 562
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1799 TGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1848

 563 ValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnTh 579
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1849 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1898

 579 rGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValT 596
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 596 yrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 612
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1949 ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1998

 613 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 629
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1999 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 2048

 629 uGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetM 646
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2049 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGA 2098

 646 etCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhe 662
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 663 LysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluTh 679
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2149 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2198

 679 rPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValP 696
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2199 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGT 2248

 696 heTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr 712
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2249 TCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 2298

 713 AlaSerThrArgProProThrLeuSerProIleProHisIleProArgSe 729
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
            partial cds.
ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
            Blasco Ibanez 17, Valencia 46010, Spain
FEATURES             Location/Qualifiers
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                     /product="retinoblastoma susceptibility protein"
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     exon            77. .192
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     exon            313. .350
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ORIGIN


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x AF043224   ..

 Align seg 1/1  to: AF043224  from: 1  to: 426

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     105 eAlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnL 122
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     126 TGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGA 175

     122 ysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIle 138
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     176 AAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATT 225

     139 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTy 155
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     155 rAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuI 172
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     276 TGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTA 325

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DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
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            FT   source          1. .4591
            FT                   /organism='Mus musculus'
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            FT   CDS             99. .2864
            FT                   /product='Rb protein'
            FT   3'UTR           2865. .4591.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN


alignment_scores:
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x E12560   ..

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     735 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 751
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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     751 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 768
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     768 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     785 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 801
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     801 sArgSerAlaGluGly 806
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    2657 AAGAAGTGCTGAAGGC 2672
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seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
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                     /strain="BALB/c"
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                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
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                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
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                     ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
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BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     751 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 768
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    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     768 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 784
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    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     785 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 801
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    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

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seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
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                     /gene="RB1"
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                     /product="retinoblastoma suspectibility protein"
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                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
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                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
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     457 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 474
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     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     474 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 490
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     491 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 506
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     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260

seq_name: gb_pat:I09384

seq_documentation_block:
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DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
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BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


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     252 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 301

     458 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 475
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     302 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 351

     475 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 491
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     352 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 401

     492 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 506
         |||||||||||||||||||||||||||||||||||||||||||||
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Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
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 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
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 -THREADS=1

Search information block:
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Query length: 797
Database: EST:*
Database sequences: 4538634
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gb_est32:AI745643     -  116.00 1747.08   1.5e-88  411   ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103     +   85.00 1279.38   1.7e-62  285   ! AA382103 EST95270 Activated T-c
gb_est9:AA072780      +   67.00 1002.10   4.7e-47  522   ! AA072780 mm76a05.r1 Stratagene
gb_est22:AI074792     -   60.00  895.28   4.2e-41  571   ! AI074792 oy03a06.s1 Soares_sene
gb_est17:AA664676     -   53.00  792.95   2.1e-35  329   ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875     +   52.00  775.50   2.0e-34  456   ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277     +   49.00  732.82   4.7e-32  304   ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882     -   43.00  645.82   3.3e-27  171   ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392     +   42.00  625.53   4.5e-26  356   ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411     -   40.00  588.60   5.1e-24  914   ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402        +   38.00  564.29   1.2e-22  386   ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485     -   38.00  558.60   2.4e-22  871   ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391        +   37.00  547.94   9.4e-22  457   ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845        +   29.00  434.27   2.0e-15  152   ! R57845 F6142 Fetal heart Homo s
gb_est11:AA258255     +   27.00  395.27   3.0e-13  525   ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628     +   25.00  366.37   1.2e-11  427   ! AA709628 vv41c11.r1 Soares 2NbM
gb_est42:AV302462     +   23.00  342.31   2.7e-10  174   ! AV302462 AV302462 RIKEN full-le
gb_est21:AA959836     +   21.00  303.15   4.0e-08  615   ! AA959836 vw54h01.s1 Soares mous
gb_est27:AA955457     +   21.00  305.00   3.2e-08  472   ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est29:AI606529     -   21.00  305.15   3.1e-08  462   ! AI606529 vb27g08.y1 Soares mous
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gb_est30:AI646097     +   21.00  302.15   4.6e-08  709   ! AI646097 vw54h07.x1 Soares mous
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gb_est34:AV147820     +   11.00  157.57      5.19  256   ! AV147820 AV147820 Mus musculus
gb_est36:AI931087     +   11.00  157.28      5.39  267   ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:D15138        +   10.00  140.46     46.59  338   ! D15138 RICC0141A Rice callus Or
gb_est1:D38851        +   10.00  139.63     51.87  381   ! D38851 RICC1624A Rice callus Or
gb_est1:D38980        +   10.00  138.83     57.45  427   ! D38980 RICR0089A Rice root Oryz
gb_est1:D40024        -   10.00  140.10     48.81  356   ! D40024 RICS1743A Rice shoot Ory
gb_est2:D47372        -   10.00  140.44     46.72  339   ! D47372 RICS12716A Rice green sh
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gb_est7:W29419        -   10.00  132.38     131.36  1075   ! W29419 mb98h11.r1 Soares mo
gb_est7:W29461        -   10.00  133.03     120.91  980   ! W29461 mb99b11.r1 Soares mou
gb_est7:W29564        -   10.00  132.14     135.51  1113   ! W29564 mc03d11.r1 Soares mo
gb_est8:AA003706      +   10.00  140.30      47.58  346   ! AA003706 mg61a04.r1 Soares m
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seq_documentation_block:
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DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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ORIGIN


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 Percent Similarity: 100.000   Percent Identity: 100.000

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     375 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 392
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     392 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 408
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     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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        ||||||||||||||||||||||||||||||||||||||||||||||||||
    151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

    425 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 442
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

    442 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 458
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

    459 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 475
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

    475 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 492
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

    492 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 508
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

    509 LysProLeuLysSerThrSerLeuSer 517
        |||||||||||||||||||||||||||
    451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
           Quality:  117.00            Length:    117
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     583 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 599
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     599 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 616
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     616 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 632
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     633 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 649
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     649 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 666
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     666 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 682
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     683 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 699
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     699 g 699
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
```

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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
           Quality:  116.00            Length:    116
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     584 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     600 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 617
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     617 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 633
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     634 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 650
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     650 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 667
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     667 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 683
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     684 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 699
         |||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
           Quality:   85.00            Length:     85
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     514 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 530
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     530 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 547
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     547 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 563
         |||||||||||||||||||||||||||||||||||||||||||||||||
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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     564 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 580
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     580 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 597
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     597 yrLys 598
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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US-09-026-459A-45 x AA072780   ..

Align seg 1/1  to: AA072780  from: 1  to: 522

     663 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 679
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     679 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 696
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     696 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 712
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     713 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 729
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     729 s 729
         |
     458 A 458

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
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ORIGIN


alignment_scores:
            Quality:   60.00             Length:     60
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

      29 ProGluGluAspProGluGlnAspSerGlyProGluAspLeuProLeuVa 45
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGT 319

      45 lArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeuCysG 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     318 CAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTC 269

      62 lnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeuThrTrp 78
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     268 AGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGG 219

      79 GluLysValSerSerValAspGlyValLeu 88
         ||||||||||||||||||||||||||||||
     218 GAGAAAGTTTCATCTGTGGATGGAGTATTG 189

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


alignment_scores:
            Quality:   53.00             Length:     53
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     382 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 398
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     398 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 415
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     415 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 431
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     432 TrpLeuSer 434
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
```

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 80 c 90 g 133 t 3 others
ORIGIN

alignment_scores:
Quality: 52.00 Length: 52
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-45 x AA210875 ..

Align seg 1/1 to: AA210875 from: 1 to: 456

```
746 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 762
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

762 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 779
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

779 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 795
    ||||||||||||||||||||||||||||||||||||||||||||||||||
125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

796 GluLys 797
    ||||||
175 GAGAAA 180
```

seq_name: gb_est13:AA361277

seq_documentation_block:

LOCUS AA361277 304 bp mRNA EST 21-APR-1997
DEFINITION EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION AA361277
VERSION AA361277.1 GI:2013596
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 304)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., , Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 12140200

COMMENT On Sep 12, 1996 this sequence version replaced gi:1407493.
Other_ESTs: THC168922
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .304
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165411"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 94 a 79 c 43 g 86 t 2 others
ORIGIN

alignment_scores:
Quality: 49.00 Length: 49
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-45 x AA361277 ..

Align seg 1/1 to: AA361277 from: 1 to: 304

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450 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 466
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

466 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 483
    ||||||||||||||||||||||||||||||||||||||||||||||||||
100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

483 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 498
    ||||||||||||||||||||||||||||||||||||||||||||||||||
150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196
```

seq_name: gb_est19:AA765882

seq_documentation_block:

LOCUS AA765882 171 bp mRNA EST 08-FEB-1998
DEFINITION oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA765882
VERSION AA765882.1 GI:2817120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044576.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

```
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Insert Length: 2415    Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00            Length:     43
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     314 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 330
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     330 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 347
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTAGCAAACTTCTGA 70

     347 snAspAsnIlePheHisMetSerLeuLeu 356
         ||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS       AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION  ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AI020392
VERSION     AI020392.1  GI:3234728
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00            Length:     42
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     693 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 709
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     709 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 726
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     726 rgValLeuLysArgSerAlaGluGly 734
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00            Length:     40
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     332 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 348
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     348 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 365
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     365 laThrTyrSerArgSerThr 371
         ||||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     731 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 747
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     747 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 764
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     764 erLysPheGlnGln 768
         ||||||||||||||
```

```
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
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                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


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 Percent Similarity: 100.000   Percent Identity: 100.000

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 US-09-026-459A-45 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     410 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 426
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     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     426 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 443
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     443 ysGlnSerLysAsp 447
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     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
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                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
            Quality:   37.00            Length:     37
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alignment_block:
 US-09-026-459A-45 x N41391   ..
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    218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

    726 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 743
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

    743 ysLeuArgPhe 746
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    318 AACTACGCTTT 328
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OM of: US-09-026-459A-45 to: Issued_Patents_NA:*   out_format : pfs

Date: Feb 13, 2000  4:02 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15938/app_query.fasta.1
 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.rni
 -GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
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 -XGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
 -YGAPEXT=60.000 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=oligo -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US09026459 -NCPU=6
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Search information block:
Query: US-09-026-459A-45
Query length: 797
Database: Issued_Patents_NA:*
Database sequences: 214294
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WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


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; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-038-760-1


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161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
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244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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806 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 855

261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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856 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 905

277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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1006 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1055

327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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1056 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1105

344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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1106 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1155

361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
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1206 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1255

394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1256 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1305

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1306 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1355

427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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1406 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1455

461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 1555

494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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seq_documentation_block:
; Sequence 2, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


alignment_scores:
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              Ratio:  1.000               Gaps:      0
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; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


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   1412 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

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; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  19..2469
US-08-470-091-1

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; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
```

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;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
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seq_documentation_block:
; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2922
US-08-959-638-7


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; Sequence 4, Application US/08482627
; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
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;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  United States
;       ZIP:  92122
;     COMPUTER READABLE FORM:
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/482,627
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/951,947
;       FILING DATE:  28-SEP-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  P-UC 1707
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
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;       NAME/KEY:  CDS
;       LOCATION:  139..2924
US-08-482-627-4


alignment_scores:
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              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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seq_documentation_block:
; Sequence 1, Application PC/TUS9410357
;  GENERAL INFORMATION:
;     APPLICANT:  The Regents of the University of California
;     APPLICANT:  and Canji, Inc.
;     TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;     TITLE OF INVENTION:  Susceptibility Gene Product
;     NUMBER OF SEQUENCES:  3
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Campbell and Flores
;       STREET:  4370 La Jolla Village Drive
;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92122
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10357
;       FILING DATE:  13-SEP-1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/121,108
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Campbell, Cathryn A.
;       REGISTRATION NUMBER:  31,815
;       REFERENCE/DOCKET NUMBER:  FP-UC 1117
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2994 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
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PCT-US94-10357-1

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; Sequence 1, Application US/07915246
; Patent No. 5401836
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris L.
;    APPLICANT:  Fallis, Lynne
;    APPLICANT:  Bellmare, Guy
;    APPLICANT:  Boivin, Rodolphe
;    TITLE OF INVENTION:  A BRASSICA REGULATORY SEQUENCE FOR
;    TITLE OF INVENTION:  ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held, and Malloy
```

```
;       STREET:  500 W. Madison St. 34th Floor
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/915,246
;       FILING DATE:  19920716
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pochopien, Donald J.
;       REGISTRATION NUMBER:  32,167
;       REFERENCE/DOCKET NUMBER:  91 P 1125
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312 707-8889
;       TELEFAX:  312 707-9155
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1505 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Brassica napus
;       STRAIN:  Westar
;       DEVELOPMENTAL STAGE:  Somatic
;       TISSUE TYPE:  Root
US-07-915-246-1


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; Sequence 1, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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US-08-234-783-1


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seq_documentation_block:
; Sequence 3, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
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;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST48USA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9200
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1680 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
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; Sequence 1, Application US/08456907
; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
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US-08-456-907-1


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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
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; Sequence 5, Application US/08246982A
; Patent No. 5686288
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/246,982A
;      FILING DATE:  May 20, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Jorge, A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  0609.3880002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
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US-08-246-982A-5


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; Sequence 5, Application US/08453265
; Patent No. 5693757
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,265
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0609.3880003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10366 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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  AUTHORS   Dryja,T.P. and Friend,S.
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    724 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 773

    127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    774 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 823

    144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    824 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 873

    161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    874 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 923

    177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    924 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 973

    194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    974 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1023

    211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1024 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1073

    227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1074 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 1123

    244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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1124 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1173

 261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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1174 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1223

 277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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1224 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1273

 294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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1274 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1323

 311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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1324 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1373

 327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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1374 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1423

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 361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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 394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
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 461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1774 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1823

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1874 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1923

 511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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1924 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1973

 527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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1974 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 2023

 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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2024 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 2073

 561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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2074 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2123

 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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 594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
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2174 TAACAGCATACAAGGATGTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2223

 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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 644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
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 661 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 677
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2374 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2423

 677 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 694
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2424 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAA 2473

 694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2474 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2523

 711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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 727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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 744 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 760
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 777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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2774 AGGAAGAGAAA 2784

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seq_documentation_block:
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DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
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  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
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BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


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             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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    406 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 455

    127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    456 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 505

    144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    506 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 555

    161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    556 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 605

    177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    606 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 655

    194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    656 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 705

    211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    706 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 755

    227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    756 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 805

    244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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    806 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 855

    261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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    294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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    956 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1005

    311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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   1006 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1055

    327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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   1056 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1105

    344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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   1106 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1155

    361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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    444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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    477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1556 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1605

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    544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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    577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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    611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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   644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
     |||||||||||||||||||||||||||||||||||||||||||||||||||
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   661 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 677
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   694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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  2156 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2205

   711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


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              Ratio:  1.000                Gaps:      0
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   127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
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VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-p110.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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ORIGIN


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VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
            retinoblastoma patients using single-strand conformation
            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
            showing incomplete penetrance and mild expression of the
            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
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            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
            FAX: 416 813-4989
            E-mail: brenda@hafiz.eric.on.ca.
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            Li,F.P. and Weinberg,R.A.
  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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ACCESSION   M15400
VERSION     M15400.1  GI:190958
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mRNA.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 243 to 4740)
  AUTHORS   Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
            and sequence
  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
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REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
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  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
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ORIGIN


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             Ratio:  0.550                Gaps:      1
 Percent Similarity:  99.617   Percent Identity: 99.617

alignment_block:
 US-09-026-459A-45 x A01444   ..

 Align seg 1/1  to: A01444  from: 1  to: 4580

     208 HisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnAr 224
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1001 CATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAG 1050

     224 gThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProH 241
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1051 AACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCAC 1100

     241 isThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIle 257
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1101 ACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1150

     258 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 274
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1151 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAA 1200
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 274 nAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspI 291
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1201 CAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATA 1250

 291 leGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCys 307
     |||||||||||||||||||||||||||||||||   ||||||||||||
1251 TAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT.GGACAGGGTTGT 1299

 308 ValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrAr 324
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1300 GTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCG 1349

 324 gValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnA 341
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1350 AGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAA 1399

 341 snPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla 357
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1400 ATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1449

 358 CysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAs 374
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1450 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAA 1499

 374 nLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuA 391
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1500 TCTTGATTCAGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTA 1549

 391 snLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAla 407
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1550 ATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCA 1599

 408 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHi 424
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1600 GAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACA 1649

 424 sArgIleMetGluSerLeu.AlaTrpLeuSerAspSerProLeuPheAsp 440
     ||||||||||||||   ||| ||||||||||||||||||||||||||||||
1650 TCGAATCATGGAATC.CTTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1698

 441 LeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSe 457
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1699 CTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1748

 457 rAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspM 474
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1749 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATA 1798

 474 etTyrLeuSerProValArgSerProLysLysLysGlySerThrThrArg 490
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1799 TGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1848

 491 ValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnTh 507
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1849 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1898

 507 rGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValT 524
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1899 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGT 1948

 524 yrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 540
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1949 ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1998

 541 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 557
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1999 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 2048

 557 uGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetM 574
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 574 etCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhe 590
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2099 TGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2148

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     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2149 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2198

 607 rPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValP 624
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2199 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTGT 2248

 624 heTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyr 640
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2249 TCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 2298

 641 AlaSerThrArgProProThrLeuSerProIleProHisIleProArgSe 657
     ||||||||||||||||||||||   ||||||||||||||||||||||||||
2299 GCTTCCACCAGGCCCCCTACCTTGCA.CCAATACCTCACATTCCTCGAAG 2347

 657 rProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleT 674
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2348 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCT 2397

 674 yrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThr 690
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2398 ATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2447

 691 ProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSe 707
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2448 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2497

 707 rPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnS 724
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2498 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACA 2547

 724 erAspArgValLeu 728
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2548 GCGACCGTGTGCTC 2561
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seq_name: gb_pat:E12560

seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .4591
            FT                   /organism='Mus musculus'
            FT                   /cell_type='B-cell precursor' FT
                /cell_line='70Z-3'
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           FT   5'UTR           1. .98
           FT   CDS             99. .2864
           FT                   /product='Rb protein'
           FT   3'UTR           2865. .4591.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT     1395 a     969 c     898 g    1329 t
ORIGIN


alignment_scores:
            Quality:   72.00             Length:     72
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x E12560   ..

 Align seg 1/1  to: E12560  from: 1  to: 4591

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     679 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 696
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     696 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 712
         ||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     713 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 729
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     729 sArgSerAlaGluGly 734
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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
     CDS             99. .2864
                     /codon_start=1
                     /product="pp105 Rb protein"
                     /protein_id="AAA39964.1"
                     /db_xref="GI:200453"
                     /translation="MPPKAPRRAAAAEPPPPPPPPREDDPAQDSGPEELPLARLEFE
                     EIEEPEFIALCQKLKVPDHVRERAWLTWEKVSSVDGILEGYIQKKKELWGICIFIAAV
                     DLDEMPFTFTELQKSIETSVYKFFDLLKEIDTSTKVDNAMSRLLKKYNVLCALYSKLE
                     RTCELIYLTQPSSALSTEINSMLVLKISWITFLLAKGEVLQMEDDLVISFQLMLCVVD
                     YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
                     CNIDEVKNVYFKNFIPFINSLGIVSSNGLPEVESLSKRYEEVYLKNKDLDARLFLDHD
                     KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
                     NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
                     MESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTLQHLDSGTDLSF
                     PWILNVLNLKAFDFYKVIESFIKVEANLTREMIKHLERCEHRIMESLAWLSDSPLFDL
                     IKQSKDGEGPDNLEPACPLSLPLQGNHTAADMYLSPLRSPKKRTSTTRVNSAANTETQ
                     AASAFHTQKPLKSTSLALFYKKVYRLAYLRLNTLCARLLSDHPELEHIIWTLFQHTLQ
                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                     EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
                     ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
                     EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
                     VSNKEEK"
BASE COUNT     1395 a     969 c     898 g    1329 t
ORIGIN      Chromosome 14.


alignment_scores:
            Quality:   72.00             Length:     72
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x MUSPP105RB   ..

 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

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    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     679 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 696
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     696 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 712
         ||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     713 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 729
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     729 sArgSerAlaGluGly 734
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    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
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  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /isolate="Patient G364"
                     /db_xref="taxon:9606"
                     /cell_type="leukocyte"
                     /map="13q14.2"
     gene            1. .340
                     /gene="RB1"
     intron          <1. .64
                     /gene="RB1"
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                     /number=16
     exon            65. .260
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
     CDS             <65. .120
                     /gene="RB1"
                     /note="exon 17"
                     /codon_start=3
                     /db_xref="GDB:G00-118-734"
                     /product="retinoblastoma suspectibility protein"
                     /protein_id="AAA82549.1"
                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
                     /gene="RB1"
                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
     intron          261. .>340
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                     /note="G00-118-734"
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BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN


alignment_scores:
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x HUMRB1501V   ..

 Align seg 1/1  to: HUMRB1501V  from: 1  to: 340

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      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     385 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 402
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     402 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 418
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     419 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 434
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     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260

seq_name: gb_pat:I09384

seq_documentation_block:
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


alignment_scores:
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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x I09384   ..

 Align seg 1/1  to: I09384  from: 1  to: 693

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     252 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 301

     386 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 403
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     302 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 351

     403 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 419
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     352 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 401

     420 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 434
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     402 GAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 446

seq_name: gb_pr1:HUMRBS15

seq_documentation_block:
LOCUS       HUMRBS15      693 bp    DNA             PRI       23-NOV-1994
DEFINITION  Human retinoblastoma susceptibility protein gene, exon 17.
ACCESSION   M27858
VERSION     M27858.1  GI:341775
KEYWORDS    nuclear protein; recessive oncogene; retinoblastoma protein;
            retinoblastoma susceptibility protein; tumor suppressor gene.
SEGMENT     15 of 23
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
FEATURES             Location/Qualifiers
     source          1. .693
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                     /map="13q14"
     intron          order(M27857.1:980. .>1280,<1. .241)
                     /note="1.0 kb gap; retinoblastoma susceptibility gene"
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     exon            250. .446
                     /note="retinoblastoma susceptibility gene"
                     /number=17
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BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN

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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x HUMRBS15   ..

 Align seg 1/1  to: HUMRBS15  from: 1  to: 693

     370 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 386
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     252 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 301

     386 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 403
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     302 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 351

     403 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 419
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     352 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 401

     420 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 434
         ||||||||||||||||||||||||||||||||||||||||||
     402 GAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 446
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OM of: US-09-026-459A-43 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15917/app_query.fasta.1
 -DB=EST -QFMT=fastap -SUFFIX=oligo.rst -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-43
Query length: 859
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence           Strd Orig    ZScore    EScore Len   ! Documentation ..
gb_est38:AL120941    +  159.00 2425.38  2.5e-126  572   ! AL120941 DKFZp762D143_r1 762 (s
gb_est32:AI745644    -  117.00 1782.71  1.6e-90   415   ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643    -  116.00 1767.42  1.1e-89   411   ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103    +   85.00 1293.97  2.6e-63   285   ! AA382103 EST95270 Activated T-c
gb_est9:AA072780     +   67.00 1013.34  1.1e-47   522   ! AA072780 mm76a05.r1 Stratagene
gb_est22:AI074792    -   60.00  905.22  1.2e-41   571   ! AI074792 oy03a06.s1 Soares_sene
gb_est17:AA664676    -   53.00  801.59  7.0e-36   329   ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875    +   52.00  783.95  6.7e-35   456   ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277    +   49.00  740.73  1.7e-32   304   ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882    -   43.00  652.62  1.4e-27   171   ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392    +   42.00  632.13  1.9e-26   356   ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411    -   40.00  594.83  2.3e-24   914   ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402       +   38.00  570.15  5.4e-23   386   ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485    -   38.00  564.45  1.1e-22   871   ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391       +   37.00  553.61  4.5e-22   457   ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845       +   29.00  438.47  1.2e-15   152   ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529    -   29.00  430.69  3.2e-15   462   ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097    +   29.00  427.69  4.7e-15   709   ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255    +   27.00  399.09  1.8e-13   525   ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628    +   25.00  369.82  7.8e-12   427   ! AA709628 vv41c11.r1 Soares 2NbM
gb_est42:AV302462    +   23.00  345.39  1.8e-10   174   ! AV302462 AV302462 RIKEN full-le
gb_est21:AA959836    +   21.00  305.85  2.9e-08   615   ! AA959836 vw54h01.s1 Soares mous
gb_est27:AA955457    +   21.00  307.70  2.3e-08   472   ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est30:AI646038    +   21.00  303.73  3.8e-08   832   ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832    +   21.00  306.32  2.7e-08   575   ! AI662832 vb27g08.x1 Soares mous
gb_est21:AA959709    +   20.00  291.55  1.8e-07   529   ! AA959709 vw54a04.s1 Soares mous
gb_est1:T24020       -   17.00  248.39  4.5e-05   349   ! T24020 seq2177 3HFLSK20 Homo sa
gb_est14:AA396353    -   17.00  245.99  6.2e-05   492   ! AA396353 vb27g08.r1 Soares mous
gb_est3:R70325       +   16.00  232.13  0.0004    397   ! R70325 yj81b10.r1 Soares breast
gb_est33:AV111279    +   16.00  234.48  0.0003    284   ! AV111279 AV111279 Mus musculus
gb_est32:C82304      +   14.00  196.53  0.0351    799   ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300     +   14.00  195.06  0.0424    986   ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est34:AV147820    +   11.00  158.43  4.65      256   ! AV147820 AV147820 Mus musculus
gb_est36:AI931087    +   11.00  158.13  4.83      267   ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:D15138       +   10.00  141.13  42.78     338   ! D15138 RICC0141A Rice callus Or
gb_est1:D38851       +   10.00  140.29  47.63     381   ! D38851 RICC1624A Rice callus Or
gb_est1:D38980       +   10.00  139.49  52.77     427   ! D38980 RICR0089A Rice root Oryz
gb_est1:D40024       -   10.00  140.77  44.82     356   ! D40024 RICS1743A Rice shoot Ory
gb_est2:D47372       -   10.00  141.11  42.89     339   ! D47372 RICS12716A Rice green sh
gb_est2:D48004       -   10.00  140.61  45.72     364   ! D48004 RICS13911A Rice green
gb_est7:W29241       -   10.00  133.91  107.95    948   ! W29241 mb96e12.r1 Soares mou
gb_est7:W29419       -   10.00  133.03  120.85   1075   ! W29419 mb98h11.r1 Soares mo
gb_est7:W29461       -   10.00  133.68  111.22    980   ! W29461 mb99b11.r1 Soares mou
gb_est7:W29564       -   10.00  132.79  124.68   1113   ! W29564 mc03d11.r1 Soares mo
gb_gss15:AQ650463    -   10.00  140.73  45.05     358   ! AQ650463 Sheared DNA-18F2.TF

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seq_documentation_block:
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DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .572
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AL120941 ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     421 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 437
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     437 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 454
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     454 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 470
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     471 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 487
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     487 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 504
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     504 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 520
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     521 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 537
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     537 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 554
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     554 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 570
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     571 LysProLeuLysSerThrSerLeuSer 579
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     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
            Quality:  117.00              Length:    117
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

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     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     661 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 678
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     678 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 694
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     695 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 711
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     711 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 728
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     728 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 744
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     745 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 761
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     761 g 761
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
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DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
            Quality:  116.00            Length:    116
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     662 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 679
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     679 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 695
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     696 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 712
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     712 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 729
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     729 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 745
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     746 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 761
         |||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
            Quality:   85.00            Length:     85
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     576 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 592
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     592 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 609
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     609 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 625
         |||||||||||||||||||||||||||||||||||||||||||||||||
```

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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     626 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 642
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     642 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 659
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     659 yrLys 660
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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US-09-026-459A-43 x AA072780   ..

Align seg 1/1  to: AA072780  from: 1  to: 522

     725 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 741
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     741 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 758
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     758 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 774
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     775 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 791
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAAGCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     791 s 791
         |
     458 A 458

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS       AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION  oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
            clone IMAGE:1664722 3' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
            repetitive element ;, mRNA sequence.
ACCESSION   AI074792
VERSION     AI074792.1  GI:3401436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2043761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 644   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
```

```
ORIGIN


alignment_scores:
            Quality:   60.00              Length:     60
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

      29 ProGluGluAspProGluGlnAspSerGlyProGluAspLeuProLeuVa 45
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGT 319

      45 lArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeuCysG 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     318 CAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTC 269

      62 lnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeuThrTrp 78
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 AGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGG 219

      79 GluLysValSerSerValAspGlyValLeu 88
         |||||||||||||||||||||||||||||||
     218 GAGAAAGTTTCATCTGTGGATGGAGTATTG 189

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN


alignment_scores:
            Quality:   53.00              Length:     53
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     444 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     460 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 477
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     477 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 493
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     494 TrpLeuSer 496
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
```

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

```
BASE COUNT      150 a      80 c      90 g     133 t       3 others
ORIGIN


alignment_scores:
            Quality:   52.00             Length:     52
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AA210875   ..

 Align seg 1/1  to: AA210875  from: 1  to: 456

     808 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 824
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     824 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 841
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     841 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 857
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     858 GluLys 859
         ||||||
     175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a      79 c      43 g      86 t       2 others
ORIGIN


alignment_scores:
            Quality:   49.00             Length:     49
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     512 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 528
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     528 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 545
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     545 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 560
         ||||||||||||||||||||||||||||||||||||||||||||||||
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS       AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION  oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA765882
VERSION     AA765882.1  GI:2817120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044576.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
```

```
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
           Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Insert Length: 2415    Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00            Length:     43
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     376 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 392
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     392 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 409
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     409 snAspAsnIlePheHisMetSerLeuLeu 418
         |||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS       AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION  ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AI020392
VERSION     AI020392.1  GI:3234728
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00            Length:     42
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     755 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 771
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     771 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 788
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     788 rgValLeuLysArgSerAlaGluGly 796
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00            Length:     40
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     394 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 410
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     410 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 427
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     427 laThrTyrSerArgSerThr 433
         ||||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402          386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00            Length:     38
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     793 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 809
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     809 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 826
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     826 erLysPheGlnGln 830
         ||||||||||||||
```

```
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
           Quality:   38.00            Length:     38
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     472 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 488
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258
```

```
     488 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 505
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     505 ysGlnSerLysAsp 509
         ||||||||||||||
     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391       457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .457
                     /organism="Homo sapiens"
                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
           Quality:   37.00            Length:     37
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x N41391   ..
```

Align seg 1/1 to: N41391 from: 1 to: 457

```
    772 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspAr 788
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

    788 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 805
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

    805 ysLeuArgPhe 808
        ||||||||||
    318 AACTACGCTTT 328
```

```
OM of: US-09-026-459A-43 to: GenEmbl:*   out_format : pfs

Date: Feb 13, 2000  8:16 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15926/app_query.fasta.1
 -DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.rge -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-43
Query length: 859
Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 10867.920000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:
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Sequence	Strd	Orig	ZScore	EScore	Len	! Documentation ..
gb_pat:I05311	+	747.00	13460.72	0.0	4597	! I05311 Sequence 1 from Patent
gb_pat:I18496	+	747.00	13463.20	0.0	3232	! I18496 Sequence 1 from patent
gb_pat:I18497	-	747.00	13463.20	0.0	3232	! I18497 Sequence 2 from patent
gb_pat:I81465	+	747.00	13463.74	0.0	2994	! I81465 Sequence 2 from patent
gb_pr2:HUMRB1MRNA	+	747.00	13460.36	0.0	4839	! L41870 Homo sapiens retinobla
gb_pr2:HUMRBA1RA	+	747.00	13460.72	0.0	4600	! M33647 Human retinoblastoma a
gb_pr2:HUMRBSA	+	747.00	13463.74	0.0	2994	! M28419 Human retinoblastoma s
gb_pat:I09369	+	696.00	12538.94	0.0	4597	! I09369 Sequence 1 from Patent
gb_pr2:HUMRBS	+	560.00	10080.66	0.0	4740	! M15400 Human retinoblastoma s
gb_pat:A01444	+	286.00	5128.60	1.2e-277	4580	! A01444 H.sapiens DNA for 4.6 k
gb_pat:E12560	+	72.00	1260.74	3.4e-62	4591	! E12560 cDNA encoding Rb (retin
gb_ro:MUSPP105RB	+	72.00	1260.74	3.4e-62	4591	! M26391 Mouse retinoblastoma su
gb_pr1:HUMRBSY79	+	68.00	1204.33	4.6e-59	480	! M19701 Human mutated retinoblas
gb_pr2:HUMRB1501V	+	66.00	1170.61	3.5e-57	340	! L49220 Homo sapiens retinoblast
gb_pat:I09384	+	65.00	1147.53	6.8e-56	693	! I09384 Sequence 17 from Patent
gb_pr1:HUMRBS15	+	65.00	1147.53	6.8e-56	693	! M27858 Human retinoblastoma sus
gb_pr1:HUMRETBLAS	+	65.00	1108.39	1.0e-53	180388	! L11910 Human retinoblastoma
gb_ro:RATRP	+	59.00	1026.02	4.0e-49	4432	! D25233 Rat mRNA for retinoblas
gb_pat:I09389	+	55.00	964.68	1.0e-45	935	! I09389 Sequence 22 from Patent
gb_pr1:HUMRBS20	+	55.00	964.68	1.0e-45	935	! M27863 Human retinoblastoma sus
gb_pr2:HUMRB23EX	+	55.00	970.31	5.0e-46	420	! L41910 Homo sapiens retinoblast
gb_pr2:HUMRB4MU2	+	55.00	968.35	6.5e-46	555	! L41904 Homo sapiens retinoblast
gb_pr2:HUMRB1777L	+	54.00	955.83	3.2e-45	252	! L49230 Homo sapiens retinoblast
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gb_pr2:HUMRB17MU2	+	51.00	896.05	6.9e-42	555	! L41924 Homo sapiens retinoblast
gb_pat:I09387	+	49.00	858.10	9.0e-40	717	! I09387 Sequence 20 from Patent
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DEFINITION  Sequence 1 from Patent EP 0259031.
ACCESSION   I05311
VERSION     I05311.1  GI:591083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4597)
  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
FEATURES             Location/Qualifiers
     source          1. .4597
                     /organism="unknown"
BASE COUNT     1489 a    842 c    812 g   1454 t
ORIGIN


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     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
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   613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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   629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
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  1976 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2025

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   746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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   829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
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seq_documentation_block:
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DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN

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    129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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    146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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    163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   2861 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 2812

    179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   2811 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 2762

    196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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    213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
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    229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
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    263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
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2461 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 2412

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2411 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 2362

 329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
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2361 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 2312

 346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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2311 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 2262

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2211 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 2162

 396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
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2011 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1962

 463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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 479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
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 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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 729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1161 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 1112

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     ||||||||||||||||||||||||||||||||||||||||||||||||||
1111 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 1062

 763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
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     ||||||||||||||||||||||||||||||||||||||||||||||||||
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DEFINITION  Sequence 2 from patent US 5710255.
ACCESSION   I81465
VERSION     I81465.1  GI:3209762
KEYWORDS    .
SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 2994)
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  AUTHORS   Shepard,H.Michael and Wen,S.Fen.
  TITLE     Characterization of a novel anti-pl10.sup.RB monoclonal antibody
  JOURNAL   Patent: US 5710255-A 2 20-JAN-1998;
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     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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     463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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VERSION     L41870.1  GI:793994
KEYWORDS    retinoblastoma protein; retinoblastoma susceptibility.
SOURCE      Homo sapiens cDNA to mRNA.
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
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  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
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  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
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            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
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  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
            Cowell,J.K. and Kaye,F.J.
  TITLE     Partial inactivation of the RB product in a family with incomplete
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  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
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COMMENT     Mutation data provided by Dr. B.L.Gallie,
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            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
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  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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  JOURNAL   Patent: WO 8906703-A 1 27-JUL-1989;
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
  MEDLINE   87149066
REFERENCE   2  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
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  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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ORIGIN      1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.


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    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATT 1292

     316 uMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleS 333
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    1293 AATGATGATTTTAAATTCTGCAAGTGATCAACCTTCAGAAAATCTGATTT 1342

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     683 leIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIle 699
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     716 eProArgSerProTyrLysPheProSerSerProLeuArgIleProGlyG 733
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
            retinoblastoma gene probe
  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
            RESEARCH DEVELOPMENT FOUNDATION
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BASE COUNT     1477 a    840 c    811 g   1451 t      1 others
ORIGIN


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    1001 CATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAG 1050

     286 gThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProH 303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1051 AACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCAC 1100

     303 isThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIle 319
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1101 ACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1150

     320 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAs 336
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     403 snPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla 419
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   603 GluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLe 619
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DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
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            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
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            CC   hypothetical: No;
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seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
```

```
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
     CDS             99. .2864
                     /codon_start=1
                     /product="pp105 Rb protein"
                     /protein_id="AAA39964.1"
                     /db_xref="GI:200453"
                     /translation="MPPKAPRRAAAAEPPPPPPPPREDDPAQDSGPEELPLARLEFE
                     EIEEPEFIALCQKLKVPDHVRERAWLTWEKVSSVDGILEGYIQKKKELWGICIFIAAV
                     DLDEMPFTFTELQKSIETSVYKFFDLLKEIDTSTKVDNAMSRLLKKYNVLCALYSKLE
                     RTCELIYLTQPSSALSTEINSMLVLKISWITFLLAKGEVLQMEDDLVISFQLMLCVVD
                     YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
                     CNIDEVKNVYFKNFIPFINSLGIVSSNGLPEVESLSKRYEEVYLKNKDLDARLFLDHD
                     KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
                     NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
                     MESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTLQHLDSGTDLSF
                     PWILNVLNLKAFDFYKVIESFIKVEANLTREMIKHLERCEHRIMESLAWLSDSPLFDL
                     IKQSKDGEGPDNLEPACPLSLPLQGNHTAADMYLSPLRSPKKRTSTTRVNSAANTETQ
                     AASAFHTQKPLKSTSLALFYKKVYRLAYLRLNTLCARLLSDHPELEHIIWTLFQHTLQ
                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                     EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
                     ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
                     EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
                     VSNKEEK"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN      Chromosome 14.


alignment_scores:
            Quality:   72.00            Length:     72
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x MUSPP105RB   ..

 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

     725 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 741
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     741 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 758
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     758 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 774
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     775 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 791
         ||||||||||||||||||||||||||||||||||||||||||||||||||||

     2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

      791 sArgSerAlaGluGly 796
          |||||||||||||||||
     2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_prl:HUMRBSY79

seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y{382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
                     /note="mutated retinoblastoma protein"
                     /codon_start=1
                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


alignment_scores:
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x HUMRBSY79   ..

 Align seg 1/1  to: HUMRBSY79  from: 1  to: 480

     134 GlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMe 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     150 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     167 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     184 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     200 nAsp 201
         ||||
     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /isolate="Patient G364"
                     /db_xref="taxon:9606"
                     /cell_type="leukocyte"
                     /map="13q14.2"
     gene            1. .340
                     /gene="RB1"
     intron          <1. .64
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=16
     exon            65. .260
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
     CDS             <65. .120
                     /gene="RB1"
                     /note="exon 17"
                     /codon_start=3
                     /db_xref="GDB:G00-118-734"
                     /product="retinoblastoma suspectibility protein"
                     /protein_id="AAA82549.1"
                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
                     /gene="RB1"
                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
     intron          261. .>340
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN


alignment_scores:
            Quality:   66.00            Length:     66
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x HUMRB1501V   ..

 Align seg 1/1  to: HUMRB1501V  from: 1  to: 340

     431 ArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTr 447
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      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     447 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 464
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     464 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     481 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 496
         ||||||||||||||||||||||||||||||||||||||||||||||||
     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260

seq_name: gb_pat:I09384

seq_documentation_block:
LOCUS       I09384        693 bp                    PAT       02-DEC-1994
DEFINITION  Sequence 17 from Patent WO 8906703.
ACCESSION   I09384
VERSION     I09384.1  GI:587914
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
  TITLE     DIAGNOSIS OF RETINOBLASTOMA
  JOURNAL   Patent: WO 8906703-A 17 27-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="unknown"
BASE COUNT      242 a    110 c    109 g    231 t      1 others
ORIGIN


alignment_scores:
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              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x I09384   ..

 Align seg 1/1  to: I09384  from: 1  to: 693

     432 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 448
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     252 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 301

     448 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 465
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     302 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 351

     465 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 481
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     352 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 401

     482 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 496
         ||||||||||||||||||||||||||||||||||||||||||||||||
     402 GAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 446
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OM of: US-09-026-459A-41 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15917/app_query.fasta.1
 -DB=EST -QFMT=fastap -SUFFIX=oligo.rst -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
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Query length: 897
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence              Strd Orig    ZScore    EScore Len   ! Documentation  ..
gb_est38:AL120941      +  159.00 2444.14  2.3e-127  572   ! AL120941 DKFZp762D143_r1 762 (s
gb_est32:AI745644      -  117.00 1796.30  2.7e-91   415   ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643      -  116.00 1780.89  2.0e-90   411   ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103      +   85.00 1303.64  7.6e-64   285   ! AA382103 EST95270 Activated T-c
gb_est9:AA072780       +   67.00 1020.73  4.3e-48   522   ! AA072780 mm76a05.r1 Stratagene
gb_est17:AA664676      -   53.00  807.30  3.4e-36   329   ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875      +   52.00  789.51  3.3e-35   456   ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277      +   49.00  745.94  8.8e-33   304   ! AA361277 EST70529 T-cell lymphc
gb_est22:AI074792      -   48.00  726.00  1.1e-31   571   ! AI074792 oy03a06.s1 Soares_sene
gb_est19:AA765882      -   43.00  657.14  7.7e-28   171   ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392      +   42.00  636.47  1.1e-26   356   ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411      -   40.00  598.84  1.4e-24   914   ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402         +   38.00  573.98  3.3e-23   386   ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485      -   38.00  568.22  7.0e-23   871   ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391         +   37.00  557.31  2.8e-22   457   ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845         +   29.00  441.28  8.2e-16   152   ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529      -   29.00  433.40  2.2e-15   462   ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097      +   29.00  430.37  3.3e-15   709   ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255      +   27.00  401.54  1.3e-13   525   ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628      +   25.00  372.04  5.9e-12   427   ! AA709628 vv41c11.r1 Soares 2NbM
gb_est42:AV302462      +   23.00  347.44  1.4e-10   174   ! AV302462 RIKEN full-le
gb_est21:AA959709      +   22.00  324.09  2.8e-09   529   ! AA959709 vw54a04.s1 Soares mous
gb_est21:AA959836      +   22.00  323.02  3.2e-09   615   ! AA959836 vw54h01.s1 Soares mous
gb_est30:AI646038      +   22.00  320.88  4.2e-09   832   ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832      +   22.00  323.50  3.0e-09   575   ! AI662832 vb27g08.x1 Soares mous
gb_est14:AA396353      -   17.00  247.21  5.3e-05   492   ! AA396353 vb27g08.r1 Soares mous
gb_est3:R70325         +   16.00  233.25  0.0003    397   ! R70325 yj81b10.r1 Soares breast
gb_est33:AV111279      +   16.00  235.62  0.0002    284   ! AV111279 AV111279 Mus musculus
gb_est27:AA955457      +   14.00  201.07  0.0196    472   ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est32:C82304        +   14.00  197.34  0.0316    799   ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300       +   14.00  195.85  0.0383    986   ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est34:AV147820      +   11.00  158.96  4.34      256   ! AV147820 AV147820 Mus musculus
gb_est36:AI931087      +   11.00  158.67  4.51      267   ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:D15138         +   10.00  141.52  40.71     338   ! D15138 RICC0141A Rice callus Or
gb_est1:D38851         +   10.00  140.67  45.38     381   ! D38851 RICC1624A Rice callus Or
gb_est1:D38980         +   10.00  139.86  50.34     427   ! D38980 RICR0089A Rice root Oryz
gb_est1:D40024         -   10.00  141.15  42.67     356   ! D40024 RICS1743A Rice shoot Ory
gb_est2:D47372         -   10.00  141.50  40.82     339   ! D47372 RICS12716A Rice green sh
gb_est2:D48004         -   10.00  140.99  43.54     364   ! D48004 RICS13911A Rice green sh
gb_est7:W29241         -   10.00  134.21  103.88    948   ! W29241 mb96e12.r1 Soares mou
gb_est7:W29419         -   10.00  133.32  116.45   1075   ! W29419 mb98h11.r1 Soares mo
gb_est7:W29461         -   10.00  133.98  107.06    980   ! W29461 mb99b11.r1 Soares mou
gb_est7:W29564         -   10.00  133.08  120.19   1113   ! W29564 mc03d11.r1 Soares mo
gb_est8:AA003706       +   10.00  141.35  41.58     346   ! AA003706 mg61a04.r1 Soares m
gb_gss15:AQ650463      -   10.00  141.11  42.89     358   ! AQ650463 Sheared DNA-18F2.TF

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="DKFZp762D143"
                     /clone_lib="762 (synonym: hmel2)"
                     /tissue_type="melanoma (MeWo cell line)"
                     /dev_stage="adult"
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BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


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             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

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       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     475 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 492
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     492 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 508
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     509 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 525
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     525 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 542
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     542 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 558
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     559 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 575
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     575 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 592
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     592 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 608
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     609 LysProLeuLysSerThrSerLeuSer 617
         |||||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
            Quality:  117.00             Length:    117
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     683 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 699
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     699 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 716
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     716 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 732
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     733 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 749
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     749 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 766
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     766 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 782
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     783 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 799
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     799 g 799
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
            Quality:  116.00             Length:    116
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     684 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 700
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     700 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 717
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     717 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 733
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     734 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     750 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     767 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     784 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 799
         |||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.;
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
            Quality:   85.00             Length:     85
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     630 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 647
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     647 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 663
         |||||||||||||||||||||||||||||||||||||||||||||||||
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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     664 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 680
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     680 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 697
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     697 yrLys 698
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
           Quality:   67.00            Length:     67
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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US-09-026-459A-41 x AA072780   ..

Align seg 1/1  to: AA072780  from: 1  to: 522

     763 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 779
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     779 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 796
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     796 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 812
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     813 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 829
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     829 s 829
         |
     458 A 458

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
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                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN
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alignment_scores:
            Quality:   53.00              Length:     53
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     482 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 498
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     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     498 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 515
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     515 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 531
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     532 TrpLeuSer 534
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     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


alignment_scores:
            Quality:   52.00              Length:     52
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AA210875   ..

 Align seg 1/1  to: AA210875  from: 1  to: 456

     846 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 862
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     862 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 879
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     879 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 895
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     896 GluLys 897
         ||||||
     175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
```

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           9712 Medical Center Drive, Rockville, MD 20850 USA
           Tel: 3018699056
           Fax: 3018699423
           Email: arkerlav@tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please check the TIGR Human Gene
           Index (http://www.tigr.org/tdb/hgi/hgi.html)
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):165411"
                     /db_xref="taxon:9606"
                     /clone_lib="T-cell lymphoma"
                     /cell_type="T-lymphocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


alignment_scores:
           Quality:   49.00            Length:     49
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     550 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 566
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     566 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 583
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     583 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 598
         ||||||||||||||||||||||||||||||||||||||||||||||
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est22:AI074792

seq_documentation_block:
LOCUS        AI074792      571 bp    mRNA            EST       24-SEP-1998
DEFINITION   oy03a06.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
             clone IMAGE:1664722 3' similar to gb:M15400
             RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);contains MER32.b3 MER32
             repetitive element ;, mRNA sequence.
ACCESSION    AI074792
VERSION      AI074792.1  GI:3401436
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 571)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2043761.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             Insert Length: 644    Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 359.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1664722"
                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      126 a    147 c    143 g    153 t      2 others
ORIGIN


alignment_scores:
           Quality:   48.00            Length:     48
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AI074792/rev   ..

 Align seg 1/1  to reverse of: AI074792  from: 1  to: 571

      29 ProGluGluAspProGluGlnAspSerGlyProGluAspLeuProLeuVa 45
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     368 CCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGT 319

      45 lArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeuCysG 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     318 CAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTATGTC 269

      62 lnLysLeuLysIleProAspHisValArgGluArgAlaTrpLeu 76
         |||||||||||||||||||||||||||||||||||||||||||
     268 AGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTA 225

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS        AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION   oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
             similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
             mRNA sequence.
ACCESSION    AA765882
VERSION      AA765882.1  GI:2817120
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 171)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044576.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
```

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           Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Insert Length: 2415   Std Error: 0.00
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .171
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1304914"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00            Length:     43
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     414 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 430
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     430 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 447
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     447 snAspAsnIlePheHisMetSerLeuLeu 456
         ||||||||||||||||||||||||||||
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS        AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION   ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
             clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
             susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION    AI020392
VERSION      AI020392.1  GI:3234728
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 356)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
             Waterston,R.
  TITLE      The WashU-HHMI Mouse EST Project
  JOURNAL    Unpublished (1996)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044708.
             Contact: Marra M/Mouse EST Project
             WashU-HHMI Mouse EST Project
             Washington University School of MedicineP
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:900436
             Seq primer: -28m13 rev1 ET from Amersham
             High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00            Length:     42
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     793 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 809
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     809 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 826
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     826 rgValLeuLysArgSerAlaGluGly 834
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS        AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION   vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
             IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
             PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
             protein (MOUSE);, mRNA sequence.
ACCESSION    AA763411
VERSION      AA763411.1  GI:2813158
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 914)
```

```
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
           Quality:   40.00            Length:     40
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x AA763411/rev   ..

 Align seq 1/1  to reverse of: AA763411  from: 1  to: 914

     432 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 448
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     448 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 465
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     465 laThrTyrSerArgSerThr 471
         ||||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTAGCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
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             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     847 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 864
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     864 erLysPheGlnGln 868
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     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485
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seq_documentation_block:
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DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
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                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


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           Quality:   38.00            Length:     38
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alignment_block:
 US-09-026-459A-41 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     510 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 526
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     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     526 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 543
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     543 ysGlnSerLysAsp 547
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     207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
LOCUS       N41391        457 bp    mRNA            EST       24-JAN-1996
DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
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FEATURES             Location/Qualifiers
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                     /db_xref="GDB:3887236"
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                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
           Quality:   37.00            Length:     37
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x N41391   ..

 Align seg 1/1  to: N41391  from: 1  to: 457

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218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

826 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 843
    ||||||||||||||||||||||||||||||||||||||||||||||||||
268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

843 ysLeuArgPhe 846
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318 AACTACGCTTT 328
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Date: Feb 13, 2000  3:59 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15938/app_query.fasta.1
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 -GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
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 -YGAPEXT=60.000 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=oligo -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US09026459 -NCPU=6
 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:
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Query length: 897
Database: Issued_Patents_NA:*
Database sequences: 214294
Database length: 59861208
Search time (sec): 316.800000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence            Strd Orig    ZScore    EScore Len  ! Documentation  ..
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; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


alignment_scores:
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 Percent Similarity: 100.000   Percent Identity: 100.000

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143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 709

160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
710 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 809

193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
810 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 859

210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
860 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

243 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 260
960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 1009

260 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 276
1010 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

277 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 293
1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 1109

293 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 310
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1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1409

393 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 410
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410 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 426

1460 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1509

427 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 443
1510 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

443 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 460
1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1609

460 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 476
1610 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1709

493 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 510
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; Sequence 7, Application US/08959638
; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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US-08-959-638-7


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; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES: 13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
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;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:  19930325
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
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US-08-038-760-1


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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


alignment_scores:
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seq_documentation_block:
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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US-08-470-091-1


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; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
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;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


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;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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; Sequence 1, Application US/07915246
; Patent No. 5401836
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris L.
;    APPLICANT:  Fallis, Lynne
;    APPLICANT:  Bellmare, Guy
;    APPLICANT:  Boivin, Rodolphe
;    TITLE OF INVENTION:  A BRASSICA REGULATORY SEQUENCE FOR
;    TITLE OF INVENTION:  ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held, and Malloy
;      STREET:  500 W. Madison St. 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/915,246
;      FILING DATE:  19920716
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien, Donald J.
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  91 P 1125
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312 707-8889
;      TELEFAX:  312 707-9155
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1505 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Brassica napus
;      STRAIN:  Westar
;      DEVELOPMENTAL STAGE:  Somatic
;      TISSUE TYPE:  Root
US-07-915-246-1
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seq_documentation_block:
; Sequence 1, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..630
US-08-234-783-1


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seq_documentation_block:
; Sequence 3, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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US-08-234-783-3


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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
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;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
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US-08-456-907-3


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; Patent No. 5686288
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
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;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/246,982A
;       FILING DATE:  May 20, 1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Goldstein, Jorge, A.
;       REGISTRATION NUMBER:  29,021
;       REFERENCE/DOCKET NUMBER:  0609.3880002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
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; Patent No. 5693757
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,265
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0609.3880003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10366 base pairs
;       TYPE:  nucleic acid
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       Copyright (c) 1993-1998 Compugen Ltd.

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            Unclassified.
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  AUTHORS   Dryja,T.P. and Friend,S.
  TITLE     Human DNA in the diagnosis of retinoblastoma
  JOURNAL   Patent: EP 0259031-A2 1 09-MAR-1988;
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REFERENCE   1  (sites)
  AUTHORS   McGee,T.L., Yandell,D.W. and Dryja,T.P.
  TITLE     Structure and partial genomic sequence of the human retinoblastoma
            susceptibility gene
  JOURNAL   Gene 80 (1), 119-128 (1989)
  MEDLINE   90006771
REFERENCE   2  (sites)
  AUTHORS   Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
  TITLE     Detection of heterozygous mutations in the RB1 gene in
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            polymorphism analysis and polymerase chain reaction sequencing
  JOURNAL   Oncogene 7 (7), 1445-1451 (1992)
  MEDLINE   92319557
REFERENCE   3  (sites)
  AUTHORS   Onadim,Z., Hogg,A., Baird,P.N. and Cowell,J.K.
  TITLE     Oncogenic point mutations in exon 20 of the RB1 gene in families
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            retinoblastoma phenotype
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
  MEDLINE   92335261
REFERENCE   4  (sites)
  AUTHORS   Onadim,Z., Hogg,A. and Cowell,J.K.
  TITLE     Mechanisms of oncogenesis in patients with familial retinoblastoma
  JOURNAL   Br. J. Cancer 68 (5), 958-964 (1993)
  MEDLINE   94031584
REFERENCE   5  (sites)
  AUTHORS   Hogg,A., Bia,B., Onadim,Z. and Cowell,J.K.
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  TITLE     Molecular mechanisms of oncogenic mutations in tumors from patients
            with bilateral and unilateral retinoblastoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
  MEDLINE   93348271
REFERENCE   6  (sites)
  AUTHORS   Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J.,
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  TITLE     Partial inactivation of the RB product in a family with incomplete
            penetrance of familial retinoblastoma and benign retinal tumors
  JOURNAL   Oncogene 9 (5), 1321-1326 (1994)
  MEDLINE   94203660
COMMENT     Mutation data provided by Dr. B.L.Gallie,
            Hospital for Sick Children
            555 Univ. Ave.
            Toronto ONT W5G 1X8
            Canada
            Ph:  416 813-5868
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VERSION     M33647.1  GI:190945
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REFERENCE   1  (bases 1 to 4600)
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  TITLE     Deletions of a DNA sequence in retinoblastomas and mesenchymal
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  AUTHORS   Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Donoso,L.A., Young,L.J.,
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  TITLE     The retinoblastoma susceptibility gene encodes a nuclear
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  2810 TCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

   877 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 893
     |||||||||||||||||||||||||||||||||||||||||||||||||||
  2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2909

   893 nLysGluGluLys 897
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seq_name: gb_pat:I18496

seq_documentation_block:
LOCUS       I18496       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 1 from patent US 5496731.
ACCESSION   I18496
VERSION     I18496.1  GI:1598851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 1 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
                     /organism="unknown"
BASE COUNT     1086 a    597 c    566 g    983 t
ORIGIN


alignment_scores:
            Quality:  820.00             Length:    820
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x I18496   ..

 Align seg 1/1  to: I18496  from: 1  to: 3232

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      7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGA 56

     94 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 111
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

    111 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 127
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

    128 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 144
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

    144 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 161
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

    161 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 177
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    178 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 194
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 356

    194 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 211
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    357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

    211 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 227
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    294 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 311
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    657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

    311 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 327
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    328 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVa 344
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    757 AAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGT 806

    344 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 361
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    807 TAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAG 856

    361 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 377
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    857 CAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

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1007 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 1056

 428 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 444
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 461 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 477
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 594 rAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProL 611
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1907 TTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCG 1956

 728 ValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrAr 744
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1957 GTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAG 2006

 744 gProProThrLeuSerProIleProHisIleProArgSerProTyrLysP 761
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2007 GCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGT 2056

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 811 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 827
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 844 uArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuP 861
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seq_name: gb_pat:I18497

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LOCUS       I18497       3232 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 2 from patent US 5496731.
ACCESSION   I18497
VERSION     I18497.1  GI:1598852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Xu,H., Hu,S. and Benedict,W.F.
  TITLE     Broad-spectrum tumor suppressor genes, gene products and methods
            for tumor suppressor gene therapy
  JOURNAL   Patent: US 5496731-A 2 05-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .3232
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BASE COUNT      983 a    566 c    597 g   1086 t
ORIGIN


alignment_scores:
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alignment_block:
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    3180 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 3131

     111 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 127
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    3130 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 3081

     128 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 144
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    3080 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 3031

     144 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 161
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    3030 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 2981

     161 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2980 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 2931

     178 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 194
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     194 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 211
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    2580 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 2531

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     344 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 361
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     361 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 377
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     378 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 394
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     394 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 411
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     411 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 427
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    1980 CTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACT 1931

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  AUTHORS   Dryja,T.P., Friend,S. and Yandell,D.W.
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  TITLE     Human retinoblastoma susceptibility gene: cloning, identification,
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  JOURNAL   Science 235 (4794), 1394-1399 (1987)
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  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
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     260 lTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrS 277
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     310 sThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProA 327
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     327 rgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPro 343
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     344 ValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSe 360
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seq_documentation_block:
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DEFINITION  H.sapiens DNA for 4.6 kb retinoblastoma gene probe.
ACCESSION   A01444
VERSION     A01444.1  GI:345125
KEYWORDS    .
SOURCE      human.
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REFERENCE   1  (bases 1 to 4580)
  AUTHORS   Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
  TITLE     A method for detecting the predisposition to retinoblastoma and a
            method for detecting a retinoblastoma gene in tumors using a
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  JOURNAL   Patent: EP 0293266-A 1 30-NOV-1988;
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DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA,
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ACCESSION   AF043224
VERSION     AF043224.1  GI:2865463
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REFERENCE   1  (bases 1 to 426)
  AUTHORS   Pellin,A., Boix-Ferrero,J., Carpio,D., Lopez-Terrada,D., Carda,C.,
            Navarro,S., Peydro-Olaya,A., Triche,T.J. and Llombart-Bosch,A.
  TITLE     Molecular alterations of the RB1, TP53, and MDM2 genes in primary
            and xenografted human osteosarcomas
  JOURNAL   Diagn. Mol. Pathol. 6 (6), 333-341 (1997)
  MEDLINE   98220047
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Pellin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1998) Pathology, University of Valencia, Avda.
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     160 euLysValSerTrpIleThrPheLeuLeu 169
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     383 TAAAAGTTTCTTGGATCACATTTTTATTA 411

seq_name: gb_pat:E12560

seq_documentation_block:
LOCUS       E12560       4591 bp    DNA             PAT       24-JUN-1998
DEFINITION  cDNA encoding Rb (retinoblastoma) protein.
ACCESSION   E12560
VERSION     E12560.1  GI:3251392
KEYWORDS    JP 1997023884-A/1.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Kobayashi,M., Yamauchi,Y. and Tanaka,A. .
  TITLE     ANTISENSE RNA EXPRESSING VECTOR
  JOURNAL   Patent: JP 1997023884-A 1 28-JAN-1997;
            CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO
COMMENT     OS   Mus musculus (mouse)
            PN   JP 1997023884-A/1
            PD   28-JAN-1997
            PF   13-JUL-1995 JP 1995177741
            PI   KOBAYASHI MASAYUKI, YAMAUCHI YUKIKA, TANAKA AKIKO PC
            C12N15/09//A61K31/70,A61K48/00,(C12N15/09,C12R1:92); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .4591
            FT                   /organism='Mus musculus'
            FT                   /cell_type='B-cell precursor' FT
                /cell_line='70Z-3'
            FT   5'UTR           1. .98
            FT   CDS             99. .2864
            FT                   /product='Rb protein'
            FT   3'UTR           2865. .4591.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT     1395 a    969 c    898 g   1329 t
ORIGIN


alignment_scores:
            Quality:   72.00            Length:     72
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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US-09-026-459A-41 x E12560   ..

Align seg 1/1  to: E12560  from: 1  to: 4591

     763 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 779
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     779 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 796
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     796 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 812
         ||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     813 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 829
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     829 sArgSerAlaGluGly 834
         |||||||||||||||||
    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_ro:MUSPP105RB

seq_documentation_block:
LOCUS       MUSPP105RB   4591 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse retinoblastoma susceptibility protein (pp105 Rb) mRNA,
            complete cds.
ACCESSION   M26391
VERSION     M26391.1  GI:200452
KEYWORDS    pp105 Rb gene; retinoblastoma susceptibility protein.
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4591)
  AUTHORS   Bernards,R., Schackleford,G.M., Gerber,M.R., Horowitz,J.M.,
            Friend,S.H., Schartl,M., Bogenmann,E., Rapaport,J., McGee,T.,
            Dryja,T. and Weinberg,R.A.
  TITLE     Structure and expression of the murine retinoblastoma gene and
            characterization of its encoded protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 6474-6478 (1989)
  MEDLINE   89367271
COMMENT     Draft entry and computer-readable copy of sequence [1] kindly
            provided by R.Bernards, 21-JUL-1989.
FEATURES             Location/Qualifiers
     source          1. .4591
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_line="70Z/3"
                     /cell_type="pre B-lymphocyte"
     CDS             99. .2864
                     /codon_start=1
                     /product="pp105 Rb protein"
                     /protein_id="AAA39964.1"
                     /db_xref="GI:200453"
                     /translation="MPPKAPRRAAAAEPPPPPPPPREDDPAQDSGPEELPLARLEFE
                     EIEEPEFIALCQKLKVPDHVRERAWLTWEKVSSVDGILEGYIQKKKELWGICIFIAAV
                     DLDEMPFTFTELQKSIETSVYKFFDLLKEIDTSTKVDNAMSRLLKKYNVLCALYSKLE
                     RTCELIYLTQPSSALSTEINSMLVLKISWITFLLAKGEVLQMEDDLVISFQLMLCVVD
                     YFIKFSPPALLREPYKTAAIPINGSPRTPRRGQNRSARIAKQLENDTRIIEVLCKEHE
                     CNIDEVKNVYFKNFIPFINSLGIVSSNGLPEVESLSKRYEEVYLKNKDLDARLFLDHD
                     KTLQTDPIDSFETERTPRKNNPDEEANVVTPHTPVRTVMNTIQQLMVILNSASDQPSE
                     NLISYFNNCTVNPKENILKRVKDVGHIFKEKFANAVGQGCVDIGVQRYKLGVRLYYRV
                     MESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTLQHLDSGTDLSF
                     PWILNVLNLKAFDFYKVIESFIKVEANLTREMIKHLERCEHRIMESLAWLSDSPLFDL
                     IKQSKDGEGPDNLEPACPLSLPLQGNHTAADMYLSPLRSPKKRTSTTRVNSAANTETQ
                     AASAFHTQKPLKSTSLALFYKKVYRLAYLRLNTLCARLLSDHPELEHIIWTLFQHTLQ
                     NEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAAQETFKRVLIREE
                     EFDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFSSSPLRIPGGNIY
                     ISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSDRVLKRSA
                     EGGNPPKPLKNVRFDIEGADEADGSKHLPAESKFQQKLAEMTSTRTRMQKQRMNESKD
                     VSNKEEK"
     BASE COUNT     1395 a    969 c    898 g   1329 t
     ORIGIN      Chromosome 14.


alignment_scores:
            Quality:   72.00            Length:     72
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x MUSPP105RB   ..

 Align seg 1/1  to: MUSPP105RB  from: 1  to: 4591

     763 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 779
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2457 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 2506

     779 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 796
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 2556

     796 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 812
         ||||||||||||||||||||||||||||||||||||||||||||||||
    2557 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAG 2606

     813 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 829
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2607 AAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACAGAGTGCTCAA 2656

     829 sArgSerAlaGluGly 834
         |||||||||||||||||
    2657 AAGAAGTGCTGAAGGC 2672

seq_name: gb_pr1:HUMRBSY79

seq_documentation_block:
LOCUS       HUMRBSY79     480 bp    mRNA            PRI       08-JAN-1995
DEFINITION  Human mutated retinoblastoma susceptibility (RB) mRNA, complete
            cds.
ACCESSION   M19701 J03809
VERSION     M19701.1  GI:190967
KEYWORDS    retinoblastoma susceptibility.
SOURCE      Human (patient with a maternal family history of retinoblastoma)
            retinoblastoma cell line Y79, cDNA to mRNA, clones Y[382,383,451].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.G. and
            Lee,W.H.
  TITLE     Molecular mechanism of retinoblastoma gene inactivation in
            retinoblastoma cell line Y79
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
  MEDLINE   88320373
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by E.Y.-H.P.Lee, 15-JUL-1988 The deletion spans exons 2-6 of the
            normal gene.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="13q14.2"
     gene            139. .300
                     /gene="RB1"
     CDS             139. .300
                     /gene="RB1"
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                     /codon_start=1
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                     /db_xref="GDB:G00-118-734"
                     /protein_id="AAA60259.1"
                     /db_xref="GI:190968"
                     /translation="MPPKTPRKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
                     VRGSITNGR"
     misc_recomb     275. .276
                     /gene="RB1"
                     /organism="Homo sapiens"
BASE COUNT      111 a    151 c    125 g     93 t
ORIGIN      Chromosome 13q14.1-q14.2.


alignment_scores:
            Quality:   68.00             Length:     68
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x HUMRBSY79   ..

 Align seg 1/1  to: HUMRBSY79  from: 1  to: 480

     172 GlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMe 188
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     275 GGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAAT 324

     188 tLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuL 205
         |||||||||||||||||||||||||||||||||||||||||||||||||
     325 GCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCA 374

     205 ysGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThr 221
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     375 AAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 424

     222 ProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAs 238
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     425 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAA 474

     238 nAsp 239
         ||||
     475 TGAT 478

seq_name: gb_pr2:HUMRB1501V

seq_documentation_block:
LOCUS       HUMRB1501V    340 bp    DNA             PRI       30-NOV-1995
DEFINITION  Homo sapiens retinoblastoma susceptibility protein (RB1) S501V 1 bp
            deletion mutant (resulting in premature stop at amino acid 518)
            gene, exon 17 (L11910 bases 78019-78359).
ACCESSION   L49220
VERSION     L49220.1  GI:1088308
KEYWORDS    mutation; retinoblastoma protein; retinoblastoma susceptibility
            protein.
SOURCE      Homo sapiens (individual_isolate Patient G364) DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Lohmann,D.R., Brandt,B., Hopping,W., Passarge,E. and Horsthemke,B.
  TITLE     Spectrum of small length germline mutations in the RB1 gene
  JOURNAL   Hum. Mol. Genet. 3 (12), 2187-2193 (1994)
  MEDLINE   95187159
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /isolate="Patient G364"
                     /db_xref="taxon:9606"
                     /cell_type="leukocyte"
                     /map="13q14.2"
     gene            1. .340
                     /gene="RB1"
     intron          <1. .64
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=16
     exon            65. .260
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
     CDS             <65. .120
                     /gene="RB1"
                     /note="exon 17"
                     /codon_start=3
                     /db_xref="GDB:G00-118-734"
                     /product="retinoblastoma suspectibility protein"
                     /protein_id="AAA82549.1"
                     /db_xref="GI:1088309"
                     /translation="VHLRILILEQICLSHGF"
     mutation        66. .67
                     /gene="RB1"
                     /note="ag (Val) in mutant/aag (Val) in wt, resulting in
                     premature stop at AA 518; G00-118-734"
     intron          261. .>340
                     /gene="RB1"
                     /note="G00-118-734"
                     /number=17
BASE COUNT      116 a     49 c     59 g    116 t
ORIGIN


alignment_scores:
            Quality:   66.00             Length:     66
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x HUMRB1501V   ..

 Align seg 1/1  to: HUMRB1501V  from: 1  to: 340

     469 ArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTr 485
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      63 AGGAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATG 112

     485 pIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleG 502
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 GATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCG 162

     502 luSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHis 518
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 AAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 212

     519 LeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSer 534
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCA 260
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```
OM of: US-09-026-459A-39 to: EST:*   out_format : pfs

Date: Feb 13, 2000  3:38 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171247_15917/app_query.fasta.1
 -DB=EST -QFMT=fastap -SUFFIX=oligo.rst -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
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 -THREADS=1

Search information block:
Query: US-09-026-459A-39
Query length: 851
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 6778.490000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence              Strd Orig    ZScore    EScore Len   ! Documentation ..
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gb_est32:AI745644      -  117.00 1788.28  7.7e-91   415   ! AI745644 tr24b06.x1 NCI_CGAP_Ov
gb_est32:AI745643      -  116.00 1772.94  5.5e-90   411   ! AI745643 tr24b05.x1 NCI_CGAP_Ov
gb_est14:AA382103      +   85.00 1297.95  1.6e-63   285   ! AA382103 EST95270 Activated T-c
gb_est9:AA072780       +   67.00 1016.37  7.6e-48   522   ! AA072780 mm76a05.r1 Stratagene
gb_est17:AA664676      -   53.00  803.95  5.2e-36   329   ! AA664676 nu64f09.s1 NCI_CGAP_Al
gb_est11:AA210875      +   52.00  786.24  5.0e-35   456   ! AA210875 zr88f11.r1 NCI_CGAP_GC
gb_est13:AA361277      +   49.00  742.88  1.3e-32   304   ! AA361277 EST70529 T-cell lymphc
gb_est19:AA765882      -   43.00  654.51  1.1e-27   171   ! AA765882 oa14a06.s1 NCI_CGAP_GC
gb_est22:AI020392      +   42.00  633.93  1.5e-26   356   ! AI020392 ub17a05.r1 Stratagene
gb_est19:AA763411      -   40.00  596.46  1.9e-24   914   ! AA763411 vw54a04.r1 Soares mous
gb_est5:N25402         +   38.00  571.73  4.4e-23   386   ! N25402 yx40c12.r1 Soares melanc
gb_est19:AA763485      -   38.00  565.99  9.3e-23   871   ! AA763485 vw54h01.r1 Soares mous
gb_est5:N41391         +   37.00  555.14  3.7e-22   457   ! N41391 yw70g06.r1 Soares_placen
gb_est3:R57845         +   29.00  439.66  1.0e-15   152   ! R57845 F6142 Fetal heart Homo s
gb_est29:AI606529      -   29.00  431.81  2.8e-15   462   ! AI606529 vb27g08.y1 Soares mous
gb_est30:AI646097      +   29.00  428.79  4.1e-15   709   ! AI646097 vw54h07.x1 Soares mous
gb_est11:AA258255      +   27.00  400.10  1.6e-13   525   ! AA258255 zr59g04.r1 Soares_NhHM
gb_est18:AA709628      +   25.00  370.75  6.9e-12   427   ! AA709628 vv41c11.r1 Soares 2NbM
gb_est42:AV302462      +   23.00  346.27  1.6e-10   174   ! AV302462 AV302462 RIKEN full-le
gb_est21:AA959709      +   22.00  323.02  3.2e-09   529   ! AA959709 vw54a04.s1 Soares mous
gb_est21:AA959836      +   22.00  321.95  3.6e-09   615   ! AA959836 vw54h01.s1 Soares mous
gb_est30:AI646038      +   22.00  319.82  4.8e-09   832   ! AI646038 vw54a10.x1 Soares mous
gb_est30:AI662832      +   22.00  322.43  3.4e-09   575   ! AI662832 vb27g08.x1 Soares mous
gb_est14:AA396353      -   17.00  246.50  5.8e-05   492   ! AA396353 vb27g08.r1 Soares mous
gb_est33:AV111279      +   16.00  234.97  0.0003    284   ! AV111279 AV111279 Mus musculus
gb_est27:AA955457      +   14.00  200.57  0.0209    472   ! AA955457 UI-R-A1-ew-g-10-0-UI.s
gb_est32:C82304        +   14.00  196.86  0.0337    799   ! C82304 C82304 Leukocyte of Japa
gb_gss7:AQ901300       +   14.00  195.38  0.0407    986   ! AQ901300 HS_5234_A1_B12_SP6E RP
gb_est36:AI931087      +   11.00  158.38  4.68      267   ! AI931087 fc77c03.y1 Zebrafish W
gb_est1:D15138         +   10.00  141.31  41.81     338   ! D15138 RICC0141A Rice callus Or
gb_est1:D38851         +   10.00  140.46  46.60     381   ! D38851 RICC1624A Rice callus Or
gb_est1:D38980         +   10.00  139.66  51.66     427   ! D38980 RICR0089A Rice root Oryz
gb_est1:D40024         -   10.00  140.94  43.82     356   ! D40024 RICS1743A Rice shoot Ory
gb_est2:D47372         -   10.00  141.29  41.92     339   ! D47372 RICS12716A Rice green sh
gb_est2:D48004         -   10.00  140.78  44.71     364   ! D48004 RICS13911A Rice green sh
gb_est7:W29241         -   10.00  134.03  106.34    948   ! W29241 mb96e12.r1 Soares mouse
gb_est7:W29419         -   10.00  133.14  119.15   1075   ! W29419 mb98h11.r1 Soares mouse
gb_est7:W29461         -   10.00  133.80  109.58    980   ! W29461 mb99b11.r1 Soares mouse
gb_est7:W29564         -   10.00  132.90  122.96   1113   ! W29564 mc03d11.r1 Soares mo
gb_est8:AA003706       +   10.00  141.14  42.71     346   ! AA003706 mg61a04.r1 Soares m
gb_est8:AA015259       -   10.00  133.22  117.95   1063   ! AA015259 mi61d01.r1 Soares
gb_est8:AA030506       -   10.00  134.24  103.49    920   ! AA030506 mi23f08.r1 Soares m
gb_est8:AA033363       -   10.00  139.40  53.41     443   ! AA033363 mi43c06.r1 Soares m
gb_gss15:AQ650463      -   10.00  140.90  44.04     358   ! AQ650463 Sheared DNA-18F2.TF

seq_name: gb_est38:AL120941

seq_documentation_block:
LOCUS       AL120941      572 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp762D143_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
            DKFZp762D143 5', mRNA sequence.
ACCESSION   AL120941
VERSION     AL120941.1  GI:5926942
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 572)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948410.
            Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES              Location/Qualifiers
     source           1. .572
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="DKFZp762D143"
                      /clone_lib="762 (synonym: hmel2)"
                      /tissue_type="melanoma (MeWo cell line)"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      180 a    128 c     98 g    166 t
ORIGIN


alignment_scores:
            Quality:  159.00              Length:    159
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AL120941   ..

 Align seg 1/1  to: AL120941  from: 1  to: 572

     413 AlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLe 429
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT 50

     429 uAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnL 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATT 100

     446 euLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGlu 462
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     101 TAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 150
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     463 GlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisAr 479
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCG 200

     479 gIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuI 496
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTA 250

     496 leLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAla 512
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     251 TTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 300

     513 CysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTy 529
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     301 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTA 350

     529 rLeuSerProValArgSerProLysLysLysGlySerThrThrArgValA 546
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     351 TCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAA 400

     546 snSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGln 562
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     401 ATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 450

     563 LysProLeuLysSerThrSerLeuSer 571
         |||||||||||||||||||||||||||
     451 AAGCCATTGAAATCTACCTCTCTTTCC 477

seq_name: gb_est32:AI745644

seq_documentation_block:
LOCUS       AI745644      415 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219219 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745644
VERSION     AI745644.1  GI:5113932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137189.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219219"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      118 a     75 c     87 g    135 t
ORIGIN


alignment_scores:
            Quality:  117.00              Length:    117
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AI745644/rev   ..

 Align seg 1/1  to reverse of: AI745644  from: 1  to: 415

     637 ValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAs 653
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     413 GTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGA 364

     653 pLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluG 670
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     363 TCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAG 314

     670 luGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArg 686
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     313 AGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGA 264

     687 LeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSe 703
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     263 CTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 214

     703 rProIleProHisIleProArgSerProTyrLysPheProSerSerProL 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     213 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCT 164

     720 euArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyr 736
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     163 TACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 114

     737 LysIleSerGluGlyLeuProThrProThrLysMetThrProArgSerAr 753
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     113 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAG 64

     753 g 753
         |
      63 G 63

seq_name: gb_est32:AI745643

seq_documentation_block:
LOCUS       AI745643      411 bp    mRNA            EST       21-JUN-1999
DEFINITION  tr24b05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219217 3'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
            mRNA sequence.
ACCESSION   AI745643
VERSION     AI745643.1  GI:5113931
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 411)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137188.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .411
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219217"
                     /clone_lib="NCI_CGAP_Ov23"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"
BASE COUNT      117 a     74 c     87 g    133 t
ORIGIN


alignment_scores:
            Quality:  116.00             Length:    116
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AI745643/rev   ..

 Align seg 1/1  to reverse of: AI745643  from: 1  to: 411

     638 LysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLe 654
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCT 361

     654 uProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluG 671
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGG 311

     671 luTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeu 687
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 AGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTG 261

     688 LysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPr 704
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 AAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 211

     704 oIleProHisIleProArgSerProTyrLysPheProSerSerProLeuA 721
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTAC 161

     721 rgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLys 737
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 111

     738 IleSerGluGlyLeuProThrProThrLysMetThrProArgSerArg 753
         |||||||||||||||||||||||||||||||||||||||||||||||||
     110 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGG 63

seq_name: gb_est14:AA382103

seq_documentation_block:
LOCUS       AA382103      285 bp    mRNA            EST       21-APR-1997
DEFINITION  EST95270 Activated T-cells II Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA382103
VERSION     AA382103.1  GI:2034432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407366.
            Other_ESTs: EST95269 THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):107475"
                     /db_xref="taxon:9606"
                     /clone_lib="Activated T-cells II"
                     /cell_type="T-lymphocyte"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       87 a     63 c     52 g     83 t
ORIGIN


alignment_scores:
            Quality:   85.00             Length:     85
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AA382103   ..

 Align seg 1/1  to: AA382103  from: 1  to: 285

     568 ThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuAr 584
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       2 ACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 51

     584 gLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluH 601
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      52 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAAC 101

     601 isIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 617
         |||||||||||||||||||||||||||||||||||||||||||||||||
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     102 ATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 151

     618 MetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIl 634
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCAT 201

     634 eCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaT 651
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     202 ATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAT 251

     651 yrLys 652
         |||||
     252 ACAAG 256

seq_name: gb_est9:AA072780

seq_documentation_block:
LOCUS       AA072780      522 bp    mRNA            EST       07-FEB-1997
DEFINITION  mm76a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:534320 5' similar to gb:M26391 Mouse retinoblastoma
            susceptibility protein (MOUSE);, mRNA sequence.
ACCESSION   AA072780
VERSION     AA072780.1  GI:1594511
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 522)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394992.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:321256
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 391.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:534320"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      162 a    128 c    100 g    132 t
ORIGIN


alignment_scores:
            Quality:   67.00            Length:     67
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:

 US-09-026-459A-39 x AA072780   ..

 Align seg 1/1  to: AA072780  from: 1  to: 522

     717 SerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLy 733
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGTTCACCCTTACGGATTCCTGGAGGTAACATCTATATATCACCCCTAAA 307

     733 sSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrP 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 GAGTCCTTATAAAATTTCAGAAGGTCTGCCAACACCCACAAAAATGACTC 357

     750 roArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlu 766
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 CGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGGGACATCTGAA 407

     767 LysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLy 783
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 AAGTTCCAGAAAATAAACAGATGGTGTGTAATAGTGACAGAGTGCTCAA 457

     783 s 783
         |
     458 A 458

seq_name: gb_est17:AA664676

seq_documentation_block:
LOCUS       AA664676      329 bp    mRNA            EST       13-FEB-1998
DEFINITION  nu64f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1215497
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA664676
VERSION     AA664676.1  GI:2619289
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 329)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1400955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source          1. .329
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1215497"
                     /clone_lib="NCI_CGAP_Alv1"
                     /tissue_type="alveolar rhabdomyosarcoma"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from alveolar
                     rhabdomyosarcoma, cDNA made by oligo-dT priming.
                     Non-directionally cloned. Size-selected on agarose gel,
                     average insert  size 600 bp. Reference:  Krizman et al.
                     (1996) Cancer Research 56:5380-5383."
BASE COUNT       94 a     62 c     65 g    108 t
ORIGIN
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alignment_scores:
            Quality:   53.00              Length:     53
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AA664676/rev   ..

 Align seg 1/1  to reverse of: AA664676  from: 1  to: 329

     436 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 452
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     294 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 245

     452 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 469
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     244 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 195

     469 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 485
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     194 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 145

     486 TrpLeuSer 488
         |||||||||
     144 TGGCTCTCA 136

seq_name: gb_est11:AA210875

seq_documentation_block:
LOCUS       AA210875      456 bp    mRNA            EST       13-AUG-1997
DEFINITION  zr88f11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682797 5'
            similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);,
            mRNA sequence.
ACCESSION   AA210875
VERSION     AA210875.1  GI:1809511
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1402285.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Homo sapiens"
                     /db_xref="GDB:5586117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:682797"
                     /clone_lib="NCI_CGAP_GCB1"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-
                     3']. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      150 a     80 c     90 g    133 t      3 others
ORIGIN


alignment_scores:
            Quality:   52.00              Length:     52
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AA210875   ..

 Align seg 1/1  to: AA210875  from: 1  to: 456

     800 PheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGl 816
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      25 TTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGG 74

     816 yGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrA 833
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      75 AGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 124

     833 rgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 849
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     125 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAA 174

     850 GluLys 851
         ||||||
     175 GAGAAA 180

seq_name: gb_est13:AA361277

seq_documentation_block:
LOCUS       AA361277      304 bp    mRNA            EST       21-APR-1997
DEFINITION  EST70529 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            retinoblastoma susceptibility protein, mRNA sequence.
ACCESSION   AA361277
VERSION     AA361277.1  GI:2013596
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1407493.
            Other_ESTs: THC168922
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
```

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            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES              Location/Qualifiers
     source           1. .304
                      /organism="Homo sapiens"
                      /db_xref="ATCC (inhost):165411"
                      /db_xref="taxon:9606"
                      /clone_lib="T-cell lymphoma"
                      /cell_type="T-lymphocyte"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XhoI"
BASE COUNT       94 a     79 c     43 g     86 t      2 others
ORIGIN


alignment_scores:
            Quality:   49.00             Length:     49
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AA361277   ..

 Align seg 1/1  to: AA361277  from: 1  to: 304

     504 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGl 520
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
      50 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCA 99

     520 nAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProL 537
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     100 GAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAA 149

     537 ysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGlu 552
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     150 AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 196

seq_name: gb_est19:AA765882

seq_documentation_block:
LOCUS        AA765882      171 bp    mRNA            EST       08-FEB-1998
DEFINITION   oa14a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304914 3'
             similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);;
             mRNA sequence.
ACCESSION    AA765882
VERSION      AA765882.1  GI:2817120
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 171)
  AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
  JOURNAL    Unpublished (1997)
COMMENT      On Jan 17, 1998 this sequence version replaced gi:2044576.
             Contact: Robert Strausberg, Ph.D.
             Tel: (301) 496-1550
             Email: Robert_Strausberg@nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Trace considered overall poor quality
             Insert Length: 2415   Std Error: 0.00
             Seq primer: -40m13 fwd. ET from Amersham
             High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .171
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1304914"
                      /clone_lib="NCI_CGAP_GCB1"
                      /tissue_type="germinal center B cell"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was prepared from human tonsillar cells enriched for
                      germinal center B cells by flow sorting (CD20+, IgD-),
                      provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                      (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                      primed with a Not I - oligo(dT) primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-
                      3']. Double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization, and was
                      constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       53 a     32 c     29 g     57 t
ORIGIN


alignment_scores:
            Quality:   43.00             Length:     43
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AA765882/rev   ..

 Align seg 1/1  to reverse of: AA765882  from: 1  to: 171

     368 ArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLe 384
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     169 CGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 120

     384 uLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuA 401
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
     119 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGA 70

     401 snAspAsnIlePheHisMetSerLeuLeu 410
         !!!!!!!!!!!!!!!!!!!!!!!!!!!!!
      69 ATGACAACATTTTTCATATGTCTTTATTG 41

seq_name: gb_est22:AI020392

seq_documentation_block:
LOCUS        AI020392      356 bp    mRNA            EST       16-JUN-1998
DEFINITION   ub17a05.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
             clone IMAGE:1367216 5' similar to gb:M26391 Mouse retinoblastoma
             susceptibility protein (MOUSE);; mRNA sequence.
ACCESSION    AI020392
VERSION      AI020392.1  GI:3234728
KEYWORDS     EST.
SOURCE       house mouse.
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 356)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
```

```
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044708.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:900436
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1367216"
                     /clone_lib="Stratagene mouse macrophage (#937306)"
                     /tissue_type="macrophage"
                     /dev_stage="WEHI-3 cell line"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      126 a     78 c     92 g     60 t
ORIGIN


alignment_scores:
            Quality:   42.00             Length:     42
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AI020392   ..

 Align seg 1/1  to: AI020392  from: 1  to: 356

     747 LysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGl 763
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       3 AAAATGACTCCGAGATCAAGAATCTTGGTCTCAATTGGTGAATCATTTGG 52

     763 yThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 GACATCTGAAAAGTTCCAGAAAATAAACCAGATGGTGTGTAATAGTGACA 102

     780 rgValLeuLysArgSerAlaGluGly 788
         |||||||||||||||||||||||||
     103 GAGTGCTCAAAAGAAGTGCTGAAGGC 128

seq_name: gb_est19:AA763411

seq_documentation_block:
LOCUS       AA763411      914 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54a04.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247598 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763411
VERSION     AA763411.1  GI:2813158
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 914)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798537.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661286
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .914
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247598"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      257 a    178 c    217 g    261 t      1 others
ORIGIN


alignment_scores:
            Quality:   40.00             Length:     40
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AA763411/rev   ..

 Align seg 1/1  to reverse of: AA763411  from: 1  to: 914

     386 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 402
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     541 TCAGAAGAAGAACGTTTGTCCATTCAGAATTTTAGCAAACTCCTAAATGA 492

     402 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 419
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     491 CAACATCTTTCATATGTCTTTACTGGCCTGTGCTCTTGAAGTTGTAATGG 442

     419 laThrTyrSerArgSerThr 425
         |||||||||||||||||||
     441 CTACGTATAGCAGAAGTACA 422

seq_name: gb_est5:N25402

seq_documentation_block:
LOCUS       N25402         386 bp    mRNA            EST       29-DEC-1995
DEFINITION  yx40c12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:264214 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N25402
VERSION     N25402.1  GI:1139843
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837670.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 244
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 244.
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Homo sapiens"
                     /db_xref="GDB:3873856"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:264214"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      114 a     78 c     87 g     96 t     11 others
ORIGIN


alignment_scores:
            Quality:   38.00             Length:     38
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x N25402   ..

 Align seg 1/1  to: N25402  from: 1  to: 386

     785 SerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAs 801
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 50

     801 pIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluS 818
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      51 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 100

     818 erLysPheGlnGln 822
         ||||||||||||||
     101 CCAAATTTCAGCAG 114

seq_name: gb_est19:AA763485

seq_documentation_block:
```

```
LOCUS       AA763485      871 bp    mRNA            EST       27-JAN-1998
DEFINITION  vw54h01.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone
            IMAGE:1247665 5' similar to gb:M15400 RETINOBLASTOMA-ASSOCIATED
            PROTEIN (HUMAN); gb:M26391 Mouse retinoblastoma susceptibility
            protein (MOUSE);, mRNA sequence.
ACCESSION   AA763485
VERSION     AA763485.1  GI:2813232
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1798647.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:661353
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1247665"
                     /clone_lib="Soares mouse mammary gland NMLMG"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      242 a    172 c    204 g    251 t      2 others
ORIGIN


alignment_scores:
            Quality:   38.00             Length:     38
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x AA763485/rev   ..

 Align seg 1/1  to reverse of: AA763485  from: 1  to: 871

     464 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIl 480
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     307 AACTTGACAAGAGAAATGATAAAACATTTAGAAAGATGTGAGCATCGAAT 258

     480 eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleL 497
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 CATGGAATCCCTTGCATGGCTTTCAGATTCACCTTTATTTGATCTCATTA 208

     497 ysGlnSerLysAsp 501
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    207 AGCAGTCCAAGGAT 194

seq_name: gb_est5:N41391

seq_documentation_block:
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DEFINITION  yw70g06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
            clone IMAGE:257626 5' similar to gb:M15400
            RETINOBLASTOMA-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.
ACCESSION   N41391
VERSION     N41391.1  GI:1165422
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 8, 1995 this sequence version replaced gi:801499.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 359
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 359.
FEATURES             Location/Qualifiers
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                     /db_xref="GDB:3887236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:257626"
                     /clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
                     /dev_stage="two placentae: one from 8 weeks and another
                     from 9 weeks post conception"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      159 a     77 c     93 g    128 t
ORIGIN


alignment_scores:
            Quality:   37.00            Length:     37
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x N41391   ..

 Align seg 1/1  to: N41391  from: 1  to: 457

     764 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspAr 780
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     218 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCG 267

     780 gValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysL 797
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     268 TGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAA 317

     797 ysLeuArgPhe 800
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     318 AACTACGCTTT 328

seq_name: gb_est3:R57845

seq_documentation_block:
LOCUS       R57845        152 bp    mRNA            EST       02-MAY-1996
DEFINITION  F6142 Fetal heart Homo sapiens cDNA clone F6142 5' end similar to
            Retinoblastoma susceptibility gene, mRNA sequence.
ACCESSION   R57845
VERSION     R57845.1  GI:827903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 152)
  AUTHORS   Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H.,
            Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
  TITLE     Analysis of expressed sequence tags from a fetal human heart cDNA
            library
  JOURNAL   Genomics 30 (2), 293-298 (1995)
  MEDLINE   96163883
COMMENT     Contact: Liew CC
            Department of Laboratory Medicine and Pathobiology
            University of Toronto
            Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
            Tel: 4169788758
            Fax: 4169785650
            Email: liewcc@utcc.utoronto.ca
            Insert Length: 1898   Std Error: 0.00
            Seq primer: GGTGGCGACGACTCCTGGAGCC
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .152
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                     /clone_lib="Fetal heart"
                     /lab_host="E. coli Y1090"
                     /note="Vector: Lambda gt22; Site_1: NotI; Site_2: SalI;
                     mRNA was purified from human fetal hearts (10-12 weeks).
                     cDNA was constructed using a NotI-Oligo dT adaptor-primer.
                      SalI adaptors were ligated, followed by digestion with
                     NotI, for direction cloning into predigested lambda gt22.
                     Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                     1329-1333)"
BASE COUNT       43 a     40 c     27 g     42 t
ORIGIN


alignment_scores:
            Quality:   29.00            Length:     29
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x R57845   ..

 Align seg 1/1  to: R57845  from: 1  to: 152

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       3 CCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGG 52

     725 yAsnIleTyrIleSerProLeuLysSerProTyrLys 737
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OM of: US-09-026-459A-39 to: Issued_Patents_NA:*   out_format : pfs

Date: Feb 13, 2000  3:58 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15938/app_query.fasta.1
 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oligo.rni
 -GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
 -LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000
 -XGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
 -YGAPEXT=60.000 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=oligo -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US09026459 -NCPU=6
 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-026-459A-39
Query length: 851
Database: Issued_Patents_NA:*
Database sequences: 214294
Database length: 59861208
Search time (sec): 316.800000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
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Sequence          Strd Orig    ZScore   EScore Len  ! Documentation  ..
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-470-091-2 -  820.00 13975.87  0.0       3232  !
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-07-812-421-26 -   10.00  165.63  0.0864     57  !  S
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/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:PCT-US95-05523-3 +   10.00  140.74  2.10      1680
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seq_documentation_block:
; Sequence 2, Application US/08204329
; Patent No. 5710255
;  GENERAL INFORMATION:
;    APPLICANT:  SHEPARD, H. M.
;    APPLICANT:  WEN, SHU F.
;    TITLE OF INVENTION:  CHARACTERIZATION OF A NOVEL ANTI-P110RB
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND & TOWNSEND & CREW LLP
;      STREET:  TWO EMBARCADERO CENTER, 8TH FLOOR
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/204,329
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05866
;      FILING DATE:  14-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RENEE A. FITTS
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16930-000400US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (cDNA)
US-08-204-329-2


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x US-08-204-329-2   ..

 Align seg 1/1  to: US-08-204-329-2  from: 1  to: 2994

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      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
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 81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
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610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

 97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
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114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
    ||||||||||||||||||||||||||||||||||||||||||||||||||
710 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
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147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
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810 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 859

164 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||
860 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
    ||||||||||||||||||||||||||||||||||||||||||||||||||
910 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
    ||||||||||||||||||||||||||||||||||||||||||||||||||
960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 1009

214 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 230
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1010 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
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247 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 264
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281 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 297
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; Patent No. 5932210
;  GENERAL INFORMATION:
;    APPLICANT:  Gregory, Richard J.
;    APPLICANT:  Wills, Ken N.
;    APPLICANT:  Maneval, Daniel C.
;    TITLE OF INVENTION:  Recombinant Adenoviral Vector and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/328,673
;      FILING DATE:  25-OCT-1994
;      APPLICATION NUMBER:  US 08/233,777
;      FILING DATE:  19-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/142,669
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-CJ 1192
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2995 base pairs
;      TYPE:  nucleic acid
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;      TOPOLOGY:  linear
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US-08-959-638-7


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; Patent No. 5998134
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Wen-Hwa
;    APPLICANT:  Lee, Eva Y-H.P
;    TITLE OF INVENTION:  Retinoblastoma Gene - Cancer Suppressor
;    TITLE OF INVENTION:  and Regulator
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,627
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,947
;      FILING DATE:  28-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 1707
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2924
US-08-482-627-4


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seq_documentation_block:
; Sequence 1, Application US/08038760
; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
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;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/038,760
;       FILING DATE:  19930325
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  7409-025-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3232 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  DNA
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;       NAME/KEY:  CDS
;       LOCATION:  19..2469
US-08-038-760-1


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; Patent No. 5496731
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:  19930325
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-038-760-2


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seq_documentation_block:
; Sequence 1, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
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;      LOCATION:  19..2469
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alignment_scores:
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seq_documentation_block:
; Sequence 2, Application US/08470091
; Patent No. 5912236
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Hong-Ji
;    APPLICANT:  Hu, Shi-Xue
;    APPLICANT:  Benedict, William F.
;    TITLE OF INVENTION:  Broad-Spectrum Tumor Suppressor Genes, Gene Products and
;    TITLE OF INVENTION:  Methods for Tumor Suppressor Gene Therapy.
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,091
;      FILING DATE:  JUN-16-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/038,760
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  7409-025-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3232 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA
US-08-470-091-2


alignment_scores:
            Quality:  820.00              Length:    820
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    APPLICANT:  and Canji, Inc.
;    TITLE OF INVENTION:  Therapeutic Use of the Retinoblastoma
;    TITLE OF INVENTION:  Susceptibility Gene Product
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10357
;      FILING DATE:  13-SEP-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/121,108
;      FILING DATE:  13-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  FP-UC 1117
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2994 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  139..2923
PCT-US94-10357-1


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; Sequence 1, Application US/07915246
; Patent No. 5401836
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris L.
;    APPLICANT:  Fallis, Lynne
;    APPLICANT:  Bellmare, Guy
;    APPLICANT:  Boivin, Rodolphe
;    TITLE OF INVENTION:  A BRASSICA REGULATORY SEQUENCE FOR
;    TITLE OF INVENTION:  ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held, and Malloy
;      STREET:  500 W. Madison St. 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/915,246
;      FILING DATE:  19920716
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien, Donald J.
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  91 P 1125
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312 707-8889
;      TELEFAX:  312 707-9155
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1505 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Brassica napus
;      STRAIN:  Westar
;      DEVELOPMENTAL STAGE:  Somatic
;      TISSUE TYPE:  Root
US-07-915-246-1
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seq_documentation_block:
; Sequence 1, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
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 Percent Similarity: 100.000   Percent Identity: 100.000

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seq_documentation_block:
; Sequence 3, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
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; Sequence 1, Application US/08456907
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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
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;      LOCATION:  1..630
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; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1680 base pairs
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;      TOPOLOGY:  unknown
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; Sequence 5, Application US/08246982A
; Patent No. 5686288
;  GENERAL INFORMATION:
;    APPLICANT:  MacDonald, Marcy E.
;    APPLICANT:  Ambrose, Christine M.
;    APPLICANT:  Duyao, Mabel P.
;    APPLICANT:  Gusella, James F.
;    TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
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;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/246,982A
;       FILING DATE:  May 20, 1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Goldstein, Jorge, A.
;       REGISTRATION NUMBER:  29,021
;       REFERENCE/DOCKET NUMBER:  0609.3880002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
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;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
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;       LOCATION:  316..9748
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; Sequence 5, Application US/08453265
; Patent No. 5693757
;  GENERAL INFORMATION:
;     APPLICANT:  MacDonald, Marcy E.
;     APPLICANT:  Ambrose, Christine M.
;     APPLICANT:  Duyao, Mabel P.
;     APPLICANT:  Gusella, James F.
;     TITLE OF INVENTION:  Huntingtin DNA, Protein And Uses Thereof
;     NUMBER OF SEQUENCES:  25
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;       STREET:  1100 New York Avenue
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/453,265
;       FILING DATE:  30-MAY-1995
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0609.3880003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10366 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
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;       LOCATION:  316..9748
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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1081.569 Million cell updates/sec

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Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	2	2953	99.9	3555	1	V58440	Modified retinobla
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	4	2889	97.8	3392	1	V58442	Modified retinobla
	5	2883	97.6	4597	1	Q70536	Human retinoblasto
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	13	2755	93.2	2994	1	V40004	Retinoblastoma pro
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	27	1629	55.1	4579	1	N81261	Probe for retinobl
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ALIGNMENTS

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AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2694
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 T;

Query Match 100.0%; Score 2955; DB 1; Length 3455;
Best Local Similarity 100.0%; Pred. No. 0;
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Qy   2221 ACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCT 2280
Db   2227 ACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCT 2286
Qy   2281 AGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 2340
Db   2287 AGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATAT 2346
Qy   2341 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTA 2400
Db   2347 AAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTA 2406
Qy   2401 TCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGT 2460
Db   2407 TCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGT 2466
Qy   2461 AACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAA 2520
Db   2467 AACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAA 2526
Qy   2521 AAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGA 2580
Db   2527 AAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGA 2586
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Qy   2581 GAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2587 GAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAG 2646

Qy   2641 CAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGAC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2647 CAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGAC 2706

Qy   2701 CTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAAC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2707 CTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAAC 2766

Qy   2761 TTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2767 TTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAA 2826

Qy   2821 TGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2827 TGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATT 2886

Qy   2881 TATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2887 TATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTT 2946

Qy   2941 CCTCTTCCAAAGTAA 2955
          |||||||||||||||
Db   2947 CCTCTTCCAAAGTAA 2961
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RESULT 2
V58440
ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69364.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Disclosure; Page 121-126; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 99.9%; Score 2953; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2953; Conservative 0; Mismatches 0; Indels : 0; Gaps 0;

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Qy      3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    108 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 167

Qy     63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    168 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 227

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    228 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 287

Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    288 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 347

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    348 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 407

Qy    303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    408 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 467

Qy    363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    468 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 527

Qy    423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    528 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 587

Qy    483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    588 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 647

Qy    543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 707

Qy    603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    708 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 767

Qy    663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    768 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 827

Qy    723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    828 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 887

Qy    783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    888 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 947

Qy    843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    948 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1007

Qy    903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1008 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1067

Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1068 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1127

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1128 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1187

Qy   1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1188 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1247

Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1248 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1307
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Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1308 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1367

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1368 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1427

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1428 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1487

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1488 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1547

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1548 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1607

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1608 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1667

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1668 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1727

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1728 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1787

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1788 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1847

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1848 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1907

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1908 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1967

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1968 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2027

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2028 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2087

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2088 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2147

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2148 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2207

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2208 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2267

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2268 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2327

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2328 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2387
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Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2388 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2447

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2448 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2507

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2508 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2567

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2568 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2627

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2628 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2687

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2688 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2747

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2748 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2807

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2808 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2867

Qy   2763 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2868 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2927

Qy   2823 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2928 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2987

Qy   2883 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 2942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2988 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 3047

Qy   2943 TCTTCCAAAGTAA 2955
          |||||||||||||
Db   3048 TCTTCCAAAGTAA 3060
```

RESULT 3
V54990
ID V54990 standard; DNA; 3555 BP.
AC V54990;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the

PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 99.9%; Score 2953; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 167

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     168 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 227

Qy     123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     228 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 287

Qy     183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     288 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 347

Qy     243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     348 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 407

Qy     303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     408 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 467

Qy     363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     468 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 527

Qy     423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     528 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 587

Qy     483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     588 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 647

Qy     543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 707

Qy     603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     708 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 767

Qy     663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     768 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 827

Qy     723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     828 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 887

Qy     783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     888 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 947

Qy     843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     948 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1007

Qy     903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1008 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1067

Qy     963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1068 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1127

Qy    1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1128 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1187

Qy    1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1188 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1247

Qy    1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1248 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1307

Qy    1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1308 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1367

Qy    1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1368 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1427

Qy    1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1428 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1487

Qy    1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1488 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1547

Qy    1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1548 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1607

Qy    1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1608 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1667

Qy    1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1668 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1727

Qy    1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1728 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1787

Qy    1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1788 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1847

Qy    1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1848 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1907

Qy    1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1908 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1967
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Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1968 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2027

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2028 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2087

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2088 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2147

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2148 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2207

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2208 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2267

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2268 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2327

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2328 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2387

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2388 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2447

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2448 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2507

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2508 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2567

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2568 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2627

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2628 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2687

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2688 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2747

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2748 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2807

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2808 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2867

Qy   2763 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2868 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2927

Qy   2823 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2928 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2987

Qy   2883 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 2942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2988 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 3047

Qy   2943 TCTTCCAAAGTAA 2955
          |||||||||||||
Db   3048 TCTTCCAAAGTAA 3060
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RESULT 4
V58442
ID V58442 standard; DNA; 3392 BP.
AC V58442;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2641
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69366.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 150-155; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3392 BP; 1137 A; 614 C; 607 G; 1034 T;

Query Match 97.8%; Score 2889; DB 1; Length 3392;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     67 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 69

Qy    127 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 129

Qy    187 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 189

Qy    247 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 249

Qy    307 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 309

Qy    367 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 369

Qy    427 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 429

Qy    487 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 489
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Qy    547 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 549

Qy    607 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 609

Qy    667 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 669

Qy    727 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 729

Qy    787 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 789

Qy    847 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 849

Qy    907 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 909

Qy    967 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 969

Qy   1027 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1029

Qy   1087 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1089

Qy   1147 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1149

Qy   1207 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1209

Qy   1267 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1269

Qy   1327 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1329

Qy   1387 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1389

Qy   1447 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1449

Qy   1507 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1509

Qy   1567 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1569

Qy   1627 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1629

Qy   1687 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1689

Qy   1747 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1749

Qy   1807 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1809

Qy   1867 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1869

Qy   1927 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1929

Qy   1987 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1989

Qy   2047 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2049

Qy   2107 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2109

Qy   2167 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2169

Qy   2227 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2229

Qy   2287 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2289

Qy   2347 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2349

Qy   2407 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2409

Qy   2467 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2469

Qy   2527 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2529

Qy   2587 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2589

Qy   2647 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGT 2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGT 2649

Qy   2707 GGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCC 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2650 GGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCC 2709

Qy   2767 AGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCA 2826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 AGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCA 2769

Qy   2827 GATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACA 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 GATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACA 2829

Qy   2887 AGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTT 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2830 AGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTT 2889

Qy   2947 CCAAAGTAA 2955
          |||||||||
Db   2890 CCAAAGTAA 2898


RESULT   5
Q70536
ID   Q70536 standard; DNA; 4597 BP.
AC   Q70536;
DT   27-MAR-1995  (first entry)
DE   Human retinoblastoma gene.
KW   Retinoblastoma; cancer; detection; diagnosis; protein; neoplasm;
KW   assay; immune complex; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             337. .2787
FT                   /*tag= a
PN   EP-608004-A.
PD   27-JUL-1994.
PF   11-AUG-1987; 307095.
PR   11-AUG-1986; US-895163.
PA   (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA   (WHED ) WHITEHEAD INST.
PA   BIOMEDICAL RES.
PI   Dryja TP,  Friend S;
DR   WPI; 94-272746/34.
DR   P-PSDB; R58568.
PT   Diagnosing the presence of defective retinoblastoma alleles -
PT   comprises comparing genetic material corresponding to a normal
PT   human retinoblastoma with DNA from a patient.
PS   Example 2(2); Figure 7; 18pp; English.
CC   A method for detecting the presence, in a tumour sample, of a protein
CC   the absence of which is associated with a neoplasm, comprises
CC   producing an antibody to the protein and then contacting the
CC   antibody with the tumour sample.  Immune complexes indicate the
CC   presence of the protein in the sample.  The method may be used in
CC   the detection and treatment of a defective human gene related to
CC   cancer, in particular retinoblastoma.
SQ   Sequence   4597 BP;    1489 A;    841 C;    812 G;    1455 T;


  Query Match             97.6%;  Score 2883;  DB 1;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2933;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     22 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 81
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy     82 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 141
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    142 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 201
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    202 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 261
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    262 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 321
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    322 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    382 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 441
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    442 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 501
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy    502 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 561
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy    562 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 621
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy    622 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 681
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy    682 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy    742 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 801
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    802 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    862 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 921
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTTGATCATGAT 1020

Qy    922 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy    982 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1041
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy   1042 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1101
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy   1102 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1161
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy   1162 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1221
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy   1222 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy   1282 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
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Qy   1342 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy   1402 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy   1462 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy   1522 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy   1582 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1642 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy   1702 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1762 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy   1822 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1882 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 1941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   1942 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2002 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2062 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2122 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2182 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2242 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2302 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2362 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
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Qy   2422 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2482 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640

Qy   2542 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2602 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2662 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2820

Qy   2722 CTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2880

Qy   2782 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2940

Qy   2842 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 2901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 3000

Qy   2902 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 3054
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RESULT 6
X04501
ID X04501 standard; cDNA; 4597 BP.
AC X04501;
DT 05-JUL-1999 (first entry)
DE Human retinoblastoma gene cDNA.
KW Retinoblastoma; Rb gene; human; predisposition; diagnosis; therapy;
KW ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 337. .2787
FT /*tag= a
FT /transl_except= (pos:2632. .2634, aa:Asp)
PN US5853988-A.
PD 29-DEC-1998.
PF 08-OCT-1992; 958290.
PR 08-JUL-1991; US-728756.
PR 11-AUG-1986; US-895163.
PR 21-JAN-1988; US-146525.
PR 23-JAN-1989; US-300667.
PR 25-SEP-1992; US-951342.
PR 08-OCT-1992; US-958290.
PA (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA (WHED) WHITEHEAD INST.
PI Dryja TP, Friend S, Yandell DW;
DR WPI; 99-094898/08.
DR P-PSDB; Y01542.
PT Isolated human retinoblastoma gene - used to develop products for
PT analysing predisposition to retinoblastoma and for the detection and
PT treatment of retinoblastoma
PS Claim 8; Fig 5; 32pp; English.
CC This is the nucleic acid sequence of a cDNA of the normal human
CC retinoblastoma gene Rb. Absence or mutation of the Rb gene (see
CC also X04502) predisposes an individual to retinoblastoma. To
CC isolate Rb cDNA, the human DNA probe pH3-8, isolated from a human
CC chromosome 13 lambda phage library, was used in a chromosome walk

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CC   to isolate and map 30 kb of genomic DNA surrounding the H3-8
CC   sequence.  Fragment p7H30.7R (ATCC 97500) was obtained, and was
CC   used as a probe to screen a cDNA library that had been constructed
CC   from an adenovirus 12-transformed human embryonic retinal cell
CC   line.  This provided clone p4.7R (ATCC 97383), which in Northern
CC   blots cross-reacted with a 4.7 kb transcript in transformed
CC   retinal cells which was not present in 4 retinoblastoma and one
CC   osteosarcoma cell samples.  Rb nucleic acids comprising the Rb
CC   gene, cDNA or a fragment of the gene, such as one of the 27 exons
CC   or 26 introns, can be used in a claimed method for detecting a
CC   deletion or point mutation in the Rb gene of a human patient.  The
CC   gene can also be used to synthesize Rb polypeptide (see Y01542) for
CC   use in the treatment of individuals determined to have a defective
CC   Rb allele.
SQ   Sequence   4597 BP;    1489 A;    841 C;    813 G;    1454 T;

  Query Match            97.6%;  Score 2883;  DB 1;  Length 4597;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2933;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      22 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy      82 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy     142 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy     202 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy     262 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy     322 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy     382 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy     442 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy     502 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy     562 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 621
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy     622 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 681
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy     682 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy     742 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy     802 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 861
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy     862 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 921
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Qy     922 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 981
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy     982 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1041
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy    1042 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy    1102 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy    1162 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy    1222 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy    1282 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1341
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy    1342 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1401
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy    1402 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1461
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy    1462 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1521
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy    1522 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1581
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy    1582 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1641
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy    1642 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1701
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy    1702 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy    1762 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1821
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy    1822 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1881
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy    1882 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 1941
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Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   1942 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2002 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2062 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2122 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2182 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2242 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2302 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2362 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Qy   2422 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2482 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2541
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGAA 2640

Qy   2542 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2602 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2662 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2820

Qy   2722 CTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2880

Qy   2782 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2940

Qy   2842 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 2901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 3000

Qy   2902 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 3054
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RESULT 7

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V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;
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  Query Match             96.5%;  Score 2851;  DB 1;  Length 3554;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2951;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 167

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     168 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 227

Qy     123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     228 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 287

Qy     183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
           |||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||
Db     288 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTC 347

Qy     243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     348 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 407

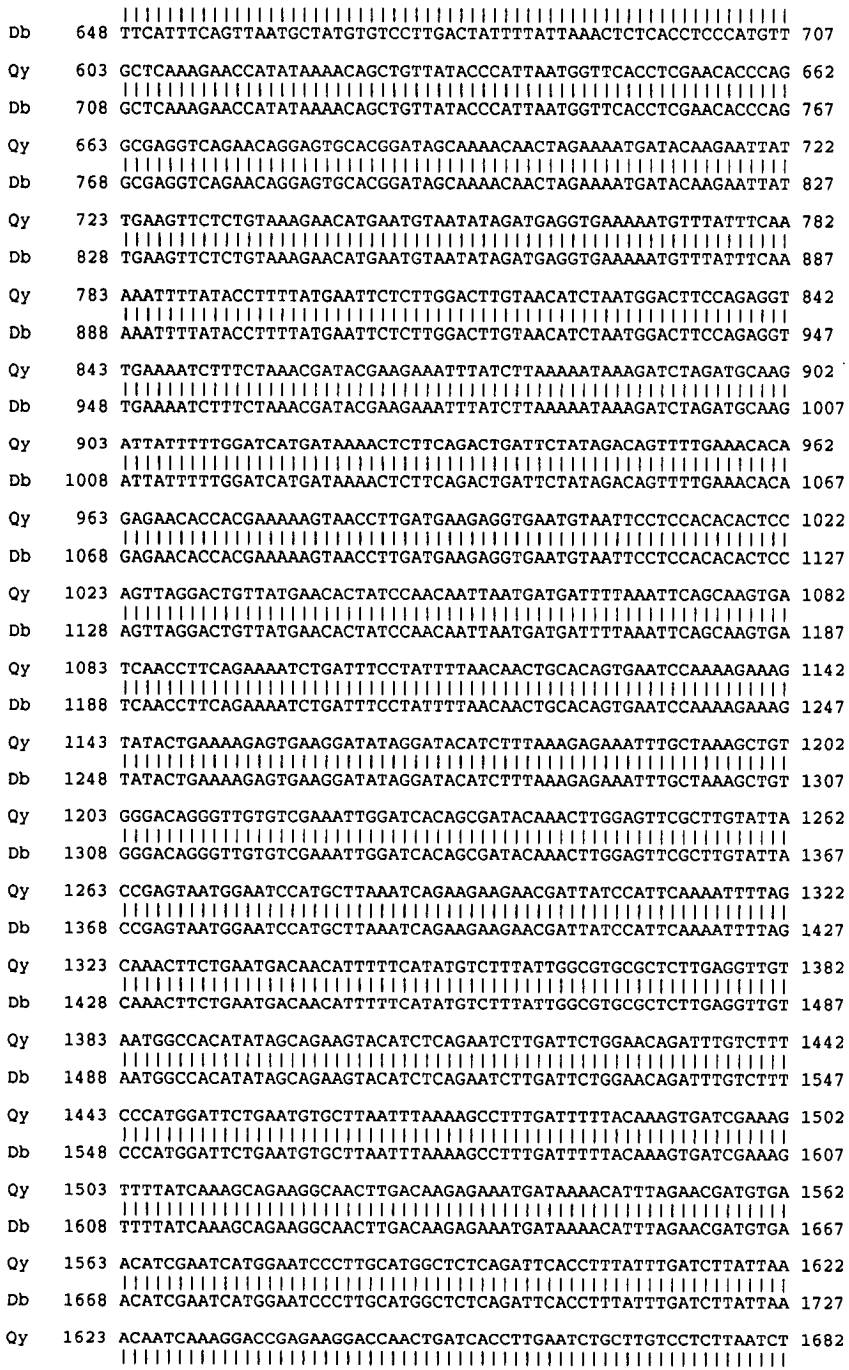
Qy     303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     408 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 467

Qy     363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     468 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 527

Qy     423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     528 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 587

Qy     483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     588 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 647

Qy     543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
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Db 648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 707
Qy 603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
Db 708 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 767
Qy 663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
Db 768 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 827
Qy 723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
Db 828 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 887
Qy 783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
Db 888 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 947
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Db 948 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1007
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Db 1008 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1067
Qy 963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
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Db 1128 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1187
Qy 1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
Db 1188 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1247
Qy 1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
Db 1248 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1307
Qy 1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
Db 1308 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1367
Qy 1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
Db 1368 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1427
Qy 1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
Db 1428 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1487
Qy 1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
Db 1488 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1547
Qy 1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
Db 1548 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1607
Qy 1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
Db 1608 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1667
Qy 1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
Db 1668 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1727
Qy 1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
Db 1728 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1787
Qy 1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
Db 1788 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1847
Qy 1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
Db 1848 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1907
Qy 1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
Db 1908 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1967
Qy 1863 GTATCGGCTAGCCTATGTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
Db 1968 GTATCGGCTAGCCTATGTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2027
Qy 1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
Db 2028 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2087
Qy 1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
Db 2088 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2147
Qy 2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
Db 2148 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2207
Qy 2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
Db 2208 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2267
Qy 2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
Db 2268 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2327
Qy 2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
Db 2328 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2387
Qy 2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
Db 2388 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2447
Qy 2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
Db 2448 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2507
Qy 2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
Db 2508 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2567
Qy 2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
Db 2568 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2627
Qy 2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
Db 2628 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2687
Qy 2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
Db 2688 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2747
Qy 2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
Db 2748 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2807
Qy 2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2762
Db 2808 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTT 2867

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Qy   2763 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2868 TCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATG 2927

Qy   2823 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2928 TGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTA 2987

Qy   2883 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 2942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2988 TACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCC 3047

Qy   2943 TCTTCCAAAGTAA 2955
          |||||||||||||
Db   3048 TCTTCCAAAGTAA 3060
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RESULT 8
N81369
ID N81369 standard; DNA; 4597 BP.
AC N81369;
DT 22-OCT-1990 (first entry)
DE Human retinoblastoma gene
KW Retinoblastoma; neoplasm; osteocarcoma; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 337. .2787
FT /*tag= a
PN EP-259031-A.
PD 09-MAR-1988.
PF 11-AUG-1987; 307095.
PR 11-AUG-1986; US-895163.
PA (MASS-) Massachusets Eye; (WHIT-) Whitehead Inst Biomed Re.
PI Dryja TP, Friend S;
DR WPI; 88-065827/10.
DR P-PSDB; P82112.
PT Diagnosis of retinoblastoma - using genetic material corresp. to a normal
PT human retinoblastoma gene or a unique sub-region
PS Disclosure; p; English.
CC This gene encodes a protein, the absence of which is associated with a
CC neoplasm. It is used to produce an antibody to the protein, contacting
CC this with the tumour sample and detecting immune complexes as indication
CC of the presence in the tumour sample of the protein. Whole sequence or
CC a unique sub-region can be used. The method identifies patients lacking
CC the defective retinoblastoma (Rb) allele and thus are not at risk of
CC developing the disease.
SQ Sequence 4597 BP; 1489 A; 839 C; 815 G; 1454 T;

Query Match 95.8%; Score 2832; DB 1; Length 4597;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2932; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy     22 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 81
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy     82 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 141
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    142 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 201
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTCATGTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    202 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 261
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    262 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 321
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    322 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    382 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 441
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    442 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 501
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy    502 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 561
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy    562 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 621
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy    622 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 681
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy    682 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy    742 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 801
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    802 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    862 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 921
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Qy    922 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy    982 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1041
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy   1042 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1101
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy   1102 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1161
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy   1162 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1221
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy   1222 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy   1282 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy   1342 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
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Qy   1402 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy   1462 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy   1522 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy   1582 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1642 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy   1702 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1762 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1821
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCGAGAAG 1920

Qy   1822 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1882 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 1941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   1942 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2002 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2062 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2122 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2182 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2242 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2302 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2362 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Qy   2422 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2482 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640

Qy   2542 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2602 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2662 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTGTGTACAC 2820

Qy   2722 CTCTGGATTCATTGTCTGTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CTCTGGATTCATTGTCTGTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGG 2880

Qy   2782 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAATTGTTTGG 2940

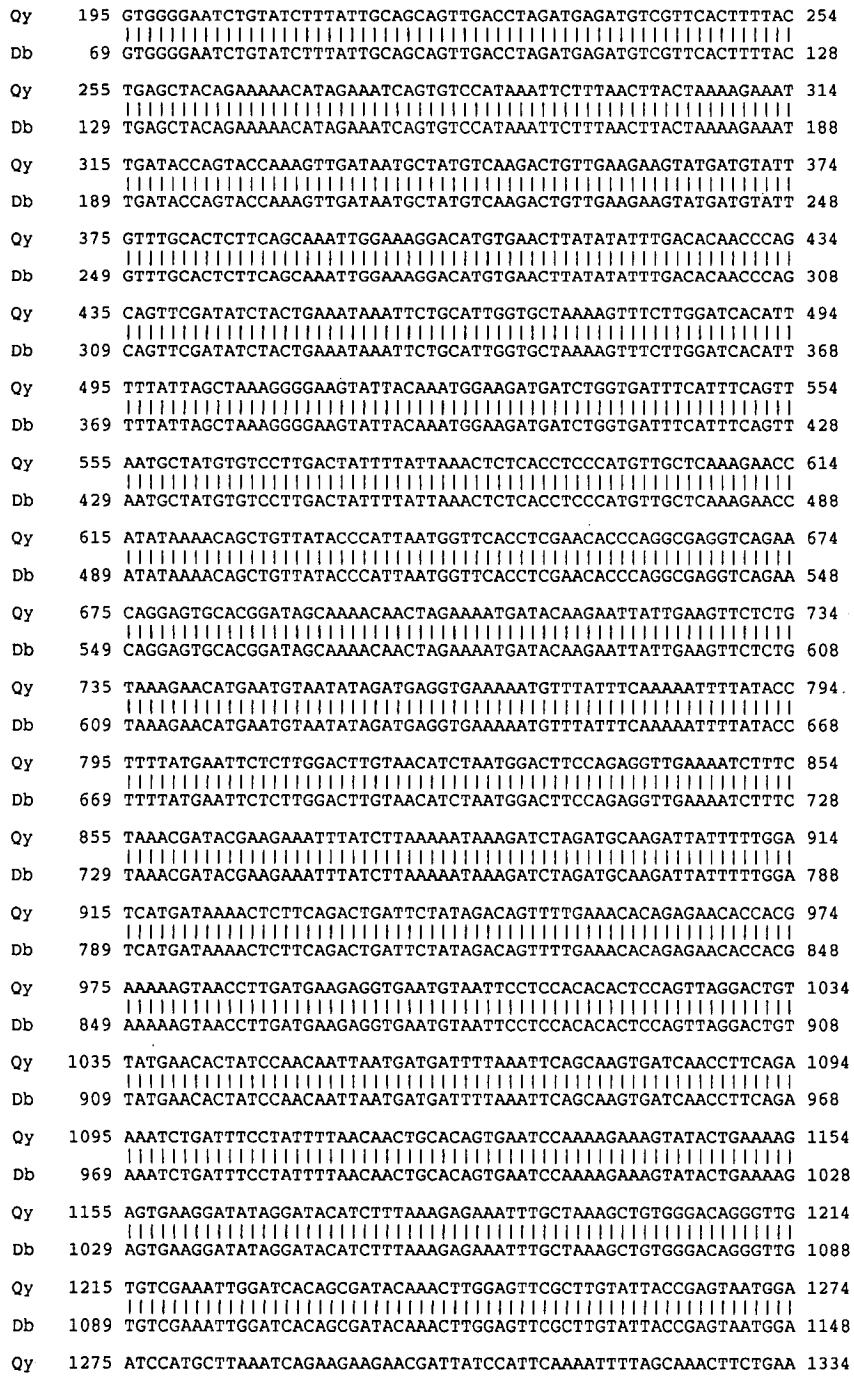
Qy   2842 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 2901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATCTTG 3000

Qy   2902 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTAA 3054
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RESULT 9
V58443
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

Query Match 95.5%; Score 2821; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2821; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    135 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 68
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Qy 195 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 254
Db 69 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 128
Qy 255 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 314
Db 129 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 188
Qy 315 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 374
Db 189 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 248
Qy 375 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 434
Db 249 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 308
Qy 435 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 494
Db 309 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 368
Qy 495 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 554
Db 369 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 428
Qy 555 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 614
Db 429 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 488
Qy 615 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 674
Db 489 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 548
Qy 675 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 734
Db 549 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 608
Qy 735 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 794
Db 609 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 668
Qy 795 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 854
Db 669 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 728
Qy 855 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 914
Db 729 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 788
Qy 915 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 974
Db 789 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 848
Qy 975 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1034
Db 849 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 908
Qy 1035 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1094
Db 909 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 968
Qy 1095 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1154
Db 969 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1028
Qy 1155 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1214
Db 1029 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1088
Qy 1215 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1274
Db 1089 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1148
Qy 1275 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1334
Db 1149 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1208
Qy 1335 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1394
Db 1209 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1268
Qy 1395 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1454
Db 1269 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1328
Qy 1455 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1514
Db 1329 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1388
Qy 1515 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1574
Db 1389 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1448
Qy 1575 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1634
Db 1449 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1508
Qy 1635 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1694
Db 1509 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1568
Qy 1695 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1754
Db 1569 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1628
Qy 1755 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1814
Db 1629 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1688
Qy 1815 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1874
Db 1689 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1748
Qy 1875 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1934
Db 1749 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1808
Qy 1935 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1994
Db 1809 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1868
Qy 1995 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2054
Db 1869 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1928
Qy 2055 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2114
Db 1929 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1988
Qy 2115 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2174
Db 1989 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2048
Qy 2175 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2234
Db 2049 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2108
Qy 2235 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2294
Db 2109 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2168
Qy 2295 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2354
Db 2169 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2228
Qy 2355 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2414

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Db    2229 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2288

Qy    2415 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2474
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2289 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2348

Qy    2475 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2534
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2349 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2408

Qy    2535 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2594
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2409 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2468

Qy    2595 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2654
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2469 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2528

Qy    2655 TAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTG 2714
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2529 TAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACACTG 2588

Qy    2715 TGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTG 2774
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2589 TGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTG 2648

Qy    2775 TTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAAT 2834
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2649 TTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAAT 2708

Qy    2835 TGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAA 2894
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2709 TGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAA 2768

Qy    2895 AATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTA 2954
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2769 AATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAGTA 2828

Qy    2955 A 2955
           |
Db    2829 A 2829
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RESULT  10
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
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SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;

  Query Match             93.5%;  Score 2763;  DB 1;  Length 3266;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2763;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     193 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 69

Qy     253 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      70 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 129

Qy     313 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 189

Qy     373 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 249

Qy     433 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 309

Qy     493 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     310 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 369

Qy     553 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     370 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 429

Qy     613 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     430 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 489

Qy     673 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     490 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 549

Qy     733 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     550 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 609

Qy     793 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     610 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 669

Qy     853 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     670 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 729

Qy     913 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     730 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 789

Qy     973 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     790 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 849

Qy    1033 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     850 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 909

Qy    1093 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     910 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 969

Qy    1153 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    970 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1029

Qy   1213 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1089

Qy   1273 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1149

Qy   1333 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1209

Qy   1393 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1269

Qy   1453 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1329

Qy   1513 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1389

Qy   1573 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1449

Qy   1633 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1509

Qy   1693 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1569

Qy   1753 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1629

Qy   1813 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1689

Qy   1873 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1749

Qy   1933 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1809

Qy   1993 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1869

Qy   2053 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1929

Qy   2113 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1989

Qy   2173 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2049

Qy   2233 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2109
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Qy   2293 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2169

Qy   2353 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2229

Qy   2413 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2289

Qy   2473 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2349

Qy   2533 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2409

Qy   2593 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2469

Qy   2653 GATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACAC 2712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 GATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTGGTGGACAC 2529

Qy   2713 TGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTC 2772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 TGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTC 2589

Qy   2773 TGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCA 2832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 TGTTTATGGCCACATTTAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCA 2649

Qy   2833 ATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTG 2892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 ATTGTTTGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTGTTATTTATACAAGATTG 2709

Qy   2893 AAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAG 2952
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 AAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAAG 2769

Qy   2953 TAA 2955
          |||
Db   2770 TAA 2772
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RESULT  11
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
```

PS Claim 35; Page 86; 105pp; English.
CC Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC By installing a working CSG, safe and specific treatment and
CC prophylaxis can be given to cancer patients.
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

Query Match 93.2%; Score 2755; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy     123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy     183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy     243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy     303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy     363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy     423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy     483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy     543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839

Qy     603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy     663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

Qy     723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

Qy     783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy     843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1139

Qy     903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

Qy     963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy    1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

Qy    1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy    1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy    1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy    1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy    1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy    1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1620 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

Qy    1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy    1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy    1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy    1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

Qy    1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1920 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy    1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy    1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy    1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy    1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy    1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279
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Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2399

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994
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RESULT  12
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;
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  Query Match           93.2%;  Score 2755;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2755;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy     63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy    303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy    363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy    423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy    483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy    543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839

Qy    603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy    663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

Qy    723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

Qy    783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy    843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1139

Qy    903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

Qy   1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099
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Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2399

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTGACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519

Qy   2283 TTCACCCTTACGGATTCGTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 TTCACCCTTACGGATTCGTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACAGCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 TGGTGGACACTGTGTACAGCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994
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RESULT 13
V40004
ID V40004 standard; DNA; 2994 BP.
AC V40004;
DT 15-FEB-1999 (first entry)
DE Retinoblastoma protein RB.
KW Retinoblastoma protein RB; E2F; transcription factor; human;
KW bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW thyroid hyperplasia; Grave's disease; psoriasis;
KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW peripheral vascular disease; therapy; ss.

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OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465). A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain. Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease. Tissue-specific expression of E2F-RB fusions is
CC   provided. The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;

  Query Match            93.2%;  Score 2755;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2755;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy     63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy    123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419

Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy    303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy    363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy    423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy    483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy    543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839

Qy    603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy    663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

Qy    723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

Qy    783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy    843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1139

Qy    903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

Qy   1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2399

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939
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Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2757
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2994


RESULT  14
X00737
ID   X00737 standard; cDNA; 2995 BP.
AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;


  Query Match           93.1%;  Score 2752;  DB 1;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2752;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 299

Qy      63 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 359

Qy     123 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 419
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Qy    183 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

Qy    243 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 539

Qy    303 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 599

Qy    363 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

Qy    423 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 719

Qy    483 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

Qy    543 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 839

Qy    603 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 899

Qy    663 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 959

Qy    723 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 1019

Qy    783 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

Qy    843 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1139

Qy    903 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1199

Qy    963 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

Qy   1023 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1319

Qy   1083 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

Qy   1143 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1439

Qy   1203 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1499

Qy   1263 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1559

Qy   1323 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1619

Qy   1383 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

Qy   1443 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1739

Qy   1503 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1799

Qy   1563 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

Qy   1623 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1919

Qy   1683 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

Qy   1743 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 2039

Qy   1803 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 2099

Qy   1863 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

Qy   1923 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2219

Qy   1983 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

Qy   2043 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2339

Qy   2103 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2399

Qy   2163 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2459

Qy   2223 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2519

Qy   2283 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

Qy   2343 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2402
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Db   2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2639

Qy   2403 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2699

Qy   2463 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2759

Qy   2523 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2819

Qy   2583 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2820 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

Qy   2643 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCT 2939

Qy   2703 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTG 2754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2940 TGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAGATGTGACTG 2991


RESULT  15
V58447
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


  Query Match           92.4%;  Score 2730;  DB 1;  Length 3461;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2730;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    226 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 297

Qy    286 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 357
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Qy    346 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 417

Qy    406 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 477

Qy    466 TTGGTGCTAAAAGTTTGTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 TTGGTGCTAAAAGTTTGTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 537

Qy    526 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 585
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 597

Qy    586 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 645
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 657

Qy    646 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 705
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    658 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 717

Qy    706 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 765
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 777

Qy    766 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 825
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 837

Qy    826 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 897

Qy    886 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 957

Qy    946 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1017

Qy   1006 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1077

Qy   1066 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1137

Qy   1126 GTGAATCCAAAAGAAAGTATAGTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1197

Qy   1186 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1257

Qy   1246 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1317

Qy   1306 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1377

Qy   1366 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1437

Qy   1426 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1485
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Db  1438 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1497

Qy  1486 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1545

Db  1498 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1557

Qy  1546 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1605

Db  1558 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1617

Qy  1606 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1665

Db  1618 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1677

Qy  1666 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1725

Db  1678 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1737

Qy  1726 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1785

Db  1738 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1797

Qy  1786 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1845

Db  1798 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1857

Qy  1846 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1905

Db  1858 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1917

Qy  1906 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1965

Db  1918 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1977

Qy  1966 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2025

Db  1978 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2037

Qy  2026 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2085

Db  2038 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2097

Qy  2086 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2145

Db  2098 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2157

Qy  2146 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2205

Db  2158 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2217

Qy  2206 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2265

Db  2218 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2277

Qy  2266 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2325

Db  2278 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2337

Qy  2326 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2385

Db  2338 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2397

Qy  2386 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2445

Db  2398 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2457

Qy  2446 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2505

Db  2458 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2517

Qy  2506 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2565

Db  2518 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2577

Qy  2566 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2625

Db  2578 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2637

Qy  2626 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2685

Db  2638 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2697

Qy  2686 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2745

Db  2698 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTCATTGTCTCTCACAG 2757

Qy  2746 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2805

Db  2758 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACATTTAATATCTTCAGCTCTT 2817

Qy  2806 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2865

Db  2818 TTTGTGGATATAAAATGTGCAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2877

Qy  2866 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2925

Db  2878 TTAGTCATTGTTATTTATACAAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGT 2937

Qy  2926 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2955

Db  2938 TGTAGCAGATTGTTTCCTCTTCCAAAGTAA 2967
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Search completed: February 13, 2000, 20:24:13
Job time: 11132 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:24:13 ; Search time 683.56 Seconds
(without alignments)
959.687 Million cell updates/sec

Title: US-09-026-459A-30_COPY_7_2628
Perfect score: 2622
Sequence: 1 ATGGATTTTACTGCATTATG.....CCTCAAACAAGGAAGAGAAA 2622

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2622	100.0	3392	1	V58442	Modified retinobla
2	2619	99.9	2994	1	Q04713	Cancer supressing
3	2619	99.9	2994	1	Q41545	Retinoblastoma gen
4	2619	99.9	3555	1	V58440	Modified retinobla
5	2619	99.9	3455	1	V58441	Modified retinobla
6	2619	99.9	3555	1	V54990	DNA sequence of th
7	2619	99.9	2994	1	V40004	Retinoblastoma pro
8	2619	99.9	2995	1	X00737	cDNA encoding a re
9	2568	97.9	4597	1	Q70536	Human retinoblasto
10	2568	97.9	2995	1	Q90059	Retinoblastoma tum
11	2568	97.9	4597	1	X04501	Human retinoblasto
12	2551	97.3	3323	1	V58443	Modified retinobla
13	2517	96.0	4597	1	N81369	Human retinoblasto
14	2517	96.0	3554	1	V58452	Modified retinobla
15	2493	95.1	3266	1	V58444	Modified retinobla
16	2460	93.8	3233	1	Q72690	Retinoblastoma 94k
17	2460	93.8	3461	1	V58447	Modified retinobla
18	2460	93.8	3323	1	V58446	Modified retinobla
19	2448	93.4	3218	1	V54991	DNA sequence of th
20	2415	92.1	2995	1	Q86398	Human Rb110 cDNA.
21	2343	89.4	3113	1	V58445	Modified retinobla
22	2242	85.5	3347	1	V58448	Modified retinobla
23	2062	78.6	3161	1	V58449	Modified retinobla
24	2061	78.6	3377	1	V58450	Modified retinobla
25	1885	71.9	3383	1	V58451	Modified retinobla
26	1548	59.0	5056	1	N90489	cDNA of human reti
27	1410	53.8	4579	1	N81261	Probe for retinobl
28	198	7.6	18303	1	X04502	Human retinoblasto
29	165	6.3	18177	1	N90490	DNA of human retin
c 30	26	1.0	26	1	V49234	rb gene antisense
c 31	26	1.0	26	1	V49235	rb gene antisense
32	24	0.9	24	1	V01247	Retinoblastoma 1 P
33	24	0.9	39	1	V58455	Primer OMRbSd2-55
34	24	0.9	39	1	V59923	Sense primer OMRbS
c 35	23	0.9	32	1	V58466	Primer for Modifie
c 36	23	0.9	32	1	V59932	PCR primer used to
37	22	0.8	52	1	Q27110	PCR primer for the
38	22	0.8	50	1	Q27131	5' PCR primer for
39	22	0.8	50	1	Q99012	Chelating peptide-
c 40	22	0.8	22	1	T11461	Retinoblastoma gen
c 41	22	0.8	22	1	T12860	PCR 3' primer for
c 42	22	0.8	22	1	V58453	Primer OMRbAS300 f
43	22	0.8	31	1	V58460	Primer for Modifie
44	22	0.8	31	1	V58464	Primer for Modifie
c 45	22	0.8	31	1	V58465	Primer for Modifie

ALIGNMENTS

RESULT 1
V58442
ID V58442 standard; DNA; 3392 BP.
AC V58442;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2641
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69366.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 150-155; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3392 BP; 1137 A; 614 C; 607 G; 1034 T;

Query Match 100.0%; Score 2622; DB 1; Length 3392;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 ATGGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCT 66

Qy      61 TGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 TGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAG 126

Qy     121 AAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 AAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCG 186

Qy     181 TTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTA 246

Qy     241 CTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 CTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAG 306

Qy     301 TATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 TATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTG 366

Qy     361 ACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCT 420
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Db    367 ACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCT 426

Qy    421 TGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATT 480

Db    427 TGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATT 486

Qy    481 TCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTG 540

Db    487 TCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTG 546

Qy    541 CTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGG 600

Db    547 CTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGG 606

Qy    601 CGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATT 660

Db    607 CGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATT 666

Qy    661 GAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAA 720

Db    667 GAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAA 726

Qy    721 AATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTT 780

Db    727 AATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTT 786

Qy    781 GAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGA 840

Db    787 GAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGA 846

Qy    841 TTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAG 900

Db    847 TTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAG 906

Qy    901 AGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCA 960

Db    907 AGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCA 966

Qy    961 GTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGAT 1020

Db    967 GTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGAT 1026

Qy   1021 CAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGT 1080

Db   1027 CAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGT 1086

Qy   1081 ATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTG 1140

Db   1087 ATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTG 1146

Qy   1141 GGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTAC 1200

Db   1147 GGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTAC 1206

Qy   1201 CGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGC 1260

Db   1207 CGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGC 1266

Qy   1261 AAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTA 1320

Db   1267 AAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTA 1326

Qy   1321 ATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTC 1380

Db   1327 ATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTC 1386

Qy   1381 CCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGT 1440

Db   1387 CCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGT 1446

Qy   1441 TTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAA 1500

Db   1447 TTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAA 1506

Qy   1501 CATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAA 1560

Db   1507 CATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAA 1566

Qy   1561 CAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTT 1620

Db   1567 CAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTT 1626

Qy   1621 CCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAG 1680

Db   1627 CCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAG 1686

Qy   1681 AAAAAAGGTTCAACTAGGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCA 1740

Db   1687 AAAAAAGGTTCAACTAGGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCA 1746

Qy   1741 GCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTG 1800

Db   1747 GCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTG 1806

Qy   1801 TATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCA 1860

Db   1807 TATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCA 1866

Qy   1861 GAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 1920

Db   1867 GAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTC 1926

Qy   1921 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTG 1980

Db   1927 ATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTG 1986

Qy   1981 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCT 2040

Db   1987 AAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCT 2046

Qy   2041 GTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTA 2100

Db   2047 GTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTA 2106

Qy   2101 TTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACC 2160

Db   2107 TTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACC 2166

Qy   2161 AGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGT 2220

Db   2167 AGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGT 2226

Qy   2221 TCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 2280

Db   2227 TCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAA 2286

Qy   2281 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCA 2340

Db   2287 ATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCA 2346

Qy   2341 ATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAAC 2400

Db   2347 ATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAAC 2406

Qy   2401 AGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAA 2460

Db   2407 AGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAA 2466

Qy   2461 CTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAG 2520

Db   2467 CTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAG 2526

Qy   2521 TCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAG 2580

Db   2527 TCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAG 2586
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Qy   2581 AAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          ||||||||||||||||||||||||||||||||||||||||||
Db   2587 AAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628


RESULT   2
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of California.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


  Query Match             99.9%;  Score 2619;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   3
Q41545
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ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


  Query Match           99.9%;  Score 2619;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
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Db    724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543

Db    784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603

Db    844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663

Db    904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723

Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783

Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843

Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903

Db   1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963

Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023

Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083

Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143

Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203

Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263

Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323

Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383

Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443

Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503

Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563

Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623

Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683

Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743

Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803

Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863

Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923

Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983

Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043

Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103

Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163

Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223

Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283

Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343

Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403

Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463

Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523

Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583

Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622

Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   4
V58440
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;

  Query Match             99.9%;  Score 2619;  DB 1;  Length 3555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 231

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 291

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 351

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 411

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 471

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 531

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 591

Qy     424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 651

Qy     484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     652 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 711

Qy     544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 771

Qy     604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 831

Qy     664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 891

Qy     724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     892 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 951

Qy     784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     952 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1011

Qy     844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1012 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1071

Qy     904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1072 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1131

Qy     964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1132 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1191

Qy    1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1192 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1251

Qy    1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1252 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1311

Qy    1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1312 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1371

Qy    1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1372 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1431

Qy    1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1432 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1491

Qy    1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1492 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1551

Qy    1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1552 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1611

Qy    1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1612 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1671

Qy    1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1672 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1731

Qy    1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1732 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1791
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Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1792 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1851

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1852 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1911

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1912 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1971

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1972 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2031

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2032 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2091

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2092 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2151

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2152 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2211

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2212 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2271

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2272 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2331

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2332 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2391

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2392 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2451

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2452 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2511

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2512 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2571

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2572 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2631

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2632 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2691

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2692 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2751

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2752 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT   5
V58441
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;
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  Query Match             99.9%;  Score 2619;  DB 1;  Length 3455;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 132

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 192

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 252

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 312

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 372

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 432

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 492

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 552

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 612

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    613 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 672
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Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    673 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 732

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    733 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 792

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    793 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 852

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    853 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 912

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    913 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 972

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    973 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1032

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1033 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1092

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1093 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1152

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1153 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1212

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1213 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1272

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1273 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1332

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1333 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1392

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1393 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1452

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1453 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1512

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1513 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1572

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1573 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1632

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1633 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1692

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1693 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1752

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1753 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1812

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1813 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1872

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1873 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1932

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1933 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1992

Qy   1924 AGAGACAGGCATTTGGAGCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1993 AGAGACAGGCATTTGGAGCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2052

Qy   1984 AATATAGACCTTAAATTGAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2053 AATATAGACCTTAAATTGAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2112

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2113 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2172

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2173 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2232

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2233 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2292

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2293 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2352

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2353 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2412

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2413 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2472

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2473 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2532

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2533 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2592

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2593 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2652

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2653 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691


RESULT   6
V54990
ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
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KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;

  Query Match             99.9%;  Score 2619;  DB 1;  Length 3555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 231

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 291

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 351

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 411

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 471

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 531

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 591

Qy     424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 651

Qy     484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 711

Qy     544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 771

Qy     604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 831

Qy     664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 891

Qy     724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     892 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 951

Qy     784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     952 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1011

Qy     844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1012 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1071

Qy     904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1072 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1131

Qy     964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1132 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1191

Qy    1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1192 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1251

Qy    1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1252 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1311

Qy    1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1312 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1371

Qy    1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1372 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1431

Qy    1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1432 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1491

Qy    1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1492 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1551

Qy    1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1552 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1611

Qy    1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1612 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1671

Qy    1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1672 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1731

Qy    1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1732 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1791
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Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1792 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1851

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1852 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1911

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1912 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1971

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1972 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2031

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2032 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2091

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2092 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2151

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2152 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2211

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2212 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2271

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2272 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2331

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2332 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2391

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2392 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2451

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2452 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2511

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2512 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2571

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2572 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2631

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2632 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2691

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2692 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2751

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2752 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT   7
V40004
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;   974 A;    618 C;    593 G;    809 T;
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  Query Match           99.9%;  Score 2619;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883
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Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   8
X00737
ID   X00737 standard; cDNA; 2995 BP.
AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;


  Query Match             99.9%;  Score 2619;  DB 1;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2619;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
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Db    544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1144 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
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Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
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Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          ||||||||||||||||||||||||||||||||||||||
Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   9
Q70536
ID   Q70536 standard; DNA; 4597 BP.
AC   Q70536;
DT   27-MAR-1995  (first entry)
DE   Human retinoblastoma gene.
KW   Retinoblastoma; cancer; detection; diagnosis; protein; neoplasm;
KW   assay; immune complex; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             337. .2787
FT                   /*tag=  a
PN   EP-608004-A.
PD   27-JUL-1994.
PF   11-AUG-1987; 307095.
PR   11-AUG-1986; US-895163.
PA   (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA   (WHED ) WHITEHEAD INST.
PA   BIOMEDICAL RES.
PI   Dryja TP,  Friend S;
DR   WPI; 94-272746/34.
DR   P-PSDB; R58568.
PT   Diagnosing the presence of defective retinoblastoma alleles -
PT   comprises comparing genetic material corresponding to a normal
PT   human retinoblastoma with DNA from a patient.
PS   Example 2(2); Figure 7; 18pp; English.
CC   A method for detecting the presence, in a tumour sample, of a protein
CC   the absence of which is associated with a neoplasm, comprises
CC   producing an antibody to the protein and then contacting the
CC   antibody with the tumour sample.  Immune complexes indicate the
CC   presence of the protein in the sample.  The method may be used in
CC   the detection and treatment of a defective human gene related to
CC   cancer, in particular retinoblastoma.
SQ   Sequence   4597 BP;    1489 A;    841 C;    812 G;    1455 T;
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  Query Match             97.9%;  Score 2568;  DB 1;  Length 4597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2618;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     166 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 225

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     226 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 285

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     286 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 345

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    346 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 405

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 465

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 525

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 585

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 645

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 705

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 765

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 825

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 885

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 945

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1005

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 TTTTTTGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1125

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1185

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1245

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1305

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1365

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1425

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1485

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1545

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1605

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1665

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1725

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1785

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1845

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1905

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1965

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1966 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2025

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2085

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2145

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2205

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2265

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2325

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2385

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2445

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2505

Qy   2344 GGTGAATCATTCGGGACTTCTCAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2506 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2565
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Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2625

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2685

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2745

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||
Db   2746 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784


RESULT 10
Q90059
ID   Q90059 standard; DNA; 2995 BP.
AC   Q90059;
DT   28-NOV-1995 (first entry)
DE   Retinoblastoma tumour suppressor gene.
KW   Recombinant; adenovirus; expression vector; TSG; small lung cancer;
KW   hepatocarcinoma; melanoma; retinoblastoma; sarcoma; sickle cell;
KW   anaemia; Tay-Sach's disease; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
PN   WO9511984-A.
PD   04-MAY-1995.
PF   25-OCT-1994; U12235.
PR   25-OCT-1993; US-142669.
PR   19-MAY-1994; US-246007.
PA   (CANJ-) CANJI INC.
PI   Gregory RJ, Maneval DC, Wills KN;
DR   WPI; 95-178876/23.
DR   P-PSDB; R74271.
PT   Adenoviral vector with deletion of viral protein IX contains
PT   foreign gene - esp. encoding tumour suppressor protein for gene
PT   therapy of tumours, reduces contamination by wild type adenovirus
PS   Disclosure; Fig 3; 92pp; English.
CC   The sequence is that of the DNA sequence encoding a retinoblastoma
CC   tumour protein. The gene can be used in a novel method involving a
CC   recombinant adenovirus expression vector to treat diseases
CC   associated with the ansence of the TSg or the presence of a mutated
CC   TSG, e.g. many forms of carcinoma, sickle cell anaemia or Tay-Sach's
CC   disease.
CC   See also Q90060-5.
SQ   Sequence   2995 BP;    975 A;    617 C;    594 G;    809 T;


  Query Match            97.9%;  Score 2568;  DB 1;  Length 2995;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2618;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 363

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 423

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 483

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 543

Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 663

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 723

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 783

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 843

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 963

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    964 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 1023

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1024 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 1083

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1084 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1143

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1144 TTTTTGGATCATGATAAAACTCTTCAGAGTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1263

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1264 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1323

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1324 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1383

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1384 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1443

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1444 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1503

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1504 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1563

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1564 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1623

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
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Db   1624 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1683

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443

Db   1684 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1743

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503

Db   1744 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563

Db   1804 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1863

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623

Db   1864 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1923

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683

Db   1924 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1983

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743

Db   1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 2043

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803

Db   2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 2103

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863

Db   2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2163

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923

Db   2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2223

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983

Db   2224 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2283

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043

Db   2284 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2343

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103

Db   2344 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2403

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163

Db   2404 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2463

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223

Db   2464 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2523

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283

Db   2524 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2583

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343

Db   2584 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2643

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403

Db   2644 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2703

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463

Db   2704 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2763

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523

Db   2764 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2823

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583

Db   2824 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2883

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622

Db   2884 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 11
X04501
ID X04501 standard; cDNA; 4597 BP.
AC X04501;
DT 05-JUL-1999 (first entry)
DE Human retinoblastoma gene cDNA.
KW Retinoblastoma; Rb gene; human; predisposition; diagnosis; therapy;
KW ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 337. .2787
FT /*tag= a
FT /transl_except= (pos:2632. .2634, aa:Asp)
PN US5853988-A.
PD 29-DEC-1998.
PF 08-OCT-1992; 958290.
PR 08-JUL-1991; US-728756.
PR 11-AUG-1986; US-895163.
PR 21-JAN-1988; US-146525.
PR 23-JAN-1989; US-300667.
PR 25-SEP-1992; US-951342.
PR 08-OCT-1992; US-958290.
PA (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA (WHED) WHITEHEAD INST.
PI Dryja TP, Friend S, Yandell DW;
DR WPI; 99-094898/08.
DR P-PSDB; Y01542.
PT Isolated human retinoblastoma gene - used to develop products for
PT analysing predisposition to retinoblastoma and for the detection and
PT treatment of retinoblastoma
PS Claim 8; Fig 5; 32pp; English.
CC This is the nucleic acid sequence of a cDNA of the normal human
CC retinoblastoma gene Rb. Absence or mutation of the Rb gene (see
CC also X04502) predisposes an individual to retinoblastoma. To
CC isolate Rb cDNA, the human DNA probe pH3-8, isolated from a human
CC chromosome 13 lambda phage library, was used in a chromosome walk
CC to isolate and map 30 kb of genomic DNA surrounding the H3-8
CC sequence. Fragment p7H30.7R (ATCC 97500) was obtained, and was
CC used as a probe to screen a cDNA library that had been constructed
CC from an adenovirus 12-transformed human embryonic retinal cell
CC line. This provided clone p4.7R (ATCC 97383), which in Northern
CC blots cross-reacted with a 4.7 kb transcript in transformed
CC retinal cells which was not present in 4 retinoblastoma and one
CC osteosarcoma cell samples. Rb nucleic acids comprising the Rb
CC gene, cDNA or a fragment of the gene, such as one of the 27 exons
CC or 26 introns, can be used in a claimed method for detecting a
CC deletion or point mutation in the Rb gene of a human patient. The
CC gene can also be used to synthesize Rb polypeptide (see Y01542) for
CC use in the treatment of individuals determined to have a defective
CC Rb allele.
SQ Sequence 4597 BP; 1489 A; 841 C; 813 G; 1454 T;

Query Match 97.9%; Score 2568; DB 1; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2618; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
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Db    166 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 225
Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
Db    226 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 285
Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
Db    286 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 345
Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
Db    346 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 405
Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
Db    406 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 465
Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
Db    466 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 525
Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
Db    526 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 585
Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
Db    586 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 645
Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
Db    646 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 705
Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
Db    706 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 765
Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
Db    766 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 825
Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
Db    826 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 885
Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
Db    886 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 945
Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
Db    946 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1005
Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
Db   1006 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065
Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
Db   1066 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1125
Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
Db   1126 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1185
Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
Db   1186 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1245
Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
Db   1246 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1305
Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
Db   1306 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1365
Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
Db   1366 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1425
Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
Db   1426 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1485
Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
Db   1486 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1545
Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
Db   1546 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1605
Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
Db   1606 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1665
Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
Db   1666 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1725
Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
Db   1726 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1785
Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
Db   1786 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1845
Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
Db   1846 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1905
Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
Db   1906 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1965
Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
Db   1966 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2025
Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
Db   2026 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2085
Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
Db   2086 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2145
Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
Db   2146 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2205
Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
Db   2206 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2265
Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
Db   2266 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2325
Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
Db   2326 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2385
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Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2445

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2505

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2506 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2565

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2625

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CGCTTTCATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2685

Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2745

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2746 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT 12
V58443
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

Query Match 97.3%; Score 2551; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     72 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 68

Qy    132 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 128

Qy    192 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 188

Qy    252 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 248

Qy    312 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 308

Qy    372 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 368

Qy    432 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 428

Qy    492 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 488

Qy    552 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 548

Qy    612 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 608

Qy    672 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 668

Qy    732 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 728

Qy    792 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 788

Qy    852 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 848

Qy    912 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 908

Qy    972 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 968

Qy   1032 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1028

Qy   1092 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1088

Qy   1152 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1148

Qy   1212 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1208
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Qy   1272 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1331
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Db   1209 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1268

Qy   1332 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1328

Qy   1392 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1388

Qy   1452 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1448

Qy   1512 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1508

Qy   1572 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1568

Qy   1632 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1628

Qy   1692 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1688

Qy   1752 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1748

Qy   1812 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1808

Qy   1872 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1931
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1868

Qy   1932 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1928

Qy   1992 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2051
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1988

Qy   2052 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2111
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Db   1989 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2048

Qy   2112 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2108

Qy   2172 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2168

Qy   2232 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2228

Qy   2292 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2288

Qy   2352 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2348

Qy   2412 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2408

Qy   2472 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2468

Qy   2532 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2528

Qy   2592 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||
Db   2529 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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RESULT 13
N81369
ID N81369 standard; DNA; 4597 BP.
AC N81369;
DT 22-OCT-1990 (first entry)
DE Human retinoblastoma gene
KW Retinoblastoma; neoplasm; osteocarcoma; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 337. .2787
FT /*tag= a
PN EP-259031-A.
PD 09-MAR-1988.
PF 11-AUG-1987; 307095.
PR 11-AUG-1986; US-895163.
PA (MASS-) Massachusets Eye; (WHIT-) Whitehead Inst Biomed Re.
PI Dryja TP, Friend S;
DR WPI; 88-065827/10.
DR P-PSDB; P82112.
PT Diagnosis of retinoblastoma - using genetic material corresp. to a normal
PT human retinoblastoma gene or a unique sub-region
PS Disclosure; p; English.
CC This gene encodes a protein, the absence of which is associated with a
CC neoplasm. It is used to produce an antibody to the protein, contacting
CC this with the tumour sample and detecting immune complexes as indication
CC of the presence in the tumour sample of the protein. Whole sequence or
CC a unique sub-region can be used. The method identifies patients lacking
CC the defective retinoblastoma (Rb) allele and thus are not at risk of
CC developing the disease.
SQ Sequence 4597 BP; 1489 A; 839 C; 815 G; 1454 T;

Query Match 96.0%; Score 2517; DB 1; Length 4597;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2617; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 225

Qy     64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    226 TTAACTTGGGAGAAAGTTTCATGTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 285

Qy    124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 345

Qy    184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 405
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Qy    244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 465

Qy    304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 525

Qy    364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 585

Qy    424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 645

Qy    484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 705

Qy    544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
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Db    706 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 765

Qy    604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 825

Qy    664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 885

Qy    724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 945

Qy    784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1005

Qy    844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065

Qy    904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1125

Qy    964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1185

Qy   1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1245

Qy   1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1305

Qy   1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1365

Qy   1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1425

Qy   1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1485

Qy   1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1545

Qy   1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1605

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1665

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1725

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1785

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1845

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1905

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 TTCCAGACCGAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1965

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1966 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2025

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2085

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2145

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2205

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2265

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2325

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2385

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2445

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2505

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2506 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2565

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2566 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2625

Qy    2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2626 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2685

Qy    2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2686 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2745

Qy    2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
           |||||||||||||||||||||||||||||||||||||||
Db    2746 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784


RESULT  14
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


  Query Match            96.0%;  Score 2517;  DB 1;  Length 3554;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2617;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 63
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 231

Qy      64 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 291

Qy     124 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 183
           |||||||||||||||||||||||||||||||||||||||||||| ||| |||||||||
Db     292 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTC 351

Qy     184 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 411

Qy     244 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 303
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 471

Qy     304 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 531

Qy     364 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 423
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 591

Qy     424 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 483
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 651

Qy     484 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 543
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 711

Qy     544 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 603
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 771

Qy     604 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 663
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 831

Qy     664 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 723
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 891

Qy     724 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 783
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     892 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 951

Qy     784 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 843
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     952 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1011

Qy     844 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 903
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1012 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1071

Qy     904 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 963
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1072 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1131

Qy     964 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1023
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1132 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1191

Qy    1024 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1083
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1192 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1251

Qy    1084 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1143
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1252 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1311

Qy    1144 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1312 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1371

Qy    1204 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1263
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1372 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1431

Qy    1264 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1323
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1432 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1491

Qy    1324 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1492 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1551

Qy    1384 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1552 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1611

Qy   1444 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1612 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1671

Qy   1504 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1672 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1731

Qy   1564 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1732 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1791

Qy   1624 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1792 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1851

Qy   1684 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1852 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1911

Qy   1744 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1912 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1971

Qy   1804 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1972 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2031

Qy   1864 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2032 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2091

Qy   1924 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2092 AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2151

Qy   1984 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2152 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2211

Qy   2044 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2212 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2271

Qy   2104 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2272 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2331

Qy   2164 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2332 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2391

Qy   2224 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2392 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2451

Qy   2284 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2452 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2511

Qy   2344 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2512 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2571

Qy   2404 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2572 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2631

Qy   2464 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2632 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2691
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Qy   2524 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2692 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2751

Qy   2584 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          |||||||||||||||||||||||||||||||||||||||
Db   2752 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790


RESULT  15
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;  1092 A;   602 C;   574 G;   998 T;


  Query Match           95.1%;  Score 2493;  DB 1;  Length 3266;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    130 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 69

Qy    190 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 129

Qy    250 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 189

Qy    310 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 249

Qy    370 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 309

Qy    430 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 369

Qy    490 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    370 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 429

Qy    550 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 489

Qy    610 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 549

Qy    670 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 609

Qy    730 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 669

Qy    790 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 729

Qy    850 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 789

Qy    910 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 849

Qy    970 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 909

Qy   1030 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 969

Qy   1090 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1029

Qy   1150 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1089

Qy   1210 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1149

Qy   1270 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1209

Qy   1330 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1269

Qy   1390 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1329

Qy   1450 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1389

Qy   1510 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1449

Qy   1570 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1509

Qy   1630 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1569

Qy   1690 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1629

Qy   1750 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1689

Qy   1810 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1749

Qy   1870 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1929
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Db   1750 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1809

Qy   1930 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1869

Qy   1990 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1929

Qy   2050 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1989

Qy   2110 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2049

Qy   2170 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2109

Qy   2230 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2169

Qy   2290 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2229

Qy   2350 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2289

Qy   2410 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2349

Qy   2470 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2409

Qy   2530 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2469

Qy   2590 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2622
          ||||||||||||||||||||||||||||||||
Db   2470 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2502
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Search completed: February 13, 2000, 20:26:46
Job time: 11285 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:26:46 ; Search time 683.56 Seconds
(without alignments)
934.432 Million cell updates/sec

Title: US-09-026-459A-32_COPY_7_2559
Perfect score: 2553
Sequence: 1 ATGGAGAAAGTTTCATCTGT.....CCTCAAACAAGGAAGAGAAA 2553

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2553	100.0	3323	1	V58443	Modified retinobla
	2	2551	99.9	2994	1	Q04713	Cancer supressing
	3	2551	99.9	2994	1	Q41545	Retinoblastoma gen
	4	2551	99.9	3555	1	V58440	Modified retinobla
	5	2551	99.9	3455	1	V58441	Modified retinobla
	6	2551	99.9	3392	1	V58442	Modified retinobla
	7	2551	99.9	3555	1	V54990	DNA sequence of th
	8	2551	99.9	2994	1	V40004	Retinoblastoma pro
	9	2551	99.9	2995	1	X00737	cDNA encoding a re
	10	2500	97.9	4597	1	Q70536	Human retinoblasto
	11	2500	97.9	2995	1	Q90059	Retinoblastoma tum
	12	2500	97.9	4597	1	X04501	Human retinoblasto
	13	2493	97.6	3266	1	V58444	Modified retinobla
	14	2485	97.3	4597	1	N81369	Human retinoblasto
	15	2460	96.4	3233	1	Q72690	Retinoblastoma 94k
	16	2460	96.4	3461	1	V58447	Modified retinobla
	17	2460	96.4	3323	1	V58446	Modified retinobla
	18	2449	95.9	3554	1	V58452	Modified retinobla
	19	2448	95.9	3218	1	V54991	DNA sequence of th
	20	2347	91.9	2995	1	Q86398	Human Rb110 cDNA.
	21	2343	91.8	3113	1	V58445	Modified retinobla
	22	2242	87.8	3347	1	V58448	Modified retinobla
	23	2062	80.8	3161	1	V58449	Modified retinobla
	24	2061	80.7	3377	1	V58450	Modified retinobla
	25	1885	73.8	3383	1	V58451	Modified retinobla
	26	1548	60.6	5056	1	N90489	cDNA of human reti
	27	1410	55.2	4579	1	N81261	Probe for retinobl
	28	198	7.8	18303	1	X04502	Human retinoblasto
	29	165	6.5	18177	1	N90490	DNA of human retin
c	30	26	1.0	26	1	V49234	rb gene antisense
c	31	26	1.0	26	1	V49235	rb gene antisense
	32	24	0.9	24	1	V01247	Retinoblastoma 1 P
c	33	23	0.9	32	1	V58466	Primer for Modifie
c	34	23	0.9	32	1	V59932	PCR primer used to
	35	22	0.9	52	1	Q27110	PCR primer for the
	36	22	0.9	50	1	Q27131	5' PCR primer for
	37	22	0.9	50	1	Q99012	Chelating peptide-
c	38	22	0.9	22	1	T11461	Retinoblastoma gen
c	39	22	0.9	22	1	T12860	PCR 3' primer for
c	40	22	0.9	22	1	V58453	Primer OMRbAS300 f
	41	22	0.9	31	1	V58460	Primer for Modifie
	42	22	0.9	31	1	V58464	Primer for Modifie
c	43	22	0.9	31	1	V58465	Primer for Modifie
c	44	22	0.9	22	1	V55002	Antisense PCR prim
	45	22	0.9	31	1	V59928	Sense primer used

ALIGNMENTS

RESULT 1
V58443
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

Query Match 100.0%; Score 2553; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 ATGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAA 66

Qy      61 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 126

Qy     121 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 186

Qy     181 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 246

Qy     241 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 306

Qy     301 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 366

Qy     361 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 420
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Db    367 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 426

Qy    421 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 480

Db    427 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 486

Qy    481 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 540

Db    487 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 546

Qy    541 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 600

Db    547 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 606

Qy    601 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 660

Db    607 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 666

Qy    661 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 720

Db    667 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 726

Qy    721 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 780

Db    727 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 786

Qy    781 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 840

Db    787 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 846

Qy    841 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 900

Db    847 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 906

Qy    901 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 960

Db    907 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 966

Qy    961 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1020

Db    967 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1026

Qy   1021 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1080

Db   1027 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1086

Qy   1081 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1140

Db   1087 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1146

Qy   1141 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1200

Db   1147 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1206

Qy   1201 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1260

Db   1207 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1266

Qy   1261 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1320

Db   1267 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1326

Qy   1321 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1380

Db   1327 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1386

Qy   1381 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1440

Db   1387 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1446

Qy   1441 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1500

Db   1447 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1506

Qy   1501 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1560

Db   1507 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1566

Qy   1561 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1620

Db   1567 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1626

Qy   1621 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1680

Db   1627 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1686

Qy   1681 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1740

Db   1687 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1746

Qy   1741 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1800

Db   1747 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1806

Qy   1801 CATATCATCTGGACCCTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1860

Db   1807 CATATCATCTGGACCCTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1866

Qy   1861 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1920

Db   1867 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1926

Qy   1921 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1980

Db   1927 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1986

Qy   1981 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2040

Db   1987 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2046

Qy   2041 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2100

Db   2047 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2106

Qy   2101 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2160

Db   2107 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2166

Qy   2161 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2220

Db   2167 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2226

Qy   2221 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2280

Db   2227 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2286

Qy   2281 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2340

Db   2287 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2346

Qy   2341 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2400

Db   2347 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2406

Qy   2401 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2460

Db   2407 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2466

Qy   2461 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2520

Db   2467 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2526

Qy   2521 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553

Db   2527 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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RESULT   2
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a .
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;

  Query Match             99.9%;  Score 2551;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 431

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 491

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 611

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 851

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 971

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 1091

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1151

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1271

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1451

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1871

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1872 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2052 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2171

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2291

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2292 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2351

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2471

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2472 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2771

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   3
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.

OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


  Query Match             99.9%;  Score 2551;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 431

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 491

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 611

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 851

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
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Db    912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 971

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662

Db    972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722

Db   1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 1091

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782

Db   1092 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1151

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842

Db   1152 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902

Db   1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1271

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962

Db   1272 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022

Db   1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082

Db   1392 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1451

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142

Db   1452 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202

Db   1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262

Db   1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322

Db   1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382

Db   1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442

Db   1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502

Db   1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1871

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562

Db   1872 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622

Db   1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682

Db   1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742

Db   2052 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802

Db   2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2171

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862

Db   2172 TATCATCTGGACCCTTTTCCABCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922

Db   2232 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2291

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982

Db   2292 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2351

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042

Db   2352 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102

Db   2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2471

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162

Db   2472 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222

Db   2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282

Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342

Db   2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402

Db   2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2771

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462

Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522

Db   2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553

Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 4
V58440
ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers

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FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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  Query Match             99.9%;  Score 2551;  DB 1;  Length 3555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 299

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 359

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 419

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 479

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 539

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 599

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 659

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 719

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 779

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 839

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 899

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    900 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 959

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1019

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1079

Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1139

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1199

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1259

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1319

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1379

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1439

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1499

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1559

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1619

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1679

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1739

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1799

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1859

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1919

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1979

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2039
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Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2099

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2159

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2219

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2279

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2339

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2399

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2459

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2519

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2579

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2639

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2699

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2759

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2760 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT   5
V58441
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;
```

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  Query Match             99.9%;  Score 2551;  DB 1;  Length 3455;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 200

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 260

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 320

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 380

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 440

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 500

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 560

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 620

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 680

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 740

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 800

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 860

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 920

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 980
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Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1040

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1100

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1160

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1220

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1280

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1340

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1400

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1460

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1520

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1580

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1640

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1700

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1760

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1820

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1880

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1940

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2000

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2060

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2120

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2180

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2240

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2300

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2360

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2420

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2480

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2540

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2600

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2660

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2661 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
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RESULT   6
V58442
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
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CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;

  Query Match            99.9%;  Score 2551;  DB 1;  Length 3392;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 137

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 197

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 257

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 317

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 377

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 437

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 497

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    498 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 557

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 617

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 677

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 737

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 797

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 857

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 917

Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 977

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1037

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1097

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1157

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1217

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1277

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1337

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1397

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1457

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1517

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1577

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1637

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1697

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1757

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1817

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1877

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1937

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1997

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2057

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2117

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
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Db    2118 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2177

Qy    2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
Db    2178 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2237

Qy    2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
Db    2238 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2297

Qy    2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
Db    2298 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2357

Qy    2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
Db    2358 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2417

Qy    2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
Db    2418 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2477

Qy    2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
Db    2478 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2537

Qy    2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
Db    2538 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2597

Qy    2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
Db    2598 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2628
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RESULT   7
V54990
ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


  Query Match            99.9%;  Score 2551;  DB 1;  Length 3555;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
Db     240 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 299

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
Db     300 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 359

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
Db     360 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 419

Qy     183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
Db     420 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 479

Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
Db     480 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 539

Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
Db     540 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 599

Qy     363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
Db     600 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 659

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACG 482
Db     660 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 719

Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
Db     720 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 779

Qy     543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
Db     780 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 839

Qy     603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
Db     840 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 899

Qy     663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
Db     900 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 959

Qy     723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
Db     960 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1019

Qy     783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
Db    1020 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1079

Qy     843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
Db    1080 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1139

Qy     903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
Db    1140 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1199
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Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1259

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1319

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1379

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1380 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1439

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1440 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1499

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1500 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1559

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1560 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1619

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1620 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1679

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1739

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1799

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1859

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1919

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1979

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2039

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2099

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2159

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2219

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2279

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2339

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2399

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2459

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2519

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2579

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2639

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2699

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2759

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2760 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT 8
V40004
ID V40004 standard; DNA; 2994 BP.
AC V40004;
DT 15-FEB-1999 (first entry)
DE Retinoblastoma protein RB.
KW Retinoblastoma protein RB; E2F; transcription factor; human;
KW bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW thyroid hyperplasia; Grave's disease; psoriasis;
KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW peripheral vascular disease; therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 139. .2925
FT /*tag= a
PN WO9821228-A1.
PD 22-MAY-1998.
PF 13-NOV-1997; U21821.
PR 14-FEB-1997; US-801092.
PR 15-NOV-1996; US-751517.
PA (CANJ-) CANJI INC.
PI Antelman D, Gregory RJ, Wills KN;
DR WPI; 98-297858/26.
DR P-PSDB; W62465.
PT New fusion polypeptide of, e.g. transcription factor - used to
PT treat, e.g. hyper-proliferative disease such as cancer and
PT restenosis
PS Example 1; Fig 2A; 91pp; English.
CC This nucleotide sequence includes a coding region for retinoblastoma
CC protein RB (see W62465). A new claimed polypeptide is a fusion of:
CC (i) a transcription factor (TF) comprising a DNA binding domain,
CC and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC suppression domain. Also new are: (1) a nucleic acid encoding the
CC fusion protein, and (2) expression vectors containing such DNA.
CC The fusion protein, particularly expressed from gene therapy
CC vectors (especially adenovirus vectors), is used to treat
CC hyperproliferative conditions, specifically cancer (particularly of

CC the bladder) or restenosis (after angioplasty), but also diabetic
CC retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC vascular disease. Tissue-specific expression of E2F-RB fusions is
CC provided. The fusion proteins are more effective in repressing
CC transcription of the E2F promoter than Rb alone and cause cell-cycle
CC arrest in a variety of cells.
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

Query Match 99.9%; Score 2551; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 431

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     432 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 491

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy     183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     552 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 611

Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy     363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     792 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 851

Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy     543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 971

Qy     603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

Qy     663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 1091

Qy     723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1092 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1151

Qy     783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1152 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

Qy     843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1271

Qy     903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1272 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

Qy     963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

Qy    1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1392 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1451

Qy    1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1452 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

Qy    1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy    1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy    1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy    1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy    1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

Qy    1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1871

Qy    1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1872 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

Qy    1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy    1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy    1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2052 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

Qy    1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2171

Qy    1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2172 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

Qy    1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2232 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2291

Qy    1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2292 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2351
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Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2471

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2472 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2771

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   9
X00737
ID   X00737 standard; cDNA; 2995 BP.
AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag=  a
FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;


  Query Match             99.9%;  Score 2551;  DB 1;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 431

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 491

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 611

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 851

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 971

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 1091

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
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Db   1092 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1151

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842

Db   1152 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902

Db   1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1271

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962

Db   1272 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022

Db   1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082

Db   1392 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1451

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142

Db   1452 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202

Db   1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262

Db   1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322

Db   1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382

Db   1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442

Db   1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502

Db   1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1871

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562

Db   1872 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622

Db   1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682

Db   1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742

Db   2052 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802

Db   2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2171

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862

Db   2172 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922

Db   2232 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2291

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982

Db   2292 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2351

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042

Db   2352 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102

Db   2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2471

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162

Db   2472 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222

Db   2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282

Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342

Db   2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402

Db   2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2771

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462

Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522

Db   2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553

Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT  10
Q70536
ID   Q70536 standard; DNA; 4597 BP.
AC   Q70536;
DT   27-MAR-1995  (first entry)
DE   Human retinoblastoma gene.
KW   Retinoblastoma; cancer; detection; diagnosis; protein; neoplasm;
KW   assay; immune complex; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             337. .2787
FT                   /*tag=  a
PN   EP-608004-A.
PD   27-JUL-1994.
PF   11-AUG-1987; 307095.
PR   11-AUG-1986; US-895163.
PA   (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA   (WHED ) WHITEHEAD INST.
PA   BIOMEDICAL RES.
PI   Dryja TP,  Friend S;
DR   WPI; 94-272746/34.
DR   P-PSDB; R58568.
```

PT Diagnosing the presence of defective retinoblastoma alleles -
PT comprises comparing genetic material corresponding to a normal
PT human retinoblastoma with DNA from a patient.
PS Example 2(2); Figure 7; 18pp; English.
CC A method for detecting the presence, in a tumour sample, of a protein
CC the absence of which is associated with a neoplasm, comprises
CC producing an antibody to the protein and then contacting the
CC antibody with the tumour sample. Immune complexes indicate the
CC presence of the protein in the sample. The method may be used in
CC the detection and treatment of a defective human gene related to
CC cancer, in particular retinoblastoma.
SQ Sequence 4597 BP; 1489 A; 841 C; 812 G; 1455 T;

Query Match 97.9%; Score 2500; DB 1; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     234 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 293

Qy      63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     294 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 353

Qy     123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 413

Qy     183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 473

Qy     243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     474 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 533

Qy     303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     534 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 593

Qy     363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     594 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 653

Qy     423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     654 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 713

Qy     483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     714 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 773

Qy     543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     774 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 833

Qy     603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     834 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 893

Qy     663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     894 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 953

Qy     723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     954 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTTGA 1013

Qy     783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1014 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1073

Qy     843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1074 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1133

Qy     903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1134 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1193

Qy     963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1194 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1253

Qy    1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1254 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1313

Qy    1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1314 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1373

Qy    1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1374 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1433

Qy    1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1434 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1493

Qy    1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1494 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1553

Qy    1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1554 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1613

Qy    1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1614 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1673

Qy    1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1674 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1733

Qy    1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1734 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1793

Qy    1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1794 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1853

Qy    1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1854 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1913

Qy    1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1914 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1973

Qy    1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1974 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2033

Qy    1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2034 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2093

Qy    1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2094 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2153
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Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2154 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2213

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2214 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2273

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2274 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2333

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2334 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2393

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2394 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2453

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2454 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2513

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2514 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2573

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2574 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2633

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2634 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2693

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2694 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2753

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2754 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT  11
Q90059
ID   Q90059 standard; DNA; 2995 BP.
AC   Q90059;
DT   28-NOV-1995  (first entry)
DE   Retinoblastoma tumour suppressor gene.
KW   Recombinant; adenovirus; expression vector; TSG; small lung cancer;
KW   hepatocarcinoma; melanoma; retinoblastoma; sarcoma; sickle cell;
KW   anaemia; Tay-Sach's disease; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
PN   WO9511984-A.
PD   04-MAY-1995.
PF   25-OCT-1994; U12235.
PR   25-OCT-1993; US-142669.
PR   19-MAY-1994; US-246007.
PA   (CANJ-) CANJI INC.
PI   Gregory RJ,  Maneval DC,  Wills KN;
DR   WPI; 95-178876/23.
DR   P-PSDB; R74271.
PT   Adenoviral vector with deletion of viral protein IX contains
PT   foreign gene - esp. encoding tumour suppressor protein for gene
PT   therapy of tumours, reduces contamination by wild type adenovirus
PS   Disclosure; Fig 3; 92pp; English.
CC   The sequence is that of the DNA sequence encoding a retinoblastoma
CC   tumour protein.  The gene can be used in a novel method involving a
CC   recombinant adenovirus expression vector to treat diseases
CC   associated with the ansence of the TSg or the presence of a mutated
CC   TSG, e.g. many forms of carcinoma, sickle cell anaemia or Tay-Sach's
CC   disease.
CC   See also Q90060-5.
SQ   Sequence   2995 BP;    975 A;    617 C;    594 G;    809 T;
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  Query Match             97.9%;  Score 2500;  DB 1;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2550;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 431

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 491

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 551

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 611

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 671

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 791

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 851

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 971

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 1091

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1151

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1152 TCATGATAAAACTCTTCAGAGTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1271

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
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Db   1272 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022

Db   1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1391

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082

Db   1392 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1451

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142

Db   1452 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202

Db   1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1571

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262

Db   1572 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322

Db   1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1691

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382

Db   1692 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1751

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442

Db   1752 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502

Db   1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1871

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562

Db   1872 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622

Db   1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1991

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682

Db   1992 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 2051

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742

Db   2052 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802

Db   2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2171

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862

Db   2172 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922

Db   2232 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2291

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982

Db   2292 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2351

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042

Db   2352 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102

Db   2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2471

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162

Db   2472 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222

Db   2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2591

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282

Db   2592 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2651

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342

Db   2652 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2711

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402

Db   2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2771

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462

Db   2772 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522

Db   2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2891

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553

Db   2892 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 12
X04501
ID X04501 standard; cDNA; 4597 BP.
AC X04501;
DT 05-JUL-1999 (first entry)
DE Human retinoblastoma gene cDNA.
KW Retinoblastoma; Rb gene; human; predisposition; diagnosis; therapy;
KW ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 337..2787
FT /*tag= a
FT /transl_except= (pos:2632..2634, aa:Asp)
PN US5853988-A.
PD 29-DEC-1998.
PF 08-OCT-1992; 958290.
PR 08-JUL-1991; US-728756.
PR 11-AUG-1986; US-895163.
PR 21-JAN-1988; US-146525.
PR 23-JAN-1989; US-300667.
PR 25-SEP-1992; US-951342.
PR 08-OCT-1992; US-958290.
PA (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA (WHED) WHITEHEAD INST.
PI Dryja TP, Friend S, Yandell DW;
DR WPI; 99-094898/08.
DR P-PSDB; Y01542.
PT Isolated human retinoblastoma gene - used to develop products for
PT analysing predisposition to retinoblastoma and for the detection and
PT treatment of retinoblastoma
PS Claim 8; Fig 5; 32pp; English.
CC This is the nucleic acid sequence of a cDNA of the normal human
CC retinoblastoma gene Rb. Absence or mutation of the Rb gene (see
CC also X04502) predisposes an individual to retinoblastoma. To

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CC   isolate Rb cDNA, the human DNA probe pH3-8, isolated from a human
CC   chromosome 13 lambda phage library, was used in a chromosome walk
CC   to isolate and map 30 kb of genomic DNA surrounding the H3-8
CC   sequence.  Fragment p7H30.7R (ATCC 97500) was obtained, and was
CC   used as a probe to screen a cDNA library that had been constructed
CC   from an adenovirus 12-transformed human embryonic retinal cell
CC   line.  This provided clone p4.7R (ATCC 97383), which in Northern
CC   blots cross-reacted with a 4.7 kb transcript in transformed
CC   retinal cells which was not present in 4 retinoblastoma and one
CC   osteosarcoma cell samples.  Rb nucleic acids comprising the Rb
CC   gene, cDNA or a fragment of the gene, such as one of the 27 exons
CC   or 26 introns, can be used in a claimed method for detecting a
CC   deletion or point mutation in the Rb gene of a human patient.  The
CC   gene can also be used to synthesize Rb polypeptide (see Y01542) for
CC   use in the treatment of individuals determined to have a defective
CC   Rb allele.
SQ   Sequence   4597 BP;    1489 A;    841 C;    813 G;    1454 T;

  Query Match           97.9%;  Score 2500;  DB 1;  Length 4597;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2550;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 62
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 293

Qy     63 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 353

Qy    123 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    354 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 413

Qy    183 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 473

Qy    243 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 533

Qy    303 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 593

Qy    363 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 653

Qy    423 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    654 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 713

Qy    483 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    714 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 773

Qy    543 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    774 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 833

Qy    603 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    834 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 893

Qy    663 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    894 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 953

Qy    723 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    954 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1013

Qy    783 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1014 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1073

Qy    843 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1074 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1133

Qy    903 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1134 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1193

Qy    963 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1194 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1253

Qy   1023 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1254 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1313

Qy   1083 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1314 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1373

Qy   1143 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1374 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1433

Qy   1203 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1434 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1493

Qy   1263 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1494 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1553

Qy   1323 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1554 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1613

Qy   1383 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1614 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1673

Qy   1443 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1674 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1733

Qy   1503 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1734 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1793

Qy   1563 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1794 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1853

Qy   1623 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1854 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1913

Qy   1683 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1914 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1973

Qy   1743 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1974 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2033

Qy   1803 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2034 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2093
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Qy   1863 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2094 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2153

Qy   1923 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2154 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2213

Qy   1983 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2214 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2273

Qy   2043 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2274 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2333

Qy   2103 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2334 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2393

Qy   2163 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2394 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2453

Qy   2223 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2454 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2513

Qy   2283 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2514 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2573

Qy   2343 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2402
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   2574 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCA 2633

Qy   2403 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2634 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2693

Qy   2463 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2694 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2753

Qy   2523 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||
Db   2754 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
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RESULT  13
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;
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  Query Match            97.6%;  Score 2493;  DB 1;  Length 3266;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     61 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 69

Qy    121 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 129

Qy    181 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 189

Qy    241 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 249

Qy    301 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 309

Qy    361 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 369

Qy    421 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 429

Qy    481 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 489

Qy    541 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 549

Qy    601 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 609

Qy    661 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 669

Qy    721 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 729

Qy    781 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 789

Qy    841 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 849

Qy    901 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 909
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Qy    961 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 969

Qy   1021 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1029

Qy   1081 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1089

Qy   1141 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1149

Qy   1201 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1209

Qy   1261 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1269

Qy   1321 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1329

Qy   1381 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1389

Qy   1441 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1449

Qy   1501 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1509

Qy   1561 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1569

Qy   1621 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1629

Qy   1681 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1689

Qy   1741 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1749

Qy   1801 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1809

Qy   1861 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1869

Qy   1921 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1929

Qy   1981 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1989

Qy   2041 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2049

Qy   2101 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2109

Qy   2161 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2169

Qy   2221 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2229

Qy   2281 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2289

Qy   2341 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2349

Qy   2401 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2409

Qy   2461 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2469

Qy   2521 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          |||||||||||||||||||||||||||||||
Db   2470 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2502
```

RESULT 14
N81369
ID N81369 standard; DNA; 4597 BP.
AC N81369;
DT 22-OCT-1990 (first entry)
DE Human retinoblastoma gene
KW Retinoblastoma; neoplasm; osteocarcoma; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 337. .2787
FT /*tag= a
PN EP-259031-A.
PD 09-MAR-1988.
PF 11-AUG-1987; 307095.
PR 11-AUG-1986; US-895163.
PA (MASS-) Massachusets Eye; (WHIT-) Whitehead Inst Biomed Re.
PI Dryja TP, Friend S;
DR WPI; 88-065827/10.
DR P-PSDB; P82112.
PT Diagnosis of retinoblastoma - using genetic material corresp. to a normal
PT human retinoblastoma gene or a unique sub-region
PS Disclosure; p; English.
CC This gene encodes a protein, the absence of which is associated with a
CC neoplasm. It is used to produce an antibody to the protein, contacting
CC this with the tumour sample and detecting immune complexes as indication
CC of the presence in the tumour sample of the protein. Whole sequence or
CC a unique sub-region can be used. The method identifies patients lacking
CC the defective retinoblastoma (Rb) allele and thus are not at risk of
CC developing the disease.
SQ Sequence 4597 BP; 1489 A; 839 C; 815 G; 1454 T;

Query Match 97.3%; Score 2485; DB 1; Length 4597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2535; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      18 TGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTAT 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     249 TGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTAT 308

Qy      78 CTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAA 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309 CTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAA 368

Qy     138 CATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAA 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     369 CATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAA 428

Qy     198 AGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAG 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     429 AGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAG 488

Qy     258 CAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTAC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     489 CAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTAC 548

Qy     318 TGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGG 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     549 TGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGG 608

Qy     378 GGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCT 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     609 GGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCT 668

Qy     438 TGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGT 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     669 TGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGT 728

Qy     498 TATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGAT 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     729 TATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGAT 788

Qy     558 AGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATG 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     789 AGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATG 848

Qy     618 TAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCT 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     849 TAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCT 908

Qy     678 TGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGA 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     909 TGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGA 968

Qy     738 AATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCT 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     969 AATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCT 1028

Qy     798 TCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGA 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1029 TCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGA 1088

Qy     858 TGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCA 917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1089 TGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCA 1148

Qy     918 ACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTA 977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1149 ACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTA 1208

Qy     978 TTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGG 1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1209 TTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGG 1268

Qy    1038 ATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATC 1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1269 ATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATC 1328

Qy    1098 ACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATC 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1329 ACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATC 1388

Qy    1158 AGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCA 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1389 AGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCA 1448

Qy    1218 TATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATC 1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1449 TATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATC 1508

Qy    1278 TCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTT 1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1509 TCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTT 1568

Qy    1338 AAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGAC 1397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1569 AAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGAC 1628

Qy    1398 AAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATG 1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1629 AAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATG 1688

Qy    1458 GCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAAC 1517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1689 GCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAAC 1748

Qy    1518 TGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGC 1577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1749 TGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGC 1808

Qy    1578 AGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAA 1637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1809 AGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAA 1868

Qy    1638 TTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAA 1697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1869 TTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCGAGAAGCCATTGAA 1928

Qy    1698 ATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAA 1757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1929 ATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAA 1988

Qy    1758 TACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCT 1817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1989 TACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCT 2048

Qy    1818 TTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAAT 1877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2049 TTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAAT 2108

Qy    1878 TATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAAT 1937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2109 TATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAAT 2168

Qy    1938 CATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTT 1997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2169 CATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTT 2228

Qy    1998 GATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAG 2057
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2229 GATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAG 2288

Qy    2058 ACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACC 2117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2289 ACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACC 2348

Qy    2118 TCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAA 2177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2349 TCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAA 2408

Qy    2178 CATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAAC 2237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2409 CATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAAC 2468

Qy    2238 AAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGA 2297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2469 AAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGA 2528

Qy    2298 GAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGC 2357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2529 GAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGC 2588

Qy    2358 TGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGA 2417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2589 TGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGA 2648

Qy    2418 TGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGA 2477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2649 TGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGA 2708

Qy    2478 AATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTC 2537
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2709 AATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTC 2768

Qy    2538 AAACAAGGAAGAGAAA 2553
           ||||||||||||||||
Db    2769 AAACAAGGAAGAGAAA 2784


RESULT  15
Q72690
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


  Query Match             96.4%;  Score 2460;  DB 1;  Length 3233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 66

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 126

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 186

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 246

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 366

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 426

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 486

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 546

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 726

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 786

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 846

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 966

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1027 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1086

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1146

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1147 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1266

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1326

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1386

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1446

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1566

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1626

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1686

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1746

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1866

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1926

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 1986

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2046

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2166

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2226

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2286

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2346

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2466
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Search completed: February 13, 2000, 20:29:20
Job time: 11439 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:34:00 ; Search time 683.56 Seconds
(without alignments)
934.432 Million cell updates/sec

Title: US-09-026-459A-38_COPY_7_2559
Perfect score: 2553
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2553

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2553	100.0	3323	1	V58446	Modified retinobla
2	2464	96.5	3461	1	V58447	Modified retinobla
3	2461	96.4	3233	1	Q72690	Retinoblastoma 94k
4	2460	96.4	2994	1	Q04713	Cancer supressing
5	2460	96.4	2994	1	Q41545	Retinoblastoma gen
6	2460	96.4	3555	1	V58440	Modified retinobla
7	2460	96.4	3455	1	V58441	Modified retinobla
8	2460	96.4	3392	1	V58442	Modified retinobla
9	2460	96.4	3323	1	V58443	Modified retinobla
10	2460	96.4	3266	1	V58444	Modified retinobla
11	2460	96.4	3555	1	V54990	DNA sequence of th
12	2460	96.4	2994	1	V40004	Retinoblastoma pro
13	2460	96.4	2995	1	X00737	cDNA encoding a re
14	2448	95.9	3554	1	V58452	Modified retinobla
15	2448	95.9	3218	1	V54991	DNA sequence of th
16	2409	94.4	4597	1	N81369	Human retinoblasto
17	2409	94.4	4597	1	Q70536	Human retinoblasto
18	2409	94.4	2995	1	Q90059	Retinoblastoma tum
19	2409	94.4	4597	1	X04501	Human retinoblasto
20	2343	91.8	3113	1	V58445	Modified retinobla
21	2256	88.4	2995	1	Q86398	Human Rb110 cDNA.
22	2242	87.8	3347	1	V58448	Modified retinobla
23	2062	80.8	3161	1	V58449	Modified retinobla
24	2061	80.7	3377	1	V58450	Modified retinobla
25	1885	73.8	3383	1	V58451	Modified retinobla
26	1548	60.6	5056	1	N90489	cDNA of human reti
27	1410	55.2	4579	1	N81261	Probe for retinobl
28	198	7.8	18303	1	X04502	Human retinoblasto
29	165	6.5	18177	1	N90490	DNA of human retin
c 30	26	1.0	26	1	V49234	rb gene antisense
c 31	26	1.0	26	1	V49235	rb gene antisense
32	25	1.0	40	1	T12226	Human retinoblasto
33	25	1.0	40	1	V11847	Human Rb PCR prime
34	24	0.9	24	1	V01247	Retinoblastoma 1 P
c 35	24	0.9	24	1	V49224	rb gene antisense
c 36	23	0.9	23	1	V49227	rb gene antisense
c 37	23	0.9	23	1	V49222	rb gene antisense
c 38	23	0.9	23	1	V49225	rb gene antisense
c 39	23	0.9	32	1	V58466	Primer for Modifie
c 40	23	0.9	32	1	V59932	PCR primer used to
41	22	0.9	52	1	Q27110	PCR primer for the
42	22	0.9	50	1	Q27131	5' PCR primer for
43	22	0.9	50	1	Q99012	Chelating peptide-
c 44	22	0.9	22	1	T11461	Retinoblastoma gen
c 45	22	0.9	22	1	T12860	PCR 3' primer for

ALIGNMENTS

RESULT 1
V58446
ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

Query Match 100.0%; Score 2553; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGTCGACCTAGATGAGATGTCGTTCACTTTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGTCGACCTAGATGAGATGTCGTTCACTTTT 126

Qy     121 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 ACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 186

Qy     181 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 ATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 246

Qy     241 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 306

Qy     301 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 366

Qy     361 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 420
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Db    367 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG 426

Qy    421 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 480

Db    427 TTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA 486

Qy    481 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 540

Db    487 CCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 546

Qy    541 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 600

Db    547 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 606

Qy    601 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 660

Db    607 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 666

Qy    661 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 720

Db    667 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 726

Qy    721 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 780

Db    727 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 786

Qy    781 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 840

Db    787 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 846

Qy    841 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 900

Db    847 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 906

Qy    901 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 960

Db    907 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 966

Qy    961 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1020

Db    967 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1026

Qy   1021 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1080

Db   1027 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1086

Qy   1081 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1140

Db   1087 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1146

Qy   1141 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1200

Db   1147 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1206

Qy   1201 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1260

Db   1207 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1266

Qy   1261 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1320

Db   1267 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1326

Qy   1321 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1380

Db   1327 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1386

Qy   1381 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1440

Db   1387 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1446

Qy   1441 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1500

Db   1447 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1506

Qy   1501 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1560

Db   1507 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1566

Qy   1561 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1620

Db   1567 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1626

Qy   1621 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1680

Db   1627 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1686

Qy   1681 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1740

Db   1687 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1746

Qy   1741 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1800

Db   1747 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1806

Qy   1801 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1860

Db   1807 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1866

Qy   1861 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1920

Db   1867 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1926

Qy   1921 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1980

Db   1927 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 1986

Qy   1981 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2040

Db   1987 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2046

Qy   2041 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2100

Db   2047 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2106

Qy   2101 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2160

Db   2107 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2166

Qy   2161 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2220

Db   2167 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2226

Qy   2221 GGTCTGCCAACACCAAGAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2280

Db   2227 GGTCTGCCAACACCAAGAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2286

Qy   2281 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2340

Db   2287 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2346

Qy   2341 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2400

Db   2347 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2406

Qy   2401 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2460

Db   2407 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2466

Qy   2461 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2520

Db   2467 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2526

Qy   2521 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553

Db   2527 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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RESULT   2
V58447
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;

  Query Match             96.5%;  Score 2464;  DB 1;  Length 3461;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2464;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     90 GGTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAG 149
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234 GGTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAG 293

Qy    150 TGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGC 209
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 TGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGC 353

Qy    210 TATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAG 269
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    354 TATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAG 413

Qy    270 GACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTC 329
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 GACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTC 473

Qy    330 TGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACA 389
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474 TGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACA 533

Qy    390 AATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTAT 449
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 AATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTAT 593

Qy    450 TAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAA 509
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594 TAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAA 653

Qy    510 TGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACT 569
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    654 TGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACT 713

Qy    570 AGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGA 629
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    714 AGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGA 773

Qy    630 GGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAAC 689
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    774 GGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAAC 833

Qy    690 ATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAA 749
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    834 ATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAA 893

Qy    750 AAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTC 809
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    894 AAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTC 953

Qy    810 TATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 869
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    954 TATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1013

Qy    870 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGAT 929
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1014 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGAT 1073

Qy    930 GATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTG 989
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1074 GATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTG 1133

Qy    990 CACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAA 1049
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1134 CACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAA 1193

Qy   1050 AGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAA 1109
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1194 AGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAA 1253

Qy   1110 ACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1169
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1254 ACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1313

Qy   1170 ATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATT 1229
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1314 ATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATT 1373

Qy   1230 GGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGA 1289
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1374 GGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGA 1433

Qy   1290 TTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGA 1349
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1434 TTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGA 1493

Qy   1350 TTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGAT 1409
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1494 TTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGAT 1553

Qy   1410 AAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTC 1469
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1554 AAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTC 1613

Qy   1470 ACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGA 1529
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1614 ACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGA 1673

Qy   1530 ATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCT 1589
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1674 ATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCT 1733

Qy   1590 TTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAA 1649
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1734 TTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAA 1793

Qy   1650 TGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCT 1709
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1794 TGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCT 1853
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Qy   1710 TTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1854 TTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA 1913

Qy   1770 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACAC 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1914 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACAC 1973

Qy   1830 CCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTC 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1974 CCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTC 2033

Qy   1890 CATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2034 CATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGC 2093

Qy   1950 ATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGA 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2094 ATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGA 2153

Qy   2010 GGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2154 GGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2213

Qy   2070 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCG 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2214 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCG 2273

Qy   2130 AAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTC 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2274 AAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTC 2333

Qy   2190 ACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCC 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2334 ACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCC 2393

Qy   2250 AAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAA 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2394 AAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAA 2453

Qy   2310 AATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2454 AATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2513

Qy   2370 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGG 2429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2514 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGG 2573

Qy   2430 AAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTAC 2489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2574 AAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTAC 2633

Qy   2490 TCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGA 2549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2634 TCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGA 2693

Qy   2550 GAAA 2553
          ||||
Db   2694 GAAA 2697
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RESULT 3
Q72690
ID Q72690 standard; DNA; 3233 BP.
AC Q72690;
DT 01-JUN-1995 (first entry)
DE Retinoblastoma 94kD therapeutic protein encoding DNA.
KW Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 19. .2469
FT /*tag= a

PN WO9421115-A.
PD 29-SEP-1994.
PF 24-MAR-1994; U03211.
PR 25-MAR-1993; US-038760.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PI Benedict WF, Xu H, Xu S;
DR WPI; 94-316534/39.
DR P-PSDB; R63564.
PT Broad spectrum tumour suppressor gene - by using retinoblastoma
PT gene product p94RB to suppress abnormal cell proliferation in the
PT treatment of cancer
PS Claim 4; Fig 1; 115pp; English.
CC Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC gene) which encodes the 94kD therapeutic retinoblastoma protein
CC R63564. Expression of this protein in an abnormally proliferating
CC cell causes that cell to enter a senescent-like state, terminating
CC the proliferation. R63564 also has the advantage of engendering a low
CC incidence of tumour suppressor gene resistance in a population of
CC treated cells.
SQ Sequence 3233 BP; 1086 A; 597 C; 567 G; 983 T;

Query Match 96.4%; Score 2461; DB 1; Length 3233;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     93 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 65

Qy    153 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 125

Qy    213 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 185

Qy    273 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 245

Qy    333 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 305

Qy    393 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 365

Qy    453 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 425

Qy    513 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 485

Qy    573 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 545

Qy    633 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 605

Qy    693 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 665

Qy    753 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 725
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Qy    813 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 785

Qy    873 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 845

Qy    933 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 905

Qy    993 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 965

Qy   1053 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1025

Qy   1113 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1085

Qy   1173 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1145

Qy   1233 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1205

Qy   1293 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1265

Qy   1353 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1325

Qy   1413 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1326 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1385

Qy   1473 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1445

Qy   1533 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1505

Qy   1593 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1565

Qy   1653 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

Qy   1713 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1685

Qy   1773 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1745

Qy   1833 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1805

Qy   1893 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1952
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1806 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1865

Qy   1953 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1866 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1925

Qy   2013 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2072
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1985

Qy   2073 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2045

Qy   2133 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2046 CCCTTACAAGTTTCCTAGTTGACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2105

Qy   2193 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2106 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2165

Qy   2253 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2166 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

Qy   2313 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2285

Qy   2373 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2286 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2345

Qy   2433 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2346 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2405

Qy   2493 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2406 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2465

Qy   2553 A 2553
          |
Db   2466 A 2466
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RESULT   4
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
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CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;

  Query Match             96.4%;  Score 2460;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1114 GGAGTTCGCTTGTATTAGCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1483 GGAGTTCGCTTGTATTAGCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy    1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy    1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy    1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy    1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy    1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy    1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy    2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy    2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502
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Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   5
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;
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  Query Match             96.4%;  Score 2460;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;

  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542
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Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622
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Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2314 AATCAGATGGTATGTAAGAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   6
V58440
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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  Query Match           96.4%;  Score 2460;  DB 1;  Length 3555;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     94 GACCTAGATGAGATGTGGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GACCTAGATGAGATGTGGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 390

Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 450

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 510

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 570
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Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 630

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 690

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 750

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 810

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 870

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 930

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 990

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1050

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1110

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1170

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1230

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1290

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1350

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1410

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1470

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1530

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1590

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1650
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Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1710

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1770

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1830

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1890

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1950

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2010

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2070

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2130

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2190

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2250

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2310

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2370

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2430

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2490

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2550

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2610

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2670

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2730

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790


RESULT   7
V58441
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


  Query Match             96.4%;  Score 2460;  DB 1;  Length 3455;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671

Qy    1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
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Db   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
Db   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
Db   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
Db   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
Db   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
Db   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
Db   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
Db   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
Db   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
Db   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
Db   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
Db   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
Db   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
Db   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
Db   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
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RESULT   8
V58442
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;
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  Query Match             96.4%;  Score 2460;  DB 1;  Length 3392;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy.    94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
Db   169 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 228

Qy   154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
Db   229 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 288

Qy   214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
Db   289 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 348

Qy   274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
Db   349 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 408

Qy   334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
Db   409 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 468

Qy   394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
Db   469 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 528

Qy   454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
Db   529 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 588

Qy   514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
Db   589 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 648

Qy   574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
Db   649 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 708

Qy   634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
Db   709 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 768

Qy   694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
Db   769 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 828

Qy   754 AAAGATCTAGATGCAAGATTATTTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
Db   829 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 888

Qy   814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
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Db    889 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 948

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
Db    949 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1008

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
Db   1009 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1068

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
Db   1069 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1128

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
Db   1129 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1188

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
Db   1189 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1248

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
Db   1249 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1308

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
Db   1309 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1368

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
Db   1369 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1428

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
Db   1429 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1488

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
Db   1489 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1548

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
Db   1549 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1608

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
Db   1609 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1668

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
Db   1669 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1728

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
Db   1729 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1788

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
Db   1789 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1848

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
Db   1849 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1908

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
Db   1909 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1968

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
Db   1969 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2028

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
Db   2029 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2088

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
Db   2089 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2148

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
Db   2149 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2208

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
Db   2209 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2268

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
Db   2269 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2328

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
Db   2329 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2388

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
Db   2389 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2448

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
Db   2449 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2508

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
Db   2509 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2568

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
Db   2569 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628
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RESULT   9
V58443
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
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SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;

  Query Match            96.4%;  Score 2460;  DB 1;  Length 3323;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 159

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     160 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 219

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 279

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     280 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 339

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     340 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 399

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 459

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     460 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 519

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     520 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 579

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 639

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 699

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 759

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 819

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 879

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 939

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 999

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1059

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1060 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1119

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1179

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1239

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1299

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1359

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1419

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1479

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1539

Qy    1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1540 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1599

Qy    1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1600 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1659

Qy    1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1660 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1719

Qy    1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1720 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1779

Qy    1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1780 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1839

Qy    1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1840 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1899

Qy    1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1900 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1959

Qy    1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1960 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2019

Qy    2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2020 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2079

Qy    2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2080 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2139

Qy    2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2140 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2199
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Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2259

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2319

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2379

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2439

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2499

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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RESULT  10
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;
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  Query Match             96.4%;  Score 2460;  DB 1;  Length 3266;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     43 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 102

Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    103 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 162

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    163 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 222

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    223 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 282

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    283 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 342

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 402

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 462

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 522

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 582

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 642

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 702

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 762

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 822

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 882

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 942

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1002

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1062

Qy   1114 GGAGTTCGCTTGTATTAGCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 GGAGTTCGCTTGTATTAGCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1122

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1182

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1242

Qy   1294 GGAACAGATTTGTCTTTGCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1302
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Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1362

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1422

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1482

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1542

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1602

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1662

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1722

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1782

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1842

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1902

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1962

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2022

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2082

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2142

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2202

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2262

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2322

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2382

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2442

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2502
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RESULT 11
V54990
ID V54990 standard; DNA; 3555 BP.
AC V54990;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 96.4%; Score 2460; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 390

Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 450

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 510

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 570

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    571 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 630

Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 690

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 750

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 810

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 870

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 930

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 990

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1050

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1110

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1170

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1230

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1290

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1350

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1410

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1470

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1530

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1590

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1650

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1710

Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1770

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1830

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1890

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1950

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2010

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2070

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2130

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2190

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2250

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2310

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2370

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2430

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2490

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2550

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2610

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2670

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2730

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT  12
V40004
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;

  Query Match             96.4%;  Score 2460;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy     274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy     334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy     394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy     454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy     514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy     574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy     634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy     694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy     754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy     814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy     874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy     934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy     994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy    1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy    1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy    1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy    1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy    1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy    1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy    1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy    1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT  13
X00737
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ID   X00737 standard; cDNA; 2995 BP.
AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;


  Query Match            96.4%;  Score 2460;  DB 1;  Length 2995;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     94 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    154 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    214 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    274 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    334 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762
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Qy    394 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    454 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    514 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    574 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    634 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    694 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    754 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    814 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy    874 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy    934 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy    994 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1054 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1114 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1174 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1234 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1294 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1354 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1414 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842
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Qy   1474 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1534 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1594 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1654 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1714 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1774 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1834 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   1894 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   1954 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2014 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2074 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2134 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2194 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2254 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2314 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2374 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2434 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2494 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT  14
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;

  Query Match             95.9%;  Score 2448;  DB 1;  Length 3554;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    106 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 165
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 402

Qy    166 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 462

Qy    226 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 285
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 522

Qy    286 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 345
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 582

Qy    346 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 405
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

Qy    406 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 465
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 702

Qy    466 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 525
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 762

Qy    526 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 585
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 822

Qy    586 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 645
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 882

Qy    646 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 942

Qy    706 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 765
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 1002

Qy    766 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 825
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1062

Qy    826 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 885
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1122

Qy    886 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 945
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1182

Qy    946 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1005
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242

Qy   1006 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1065
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1302

Qy   1066 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1125
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1362

Qy   1126 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1185
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1422

Qy   1186 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1245
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1482

Qy   1246 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1305
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1542

Qy   1306 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1365
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1602

Qy   1366 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1425
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1662

Qy   1426 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1485
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Db   1663 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1722

Qy   1486 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1545
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Db   1723 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1782

Qy   1546 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1605
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1842

Qy   1606 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1665
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Db   1843 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1902

Qy   1666 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1725
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1962

Qy   1726 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1785
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Db   1963 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2022

Qy   1786 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1845
Db   2023 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2082

Qy   1846 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1905
Db   2083 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2142

Qy   1906 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1965
Db   2143 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2202

Qy   1966 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2025
Db   2203 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2262

Qy   2026 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2085
Db   2263 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2322

Qy   2086 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2145
Db   2323 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2382

Qy   2146 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2205
Db   2383 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2442

Qy   2206 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2265
Db   2443 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2502

Qy   2266 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2325
Db   2503 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2562

Qy   2326 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2385
Db   2563 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2622

Qy   2386 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2445
Db   2623 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2682

Qy   2446 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2505
Db   2683 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2742

Qy   2506 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
Db   2743 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT 15
V54991
ID V54991 standard; DNA; 3218 BP.
AC V54991;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2457
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71355.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 153-157; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T;

Query Match 95.9%; Score 2448; DB 1; Length 3218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    106 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 165
Db      7 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 66

Qy    166 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 225
Db     67 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 126

Qy    226 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 285
Db    127 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 186

Qy    286 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 345
Db    187 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 246

Qy    346 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 405
Db    247 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 306

Qy    406 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 465
Db    307 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 366

Qy    466 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 525
Db    367 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 426

Qy    526 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 585
Db    427 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 486

Qy    586 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 645
Db    487 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 546

Qy    646 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 705
Db    547 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 606

Qy    706 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 765
Db    607 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 666
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Qy    766 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 825
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Db    667 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 726

Qy    826 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 885
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Db    727 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 786

Qy    886 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 945
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Db    787 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 846

Qy    946 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1005
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Db    847 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 906

Qy   1006 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1065
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Db    907 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 966

Qy   1066 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1125
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Qy   1126 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1185
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Db   1027 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1086

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Db   1087 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1146

Qy   1246 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1305
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Db   1147 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1206

Qy   1306 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1365
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Db   1207 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1266

Qy   1366 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1425
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Db   1267 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1326

Qy   1426 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1485
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Qy   1486 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1545
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Db   1387 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1446

Qy   1546 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1605
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Db   1447 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1506

Qy   1606 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1665
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Qy   1666 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1725
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Db   1567 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1626

Qy   1726 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1785
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Db   1687 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1746

Qy   1846 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1905
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Db   1747 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1806

Qy   1906 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1965
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Db   1807 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1866

Qy   1966 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2025
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Db   1867 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1926

Qy   2026 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2085
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Qy   2086 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2145
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Qy   2146 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2205
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Db   2047 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2106

Qy   2206 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2265
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Qy   2266 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2325
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Qy   2326 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2385
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Qy   2386 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2445
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Qy   2446 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2505
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Db   2347 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2406

Qy   2506 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2553
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2454
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Search completed: February 13, 2000, 20:36:22
Job time: 11861 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:36:22 ; Search time 683.56 Seconds
(without alignments)
984.942 Million cell updates/sec

Title: US-09-026-459A-40_COPY_7_2697
Perfect score: 2691
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2691

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2691	100.0	3461	1	V58447	Modified retinobla
	2	2464	91.6	3323	1	V58446	Modified retinobla
	3	2461	91.5	3233	1	Q72690	Retinoblastoma 94k
	4	2460	91.4	2994	1	Q04713	Cancer supressing
	5	2460	91.4	2994	1	Q41545	Retinoblastoma gen
	6	2460	91.4	3555	1	V58440	Modified retinobla
	7	2460	91.4	3455	1	V58441	Modified retinobla
	8	2460	91.4	3392	1	V58442	Modified retinobla
	9	2460	91.4	3323	1	V58443	Modified retinobla
	10	2460	91.4	3266	1	V58444	Modified retinobla
	11	2460	91.4	3555	1	V54990	DNA sequence of th
	12	2460	91.4	2994	1	V40004	Retinoblastoma pro
	13	2460	91.4	2995	1	X00737	cDNA encoding a re
	14	2448	91.0	3554	1	V58452	Modified retinobla
	15	2448	91.0	3218	1	V54991	DNA sequence of th
	16	2409	89.5	4597	1	N81369	Human retinoblasto
	17	2409	89.5	4597	1	Q70536	Human retinoblasto
	18	2409	89.5	2995	1	Q90059	Retinoblastoma tum
	19	2409	89.5	4597	1	X04501	Human retinoblasto
	20	2343	87.1	3113	1	V58445	Modified retinobla
	21	2256	83.8	2995	1	Q86398	Human Rb110 cDNA.
	22	2242	83.3	3347	1	V58448	Modified retinobla
	23	2062	76.6	3161	1	V58449	Modified retinobla
	24	2061	76.6	3377	1	V58450	Modified retinobla
	25	1885	70.0	3383	1	V58451	Modified retinobla
	26	1548	57.5	5056	1	N90489	cDNA of human reti
	27	1410	52.4	4579	1	N81261	Probe for retinobl
	28	198	7.4	18303	1	X04502	Human retinoblasto
	29	165	6.1	18177	1	N90490	DNA of human retin
c	30	26	1.0	26	1	V49234	rb gene antisense
c	31	26	1.0	26	1	V49235	rb gene antisense
	32	25	0.9	40	1	T12226	Human retinoblasto
	33	25	0.9	40	1	V11847	Human Rb PCR prime
	34	24	0.9	24	1	V01247	Retinoblastoma 1 P
c	35	24	0.9	24	1	V49224	rb gene antisense
c	36	23	0.9	23	1	V49227	rb gene antisense
c	37	23	0.9	23	1	V49222	rb gene antisense
c	38	23	0.9	23	1	V49225	rb gene antisense
c	39	23	0.9	32	1	V58466	Primer for Modifie
c	40	23	0.9	32	1	V59932	PCR primer used to
	41	22	0.8	52	1	Q27110	PCR primer for the
	42	22	0.8	50	1	Q27131	5' PCR primer for
	43	22	0.8	50	1	Q99012	Chelating peptide-
c	44	22	0.8	22	1	T11461	Retinoblastoma gen
c	45	22	0.8	22	1	T12860	PCR 3' primer for

ALIGNMENTS

RESULT 1
V58447
ID V58447 standard; DNA; 3461 BP.
AC V58447;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2700
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69371.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 188-192; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3461 BP; 1141 A; 675 C; 627 G; 1018 T;

Query Match 100.0%; Score 2691; DB 1; Length 3461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CCGGCACCGCCGCCGCCGCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy     181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTGGTCGACCTAGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTGGTCGACCTAGAT 246

Qy     241 GAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTC 306

Qy     301 TTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 TTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTG 366

Qy     361 TTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTT 420
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Db    367 TTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTT 426

Qy    421 ATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTA 480

Db    427 ATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTA 486

Qy    481 AAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGAT 540

Db    487 AAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGAT 546

Qy    541 CTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 600

Db    547 CTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 606

Qy    601 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGA 660

Db    607 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGA 666

Qy    661 ACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACA 720

Db    667 ACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACA 726

Qy    721 AGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 780

Db    727 AGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 786

Qy    781 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTT 840

Db    787 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTT 846

Qy    841 CCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 900

Db    847 CCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 906

Qy    901 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTT 960

Db    907 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTT 966

Qy    961 GAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCA 1020

Db    967 GAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCA 1026

Qy   1021 CACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1080

Db   1027 CACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1086

Qy   1081 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCA 1140

Db   1087 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCA 1146

Qy   1141 AAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1200

Db   1147 AAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1206

Qy   1201 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGC 1260

Db   1207 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGC 1266

Qy   1261 TTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAA 1320

Db   1267 TTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAA 1326

Qy   1321 AATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1380

Db   1327 AATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1386

Qy   1381 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGAT 1440

Db   1387 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGAT 1446

Qy   1441 TTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1500

Db   1447 TTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1506

Qy   1501 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAA 1560

Db   1507 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAA 1566

Qy   1561 CGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1620

Db   1567 CGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1626

Qy   1621 CTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1680

Db   1627 CTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1686

Qy   1681 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGA 1740

Db   1687 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGA 1746

Qy   1741 TCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1800

Db   1747 TCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1806

Qy   1801 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTAT 1860

Db   1807 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTAT 1866

Qy   1861 AAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1920

Db   1867 AAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1926

Qy   1921 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1980

Db   1927 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1986

Qy   1981 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATA 2040

Db   1987 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATA 2046

Qy   2041 TGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 2100

Db   2047 TGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 2106

Qy   2101 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCT 2160

Db   2107 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCT 2166

Qy   2161 ATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 2220

Db   2167 ATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 2226

Qy   2221 GCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2280

Db   2227 GCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2286

Qy   2281 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGT 2340

Db   2287 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGT 2346

Qy   2341 CCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2400

Db   2347 CCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2406

Qy   2401 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATG 2460

Db   2407 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATG 2466

Qy   2461 GTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCA 2520

Db   2467 GTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCA 2526

Qy   2521 CTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2580

Db   2527 CTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2586
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Qy   2581 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2587 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATG 2646

Qy   2641 CAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2647 CAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2697


RESULT   2
V58446
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;


  Query Match           91.6%;  Score 2464;  DB 1;  Length 3323;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2464;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    228 GGTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAG 287
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 GGTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAG 155

Qy    288 TGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGC 347
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 TGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGC 215

Qy    348 TATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAG 407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 TATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAG 275

Qy    408 GACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTC 467
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 GACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTC 335

Qy    468 TGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACA 527
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336 TGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACA 395

Qy    528 AATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTAT 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 AATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTAT 455

Qy    588 TAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAA 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456 TAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAA 515

Qy    648 TGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACT 707
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 TGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACT 575

Qy    708 AGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGA 767
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 AGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGA 635

Qy    768 GGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAAC 827
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 GGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAAC 695

Qy    828 ATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAA 887
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 ATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAA 755

Qy    888 AAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTC 947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756 AAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTC 815

Qy    948 TATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1007
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816 TATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 875

Qy   1008 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGAT 1067
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    876 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGAT 935

Qy   1068 GATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTG 1127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936 GATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTG 995

Qy   1128 CACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAA 1187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    996 CACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAA 1055

Qy   1188 AGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAA 1247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1056 AGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAA 1115

Qy   1248 ACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1116 ACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1175

Qy   1308 ATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATT 1367
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1176 ATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATT 1235

Qy   1368 GGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGA 1427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1236 GGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGA 1295

Qy   1428 TTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGA 1487
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296 TTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGA 1355

Qy   1488 TTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGAT 1547
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356 TTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGAT 1415

Qy   1548 AAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTC 1607
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416 AAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTC 1475

Qy   1608 ACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGA 1667
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476 ACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGA 1535

Qy   1668 ATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCT 1727
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536 ATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCT 1595
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Qy   1728 TTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAA 1787
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1596 TTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAA 1655

Qy   1788 TGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCT 1847
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 TGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCT 1715

Qy   1848 TTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA 1907
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1716 TTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA 1775

Qy   1908 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACAC 1967
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1776 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACAC 1835

Qy   1968 CCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTC 2027
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1836 CCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTC 1895

Qy   2028 CATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGC 2087
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1896 CATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGC 1955

Qy   2088 ATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGA 2147
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1956 ATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGA 2015

Qy   2148 GGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2207
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2016 GGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2075

Qy   2208 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCG 2267
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2076 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCG 2135

Qy   2268 AAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTC 2327
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2136 AAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTC 2195

Qy   2328 ACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCC 2387
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2196 ACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCC 2255

Qy   2388 AAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAA 2447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2256 AAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAA 2315

Qy   2448 AATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2507
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2316 AATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2375

Qy   2508 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGG 2567
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2376 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGG 2435

Qy   2568 AAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTAC 2627
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2436 AAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTAC 2495

Qy   2628 TCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGA 2687
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2496 TCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGA 2555

Qy   2688 GAAA 2691
          ||||
Db   2556 GAAA 2559


RESULT   3
Q72690
ID   Q72690 standard; DNA; 3233 BP.
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AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag= a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


  Query Match             91.5%;  Score 2461;  DB 1;  Length 3233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    231 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 CGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGT 65

Qy    291 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 125

Qy    351 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGAC 185

Qy    411 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 ATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGC 245

Qy    471 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 ATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAAT 305

Qy    531 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 GGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAA 365

Qy    591 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 ACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 425

Qy    651 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGA 485

Qy    711 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 AAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGT 545

Qy    771 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 GAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 605
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Qy    831 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAA 665

Qy    891 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 TAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 725

Qy    951 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 1010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGT 785

Qy   1011 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 1070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT 845

Qy   1071 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 TTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 905

Qy   1131 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGA 965

Qy   1191 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 GAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1025

Qy   1251 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATT 1085

Qy   1311 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 ATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGC 1145

Qy   1371 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 GTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1205

Qy   1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTT 1265

Qy   1491 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 TTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1325

Qy   1551 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1326 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACC 1385

Qy   1611 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 TTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC 1445

Qy   1671 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1505

Qy   1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC 1565

Qy   1791 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 AGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

Qy   1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACG 1685

Qy   1911 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 CCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCT 1745

Qy   1971 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 GCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1805

Qy   2031 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 2090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1806 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATA 1865

Qy   2091 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1866 CAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1925

Qy   2151 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 2210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATAT 1985

Qy   2211 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 TTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAG 2045

Qy   2271 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2046 CCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2105

Qy   2331 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2106 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAG 2165

Qy   2391 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2166 ATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

Qy   2451 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCC 2285

Qy   2511 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2286 TCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAG 2345

Qy   2571 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2346 TAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2405

Qy   2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2406 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAA 2465

Qy   2691 A 2691
          |
Db   2466 A 2466
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RESULT   4
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
```

PA (REGC) Univ of Caifornia.
PI Lee WH, Huang HJS;
DR WPI; 90-178822/23.
DR P-PSDB; R05305.
PT Controlling cancer -
PT by replacing ineffective cancer suppressing gene with cloned,
PT active gene.
PS Claim 35; Page 86; 105pp; English.
CC Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC By installing a working CSG, safe and specific treatment and
CC prophylaxis can be given to cancer patients.
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

Query Match 91.4%; Score 2460; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382
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Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 5
Q41545
ID Q41545 standard; DNA; 2994 BP.
AC Q41545;
DT 24-AUG-1993 (first entry)
DE Retinoblastoma gene.
KW RB gene product; p56RB portion; cell cycle progression control;
KW combination; therapeutic methods; arrest; tumourigenesis;
KW regulation; physiological processes; blood cell prodn.;
KW gamete prodn.; ss.
OS Homo sapiens SR-40 cell line.
FH Key Location/Qualifiers
FT cds 139. .2925
FT /*tag= a
FT /note= "Rb protein"
PN WO9308267-A.
PD 29-APR-1993.
PF 16-OCT-1992; U08918.
PR 17-OCT-1991; US-778510.
PA (REGC) UNIV CALIFORNIA.
PI Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR WPI; 93-152462/18.
DR P-PSDB; R36534.
PT Method of controlling cell cycle progression - uses purified
PT retinoblastoma protein or fragment, for use in combination with
PT therapeutic methods to arrest tumorigenesis
PS Disclosure; Fig 9; 68pp; English.
CC The sequence is that of the retinoblastoma gene which encodes the
CC retinoblastoma (RB) protein which may be used as part of a method of
CC controlling cell cycle progression which may be used in combination
CC with therapeutic methods to arrest tumourigenesis in organisms. The
CC cell cycle can be reversibly arrested in a convenient and safe
CC manner. The protein is used in a compsn. is relatively inexpensive
CC and readily obtainable, and shows little or no toxic effects on
CC healthy cells. It is also compatible with other methods and devices
CC for regulating certain physiological processes of the body, such as
CC blood cell prodn. and gamete prodn. Fragments of the protein are
CC soluble in low concns. of glycerol thus enhancing their value in
CC pharmaceutical applicns.
SQ Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T;

Query Match 91.4%; Score 2460; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTGAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422
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Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2452 AATCAGATGGTATGTAAGCAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAAGCAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 6
V58440
ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69364.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Disclosure; Page 121-126; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 91.4%; Score 2460; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 390

Qy    292 CATAAATTCTTTAACTTAGTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 CATAAATTCTTTAACTTAGTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 450
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Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 510

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 570

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 630

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 690

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 750

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 810

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 870

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 930

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 990

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1050

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1110

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1170

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1230

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1290

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1350

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1410

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1470

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1530

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1590

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1650

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1710

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1770

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1830

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1890

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1950

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2010

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2070

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2130

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2190

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2250

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2310

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2370

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2430

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2490

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2550

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2610

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
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Db   2611 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2670

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631

Db   2671 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2730

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691

Db   2731 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT 7
V58441
ID V58441 standard; DNA; 3455 BP.
AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2694
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 T;

Query Match 91.4%; Score 2460; DB 1; Length 3455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291

Db    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351

Db    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411

Db    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471

Db    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531

Db    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591

Db    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651

Db    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711

Db    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771

Db    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831

Db    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891

Db    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951

Db    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011

Db    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071

Db   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131

Db   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191

Db   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251

Db   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311

Db   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371

Db   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431

Db   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491

Db   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551

Db   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611

Db   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671

Db   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
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Db    1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731

Qy    1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
Db    1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791

Qy    1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
Db    1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851

Qy    1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
Db    1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911

Qy    1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
Db    1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971

Qy    1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
Db    1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031

Qy    2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
Db    2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091

Qy    2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
Db    2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151

Qy    2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
Db    2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211

Qy    2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
Db    2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271

Qy    2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
Db    2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331

Qy    2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
Db    2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391

Qy    2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
Db    2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451

Qy    2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
Db    2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511

Qy    2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
Db    2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571

Qy    2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
Db    2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631

Qy    2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
Db    2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
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RESULT 8
V58442
ID V58442 standard; DNA; 3392 BP.
AC V58442;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2641
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69366.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 150-155; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3392 BP; 1137 A; 614 C; 607 G; 1034 T;

Query Match 91.4%; Score 2460; DB 1; Length 3392;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
Db     169 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 228

Qy     292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
Db     229 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 288

Qy     352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
Db     289 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 348

Qy     412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
Db     349 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 408

Qy     472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
Db     409 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 468

Qy     532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
Db     469 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 528

Qy     592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
Db     529 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 588

Qy     652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
Db     589 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 648

Qy     712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
Db     649 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 708

Qy     772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
Db     709 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 768

Qy     832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
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Db    769 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 828

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 888

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 948

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1008

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1068

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1128

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1188

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1248

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1308

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1368

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1428

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1488

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1548

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1608

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1668

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1728

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1788

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1848

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1849 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1908

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1968

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2028

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2088

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2148

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2208

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2268

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2328

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2388

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2448

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2508

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2568

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628
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RESULT 9
V58443
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -

PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

Query Match 91.4%; Score 2460; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 159

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 219

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 279

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 339

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 399

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    400 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 459

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 519

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    520 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 579

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 639

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 699

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    700 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 759

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 819

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 879

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 939

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 999

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1059

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1119

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1179

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1239

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1240 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1299

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1359

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1419

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1479

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1539

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1599

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1659

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1719

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1779

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1839

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1899

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1959

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2019

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2079
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Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2139

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2199

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2200 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2259

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2260 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2319

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2320 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2379

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2380 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2439

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2440 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2499

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2500 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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RESULT  10
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;
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  Query Match             91.4%;  Score 2460;  DB 1;  Length 3266;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     43 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 102

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    103 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 162

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    163 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 222

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    223 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 282

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    283 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 342

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 402

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 462

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 522

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 582

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 642

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 702

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 762

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 822

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 882

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 942

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1002

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1062

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1122

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1182
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Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1242

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1302

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1362

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1422

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1482

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1542

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1602

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1662

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1722

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1782

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1842

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 1902

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 1962

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2022

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2082

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2142

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2202

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2262

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2322

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2382

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2442

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2502
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RESULT 11
V54990
ID V54990 standard; DNA; 3555 BP.
AC V54990;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 91.4%; Score 2460; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    232 GACCTAGATGAGATGTCGTTGACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 390

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 450

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    451 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 510
Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 570

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 630

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 690

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 750

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 810

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 870

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 930

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 990

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1050

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1110

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1170

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1230

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1290

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1350

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1410

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1470

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1530

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1531 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1590
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Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1650

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1710

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1770

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1830

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1831 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1890

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1950

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2010

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2070

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2130

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2190

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2250

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2310

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2370

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2430

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2490

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2550

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2610

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2670
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Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2730

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790


RESULT  12
V40004
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag=  a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;


  Query Match             91.4%;  Score 2460;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy    292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy    352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642

Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862
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Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT  13
X00737
ID   X00737 standard; cDNA; 2995 BP.
AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;
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  Query Match             91.4%;  Score 2460;  DB 1;  Length 2995;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     232 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     463 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

Qy     292 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG 582

Qy     352 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 TCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACA 642
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Qy    412 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCA 702

Qy    472 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 TTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 762

Qy    532 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

Qy    592 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGT 882

Qy    652 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 942

Qy    712 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 1002

Qy    772 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 1062

Qy    832 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

Qy    892 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 1182

Qy    952 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 1242

Qy   1012 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT 1302

Qy   1072 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 1362

Qy   1132 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

Qy   1192 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1482

Qy   1252 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTA 1542

Qy   1312 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 1602

Qy   1372 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1662

Qy   1432 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722
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Qy   1492 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA 1782

Qy   1552 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 CATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCT 1842

Qy   1612 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 TTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT 1902

Qy   1672 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1962

Qy   1732 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

Qy   1792 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 2082

Qy   1852 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 1911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2083 CTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC 2142

Qy   1912 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2143 CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTG 2202

Qy   1972 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2203 CAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 2262

Qy   2032 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

Qy   2092 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAG 2382

Qy   2152 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATT 2442

Qy   2212 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGC 2502

Qy   2272 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2562

Qy   2332 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2563 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

Qy   2392 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATA 2682

Qy   2452 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2683 AATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCT 2742

Qy   2512 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2743 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGT 2802

Qy   2572 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2631
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Db   2803 AAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2862

Qy   2632 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT  14
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


  Query Match             91.0%;  Score 2448;  DB 1;  Length 3554;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2448;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    244 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 402

Qy    304 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 462

Qy    364 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 522

Qy    424 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 582

Qy    484 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

Qy    544 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 702

Qy    604 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 762

Qy    664 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 822

Qy    724 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 882

Qy    784 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 942

Qy    844 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 1002

Qy    904 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 1062

Qy    964 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1122

Qy   1024 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1182

Qy   1084 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242

Qy   1144 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1302

Qy   1204 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1362

Qy   1264 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1422

Qy   1324 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1482

Qy   1384 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1542

Qy   1444 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1602

Qy   1504 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1662

Qy   1564 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1722

Qy   1624 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1782

Qy   1684 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1842

Qy   1744 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1803
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Db    1843 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1902

Qy    1804 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1863
Db    1903 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1962

Qy    1864 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1923
Db    1963 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 2022

Qy    1924 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1983
Db    2023 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 2082

Qy    1984 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2043
Db    2083 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2142

Qy    2044 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2103
Db    2143 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2202

Qy    2104 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2163
Db    2203 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2262

Qy    2164 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2223
Db    2263 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2322

Qy    2224 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2283
Db    2323 TCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2382

Qy    2284 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2343
Db    2383 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2442

Qy    2344 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2403
Db    2443 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2502

Qy    2404 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2463
Db    2503 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2562

Qy    2464 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2523
Db    2563 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2622

Qy    2524 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2583
Db    2623 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2682

Qy    2584 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2643
Db    2683 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2742

Qy    2644 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
Db    2743 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT 15
V54991
ID V54991 standard; DNA; 3218 BP.
AC V54991;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2457
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71355.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 153-157; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T;

Query Match 91.0%; Score 2448; DB 1; Length 3218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     244 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 303
Db       7 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTT 66

Qy     304 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 363
Db      67 AACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTG 126

Qy     364 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 423
Db     127 AAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATA 186

Qy     424 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 483
Db     187 TATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAA 246

Qy     484 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 543
Db     247 GTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 306

Qy     544 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 603
Db     307 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCC 366

Qy     604 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 663
Db     367 ATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACA 426

Qy     664 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 723
Db     427 CCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGA 486

Qy     724 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 783
Db     487 ATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTAT 546
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Qy    784 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 TTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 606

Qy    844 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGAT 666

Qy    904 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 GCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAA 726

Qy    964 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 ACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACAC 786

Qy   1024 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCA 846

Qy   1084 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 AGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 906

Qy   1144 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAA 966

Qy   1204 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 GCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTG 1026

Qy   1264 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 TATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAAT 1086

Qy   1324 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 TTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAG 1146

Qy   1384 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 GTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1206

Qy   1444 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATC 1266

Qy   1504 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1563
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Db   1267 GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGA 1326

Qy   1564 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 TGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTT 1386

Qy   1624 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1683
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Db   1387 ATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTT 1446

Qy   1684 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 AATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1506

Qy   1744 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA 1566

Qy   1804 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAA 1626

Qy   1864 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 AAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAG 1686

Qy   1924 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTAT 1746

Qy   1984 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 GAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1806

Qy   2044 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCT 1866

Qy   2104 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 CATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATT 1926

Qy   2164 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 ATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCT 1986

Qy   2224 TCCACCAGGCCCCCTACGTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2283
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Db   1987 TCCACCAGGCCCCCTACGTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTT 2046

Qy   2284 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2343
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Db   2047 CCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2106

Qy   2344 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTA 2166

Qy   2404 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2463
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Db   2167 GTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTA 2226

Qy   2464 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 TGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTG 2286

Qy   2524 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2583
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Db   2287 AAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCA 2346

Qy   2584 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 GGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2406

Qy   2644 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2454
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Search completed: February 13, 2000, 20:38:45
Job time: 12004 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:38:45 ; Search time 683.56 Seconds
(without alignments)
943.216 Million cell updates/sec

Title: US-09-026-459A-42_COPY_7_2583
Perfect score: 2577
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2577

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2577	100.0	3347	1	V58448	Modified retinobla
2	2242	87.0	2994	1	Q04713	Cancer supressing
3	2242	87.0	2994	1	Q41545	Retinoblastoma gen
4	2242	87.0	3233	1	Q72690	Retinoblastoma 94k
5	2242	87.0	3461	1	V58447	Modified retinobla
6	2242	87.0	3554	1	V58452	Modified retinobla
7	2242	87.0	3555	1	V58440	Modified retinobla
8	2242	87.0	3455	1	V58441	Modified retinobla
9	2242	87.0	3392	1	V58442	Modified retinobla
10	2242	87.0	3323	1	V58443	Modified retinobla
11	2242	87.0	3266	1	V58444	Modified retinobla
12	2242	87.0	3113	1	V58445	Modified retinobla
13	2242	87.0	3323	1	V58446	Modified retinobla
14	2242	87.0	3555	1	V54990	DNA sequence of th
15	2242	87.0	3218	1	V54991	DNA sequence of th
16	2242	87.0	2994	1	V40004	Retinoblastoma pro
17	2242	87.0	2995	1	X00737	cDNA encoding a re
18	2191	85.0	4597	1	N81369	Human retinoblasto
19	2191	85.0	4597	1	Q70536	Human retinoblasto
20	2191	85.0	2995	1	Q90059	Retinoblastoma tum
21	2191	85.0	4597	1	X04501	Human retinoblasto
22	2062	80.0	3161	1	V58449	Modified retinobla
23	2061	80.0	3377	1	V58450	Modified retinobla
24	2038	79.1	2995	1	Q86398	Human Rb110 cDNA.
25	1885	73.1	3383	1	V58451	Modified retinobla
26	1548	60.1	5056	1	N90489	cDNA of human reti
27	1410	54.7	4579	1	N81261	Probe for retinobl
28	198	7.7	18303	1	X04502	Human retinoblasto
29	165	6.4	18177	1	N90490	DNA of human retin
c 30	26	1.0	26	1	V49234	rb gene antisense
c 31	26	1.0	26	1	V49235	rb gene antisense
32	25	1.0	40	1	T12226	Human retinoblasto
33	25	1.0	40	1	V11847	Human Rb PCR prime
34	24	0.9	24	1	V01247	Retinoblastoma 1 P
c 35	24	0.9	24	1	V49224	rb gene antisense
c 36	23	0.9	23	1	V49227	rb gene antisense
c 37	23	0.9	23	1	V49222	rb gene antisense
c 38	23	0.9	23	1	V49225	rb gene antisense
c 39	23	0.9	32	1	V58466	Primer for Modifie
c 40	23	0.9	32	1	V59932	PCR primer used to
41	22	0.9	52	1	Q27110	PCR primer for the
42	22	0.9	50	1	Q27131	5' PCR primer for
43	22	0.9	50	1	Q99012	Chelating peptide-
c 44	22	0.9	22	1	T11461	Retinoblastoma gen
c 45	22	0.9	22	1	T12860	PCR 3' primer for

ALIGNMENTS

RESULT 1
V58448
ID V58448 standard; DNA; 3347 BP.
AC V58448;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2586
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69372.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 196-200; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3347 BP; 1096 A; 650 C; 617 G; 984 T;

Query Match 100.0%; Score 2577; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy     181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 246

Qy     241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

Qy     301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGTCGAATCTACTGAAATAAATTCTGCATTG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGTCGAATCTACTGAAATAAATTCTGCATTG 366

Qy     361 GTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAA 420
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Db    367 GTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAA 426

Qy    421 GATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTC 480

Db    427 GATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTC 486

Qy    481 TCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCA 540

Db    487 TCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCA 546

Qy    541 CCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAAT 600

Db    547 CCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAAT 606

Qy    601 GATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAA 660

Db    607 GATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAA 666

Qy    661 AATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAAT 720

Db    667 AATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAAT 726

Qy    721 GGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAA 780

Db    727 GGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAA 786

Qy    781 GATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGAC 840

Db    787 GATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGAC 846

Qy    841 AGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATT 900

Db    847 AGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATT 906

Qy    901 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTA 960

Db    907 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTA 966

Qy    961 AATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTG 1020

Db    967 AATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTG 1026

Qy   1021 AATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAA 1080

Db   1027 AATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAA 1086

Qy   1081 TTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGA 1140

Db   1087 TTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGA 1146

Qy   1141 GTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1200

Db   1147 GTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCC 1206

Qy   1201 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGC 1260

Db   1207 ATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGC 1266

Qy   1261 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1320

Db   1267 GCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1326

Qy   1321 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1380

Db   1327 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTAC 1386

Qy   1381 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1440

Db   1387 AAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACAT 1446

Qy   1441 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1500

Db   1447 TTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTA 1506

Qy   1501 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1560

Db   1507 TTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCT 1566

Qy   1561 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1620

Db   1567 TGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCT 1626

Qy   1621 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1680

Db   1627 GTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAG 1686

Qy   1681 ACACAAGCAACCTCAGCGTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTG 1740

Db   1687 ACACAAGCAACCTCAGCGTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTG 1746

Qy   1741 TTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 1800

Db   1747 TTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTT 1806

Qy   1801 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAG 1860

Db   1807 CTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAG 1866

Qy   1861 AATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTAT 1920

Db   1867 AATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTAT 1926

Qy   1921 GGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAG 1980

Db   1927 GGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAG 1986

Qy   1981 GATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTAT 2040

Db   1987 GATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTAT 2046

Qy   2041 GATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2100

Db   2047 GATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTG 2106

Qy   2101 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCT 2160

Db   2107 CAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCT 2166

Qy   2161 TACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTG 2220

Db   2167 TACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTG 2226

Qy   2221 AAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCA 2280

Db   2227 AAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCA 2286

Qy   2281 AGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAAT 2340

Db   2287 AGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAAT 2346

Qy   2341 CAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2400

Db   2347 CAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCT 2406

Qy   2401 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAA 2460

Db   2407 AAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAA 2466

Qy   2461 CATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACA 2520

Db   2467 CATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACA 2526

Qy   2521 CGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2577

Db   2527 CGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2583
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RESULT   2
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;
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Query Match 87.0%; Score 2242; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy     396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy     456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy     516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy     576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy     636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy     696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy     756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy     816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy     876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy     936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy     996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy    1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy    1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy    1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy    1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy    1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy    1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy    1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy    1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy    1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy    1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy    1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy    1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy    1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy    1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy    1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy    1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy    2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy    2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy    2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy    2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy    2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy    2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy    2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy    2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy    2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy    2556 TACCTCAAACAAGGAAGAGAAA 2577
           |||||||||||||||||||||||
Db    2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT   3
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag=  a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;
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  Query Match             87.0%;  Score 2242;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     681 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

Qy     396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 800

Qy     456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     801 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 860

Qy     516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy     576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy     636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy     696 TTCTCTTGGACTTGTAAGATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy     756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy     816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy     876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy     936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy     996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy    1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy    1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy    1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
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Db   1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2901 TACCTCAAACAAGGAAGAGAAA 2922
```

RESULT 4

Q72690

ID Q72690 standard; DNA; 3233 BP.

AC Q72690;

DT 01-JUN-1995 (first entry)

DE Retinoblastoma 94kD therapeutic protein encoding DNA.

KW Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT cds 19. .2469

FT /*tag= a

PN WO9421115-A.

PD 29-SEP-1994.

PF 24-MAR-1994; U03211.

PR 25-MAR-1993; US-038760.

PA (BAYU) BAYLOR COLLEGE MEDICINE.

PI Benedict WF, Xu H, Xu S;

DR WPI; 94-316534/39.

DR P-PSDB; R63564.

PT Broad spectrum tumour suppressor gene - by using retinoblastoma

PT gene product p94RB to suppress abnormal cell proliferation in the

PT treatment of cancer

PS Claim 4; Fig 1; 115pp; English.

CC Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor

CC gene) which encodes the 94kD therapeutic retinoblastoma protein

CC R63564. Expression of this protein in an abnormally proliferating

CC cell causes that cell to enter a senescent-like state, terminating

CC the proliferation. R63564 also has the advantage of engendering a low

CC incidence of tumour suppressor gene resistance in a population of

CC treated cells.

SQ Sequence 3233 BP; 1086 A; 597 C; 567 G; 983 T;

Query Match 87.0%; Score 2242; DB 1; Length 3233;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 284

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 344

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 404

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
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Db    405 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 464

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635

Db    465 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 524

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695

Db    525 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 584

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755

Db    585 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 644

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815

Db    645 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 704

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875

Db    705 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 764

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935

Db    765 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 824

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995

Db    825 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 884

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055

Db    885 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 944

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115

Db    945 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1004

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175

Db   1005 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1064

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235

Db   1065 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1124

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295

Db   1125 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1184

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355

Db   1185 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1244

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415

Db   1245 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1304

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475

Db   1305 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1364

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535

Db   1365 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1424

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595

Db   1425 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1484

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655

Db   1485 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1544

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715

Db   1545 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1604

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775

Db   1605 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1664

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835

Db   1665 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1724

Qy   1836 GACCCTTTTCCAGCACAGCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895

Db   1725 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1784

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955

Db   1785 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1844

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015

Db   1845 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1904

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075

Db   1905 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1964

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135

Db   1965 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2024

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195

Db   2025 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2084

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255

Db   2085 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2144

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315

Db   2145 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2204

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375

Db   2205 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2264

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435

Db   2265 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2324

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495

Db   2325 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2384

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555

Db   2385 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2444

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577

Db   2445 TACCTCAAACAAGGAAGAGAAA 2466
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RESULT 5
V58447
ID V58447 standard; DNA; 3461 BP.
AC V58447;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.

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KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;

  Query Match            87.0%;  Score 2242;  DB 1;  Length 3461;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 515

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 575

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 635

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 695

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 755

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 815

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 875

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    876 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 935

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 995

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    996 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1055

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1056 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1115

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1116 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1175

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1176 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1235

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1236 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1295

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1355

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1415

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1475

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1535

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1595

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1596 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1655

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1656 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1715

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1716 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1775

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1776 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1835

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1836 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1895

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1896 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1955

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1956 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2015

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2016 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2075

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2076 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2135

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2136 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2195
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Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2196 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2255

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2256 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2315

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2316 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2375

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2376 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2435

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2436 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2495

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2496 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2555

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2556 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2615

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2616 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2675

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2676 TACCTCAAACAAGGAAGAGAAA 2697
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RESULT   6
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;
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  Query Match            87.0%;  Score 2242;  DB 1;  Length 3554;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 608

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 668

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 728

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 788

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 848

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 908

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 968

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1028

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1088

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1148

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1208

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1268

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1328

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1388

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1448

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1508

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1568

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1628
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Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1688

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1748

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1808

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1868

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1928

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1988

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1989 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2048

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2108

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2168

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2228

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2288

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2348

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2468

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2528

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2588

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2589 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2648

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2649 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708
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Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2768

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2769 TACCTCAAACAAGGAAGAGAAA 2790
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RESULT 7
V58440
ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69364.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Disclosure; Page 121-126; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 87.0%; Score 2242; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 608

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 668

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 728

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 788

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 848

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 908

Qy    696 TTCTCTTGGACTTGTAACATGTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 968
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Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1028

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1088

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1148

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1208

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1268

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1328

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1388

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1448

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1508

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1568

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1628

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1688

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1748

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1808

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1868

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1928

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1988

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1989 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2048
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Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2108

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2168

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2228

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2288

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2348

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2468

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2528

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2588

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2589 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2648

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2649 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2768

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2769 TACCTCAAACAAGGAAGAGAAA 2790
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RESULT   8
V58441
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
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DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;

  Query Match             87.0%;  Score 2242;  DB 1;  Length 3455;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     450 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 509

Qy     396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     510 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 569

Qy     456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     570 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 629

Qy     516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     630 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 689

Qy     576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     690 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 749

Qy     636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     750 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 809

Qy     696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     810 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 869

Qy     756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 929

Qy     816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     930 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 989

Qy     876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     990 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1049

Qy     936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1050 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1109

Qy     996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1110 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1169

Qy    1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1170 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1229

Qy    1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1230 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1289

Qy    1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1290 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1349

Qy    1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1350 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1409

Qy    1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1410 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1469

Qy    1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1470 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1529

Qy    1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1530 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1589

Qy    1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1590 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1649

Qy    1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1650 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1709

Qy    1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1710 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1769

Qy    1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1770 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1829

Qy    1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1830 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1889

Qy    1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1890 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1949

Qy    1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1950 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2009

Qy    1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2010 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2069

Qy    1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2070 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2129

Qy    2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2130 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2189

Qy    2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2190 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2249

Qy    2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2250 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2309

Qy    2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2310 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2369

Qy    2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
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Db   2370 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2429

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375

Db   2430 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2489

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435

Db   2490 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2549

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495

Db   2550 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2609

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555

Db   2610 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2669

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577

Db   2670 TACCTCAAACAAGGAAGAGAAA 2691


RESULT   9
V58442
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


  Query Match             87.0%;  Score 2242;  DB 1;  Length 3392;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395

Db    387 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 446

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455

Db    447 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 506

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515

Db    507 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 566

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575

Db    567 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 626

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635

Db    627 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 686

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695

Db    687 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 746

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755

Db    747 TTCTCTTGGACTTGTAAGATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 806

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815

Db    807 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 866

Qy    816 AACTCTTCAGACTGATTGTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875

Db    867 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 926

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935

Db    927 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 986

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995

Db    987 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1046

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055

Db   1047 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1106

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115

Db   1107 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1166

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175

Db   1167 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1226

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235

Db   1227 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1286

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295

Db   1287 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1346

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355

Db   1347 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1406

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415

Db   1407 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1466

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475

Db   1467 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1526

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535

Db   1527 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1586

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595

Db   1587 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1646

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
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Db   1647 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1706

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1707 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1766

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1767 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1826

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1827 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1886

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1887 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1946

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1947 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2006

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2007 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2066

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2067 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2126

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2127 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2186

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2187 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2246

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2247 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2306

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2307 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2366

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2367 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2426

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2427 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2486

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2487 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2546

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2547 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2606

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2607 TACCTCAAACAAGGAAGAGAAA 2628
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RESULT  10
V58443
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998 (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;
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  Query Match           87.0%;  Score 2242;  DB 1;  Length 3323;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 377

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 437

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 497

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    498 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 557

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 617

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 677

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 737

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 797

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 857

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 917

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
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Db    918 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 977

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055

Db    978 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1037

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115

Db   1038 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1097

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175

Db   1098 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1157

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235

Db   1158 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1217

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295

Db   1218 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1277

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355

Db   1278 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1337

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415

Db   1338 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1397

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475

Db   1398 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1457

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535

Db   1458 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1517

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595

Db   1518 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1577

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655

Db   1578 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1637

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715

Db   1638 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1697

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775

Db   1698 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1757

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835

Db   1758 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1817

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895

Db   1818 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1877

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955

Db   1878 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1937

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015

Db   1938 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1997

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075

Db   1998 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2057

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135

Db   2058 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2117

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195

Db   2118 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2177

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255

Db   2178 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2237

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315

Db   2238 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2297

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375

Db   2298 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2357

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435

Db   2358 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2417

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495

Db   2418 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2477

Qy   2496 GGCAGAAATGACTTCTAGTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555

Db   2478 GGCAGAAATGACTTCTAGTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2537

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577

Db   2538 TACCTCAAACAAGGAAGAGAAA 2559
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RESULT 11
V58444
ID V58444 standard; DNA; 3266 BP.
AC V58444;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2505
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69368.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 166-170; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T;

Query Match 87.0%; Score 2242; DB 1; Length 3266;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 320

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 380

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 440

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 500

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 560

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 620

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 680

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 740

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 800

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 860

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 920

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 980

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1040

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1100

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1160

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1220

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1280

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1340

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1400

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1460

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1520

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1580

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1640

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1700

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1760

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1820

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1880

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1940

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2000

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2060

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2120

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2180

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2240

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2300

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2360

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2420
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Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2480

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||||
Db   2481 TACCTCAAACAAGGAAGAGAAA 2502


RESULT  12
V58445
ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;


  Query Match             87.0%;  Score 2242;  DB 1;  Length 3113;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    108 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 167

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    168 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 227

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    228 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 287

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    288 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 347

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    348 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 407

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    408 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 467

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    468 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 527

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    528 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 587

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    588 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 647

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    648 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 707

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    708 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 767

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    768 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 827

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    828 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 887

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    888 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 947

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    948 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1007

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1008 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1067

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1068 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1127

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1128 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1187

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1188 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1247

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1248 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1307

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1308 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1367

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1368 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1427

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1428 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1487

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1488 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1547

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1548 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1607
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Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1608 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1667

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1668 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1727

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1728 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1787

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1788 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1847

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1848 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1907

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1908 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1967

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1968 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2027

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2028 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2087

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2088 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2147

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2148 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2207

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2208 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2267

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2268 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2327

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2328 TACCTCAAACAAGGAAGAGAAA 2349
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RESULT  13
V58446
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;
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  Query Match             87.0%;  Score 2242;  DB 1;  Length 3323;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 377

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 437

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 497

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    498 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 557

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 617

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 677

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 737

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 797

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 857

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 917

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 977

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1037

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1097

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1157
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Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1217

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1277

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1337

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1397

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1457

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1517

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1577

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1637

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1697

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1757

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1817

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1877

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1937

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1997

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2057

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2117

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2177

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2237

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2238 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2297

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2298 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2357

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2358 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2417

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2418 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2477

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2478 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2537

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2538 TACCTCAAACAAGGAAGAGAAA 2559
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RESULT 14
V54990
ID V54990 standard; DNA; 3555 BP.
AC V54990;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key   Location/Qualifiers
FT CDS   7. .2793
FT   /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

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  Query Match           87.0%;  Score 2242;  DB 1;  Length 3555;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    549 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 608

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 668

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 728

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 788

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 848

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 908

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 968

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1028

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1088

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1148

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1208

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1268

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1328

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1388

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1448

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1508

Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1568

Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1628

Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1688

Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1748

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1808

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1868

Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1928

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1988

Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1989 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2048

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2108

Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2168

Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2228

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2288

Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2348

Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2468

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2528

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2588

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2589 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2648

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2649 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2768
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Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
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Db   2769 TACCTCAAACAAGGAAGAGAAA 2790


RESULT  15
V54991
ID   V54991 standard; DNA; 3218 BP.
AC   V54991;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2457
FT                   /*tag= a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71355.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 153-157; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3218 BP;    1080 A;    595 C;    561 G;    982 T;


  Query Match             87.0%;  Score 2242;  DB 1;  Length 3218;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    336 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    213 ATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 272

Qy    396 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    273 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 332

Qy    456 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAC 392

Qy    516 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 452

Qy    576 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 512

Qy    636 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    513 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 572

Qy    696 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 755
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Db    573 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 632

Qy    756 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 692

Qy    816 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 752

Qy    876 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 812

Qy    936 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 872

Qy    996 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 932

Qy   1056 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1115
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Db    933 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 992

Qy   1116 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1175
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Db     993 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1052

Qy   1176 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1235
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Db    1053 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1112

Qy   1236 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1295
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Qy   1296 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1355
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Qy   1356 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1415
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Qy   1416 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1475
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Qy   1476 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1535
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Db    1353 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1412

Qy   1536 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1595
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Db    1413 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1472

Qy   1596 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1655
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Qy   1656 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1533 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1592

Qy   1716 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1593 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1652
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Qy   1776 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1835
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Db   1653 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1712

Qy   1836 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1895
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Qy   1896 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1955
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Qy   1956 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2015
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Db   1833 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1892

Qy   2016 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2075
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Qy   2076 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2135
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Qy   2136 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2195
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Db   2013 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2072

Qy   2196 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2255
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Db   2073 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2132

Qy   2256 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2133 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2192

Qy   2316 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2375
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Db   2193 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2252

Qy   2376 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2253 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2312

Qy   2436 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2495
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Db   2313 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2372

Qy   2496 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2555
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Db   2373 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2432

Qy   2556 TACCTCAAACAAGGAAGAGAAA 2577
          |||||||||||||||||||||
Db   2433 TACCTCAAACAAGGAAGAGAAA 2454
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Search completed: February 13, 2000, 20:40:56
Job time: 12135 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:40:56 ; Search time 683.56 Seconds
(without alignments)
875.138 Million cell updates/sec

Title: US-09-026-459A-44_COPY_7_2397
Perfect score: 2391
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2391

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2391	100.0	3161	1	V58449	Modified retinobla
2	2062	86.2	2994	1	Q04713	Cancer supressing
3	2062	86.2	2994	1	Q41545	Retinoblastoma gen
4	2062	86.2	3233	1	Q72690	Retinoblastoma 94k
5	2062	86.2	3461	1	V58447	Modified retinobla
6	2062	86.2	3347	1	V58448	Modified retinobla
7	2062	86.2	3554	1	V58452	Modified retinobla
8	2062	86.2	3555	1	V58440	Modified retinobla
9	2062	86.2	3455	1	V58441	Modified retinobla
10	2062	86.2	3392	1	V58442	Modified retinobla
11	2062	86.2	3323	1	V58443	Modified retinobla
12	2062	86.2	3266	1	V58444	Modified retinobla
13	2062	86.2	3113	1	V58445	Modified retinobla
14	2062	86.2	3323	1	V58446	Modified retinobla
15	2062	86.2	3555	1	V54990	DNA sequence of th
16	2062	86.2	3218	1	V54991	DNA sequence of th
17	2062	86.2	2994	1	V40004	Retinoblastoma pro
18	2062	86.2	2995	1	X00737	cDNA encoding a re
19	2061	86.2	3377	1	V58450	Modified retinobla
20	2011	84.1	4597	1	N81369	Human retinoblasto
21	2011	84.1	4597	1	Q70536	Human retinoblasto
22	2011	84.1	2995	1	Q86398	Human Rb110 cDNA.
23	2011	84.1	2995	1	Q90059	Retinoblastoma tum
24	2011	84.1	4597	1	X04501	Human retinoblasto
25	1885	78.8	3383	1	V58451	Modified retinobla
26	1548	64.7	5056	1	N90489	cDNA of human reti
27	1410	59.0	4579	1	N81261	Probe for retinobl
28	198	8.3	18303	1	X04502	Human retinoblasto
29	165	6.9	18177	1	N90490	DNA of human retin
c 30	26	1.1	26	1	V49234	rb gene antisense
c 31	26	1.1	26	1	V49235	rb gene antisense
32	25	1.0	40	1	T12226	Human retinoblasto
33	25	1.0	40	1	V11847	Human Rb PCR prime
34	24	1.0	24	1	V01247	Retinoblastoma 1 P
c 35	24	1.0	24	1	V49224	rb gene antisense
c 36	23	1.0	23	1	V49227	rb gene antisense
c 37	23	1.0	23	1	V49222	rb gene antisense
c 38	23	1.0	23	1	V49225	rb gene antisense
39	22	0.9	52	1	Q27110	PCR primer for the
40	22	0.9	50	1	Q27131	5' PCR primer for
41	22	0.9	50	1	Q99012	Chelating peptide-
c 42	22	0.9	22	1	T11461	Retinoblastoma gen
c 43	22	0.9	22	1	T12860	PCR 3' primer for
c 44	22	0.9	22	1	V49228	rb gene antisense
c 45	22	0.9	22	1	V58453	Primer OMRbAS300 f

ALIGNMENTS

RESULT 1
V58449
ID V58449 standard; DNA; 3161 BP.
AC V58449;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2400
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69373.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 203-207; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3161 BP; 1037 A; 619 C; 586 G; 919 T;

Query Match 100.0%; Score 2391; DB 1; Length 3161;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
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Db       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy     181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 246

Qy     241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

Qy     301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGCTGTTATACCCATTAATGGTTCACCTCGA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGCTGTTATACCCATTAATGGTTCACCTCGA 366

Qy     361 ACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACA 420
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Db    367 ACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACA 426

Qy    421 AGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 480

Db    427 AGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 486

Qy    481 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTT 540

Db    487 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTT 546

Qy    541 CCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 600

Db    547 CCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 606

Qy    601 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTT 660

Db    607 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTT 666

Qy    661 GAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCA 720

Db    667 GAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCA 726

Qy    721 CACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 780

Db    727 CACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 786

Qy    781 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCA 840

Db    787 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCA 846

Qy    841 AAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 900

Db    847 AAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 906

Qy    901 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGC 960

Db    907 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGC 966

Qy    961 TTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAA 1020

Db    967 TTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAA 1026

Qy   1021 AATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1080

Db   1027 AATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1086

Qy   1081 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGAT 1140

Db   1087 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGAT 1146

Qy   1141 TTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1200

Db   1147 TTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1206

Qy   1201 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAA 1260

Db   1207 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAA 1266

Qy   1261 CGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1320

Db   1267 CGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGAT 1326

Qy   1321 CTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1380

Db   1327 CTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1386

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Db   1387 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGA 1446

Qy   1441 TCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1500

Db   1447 TCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1506

Qy   1501 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTAT 1560

Db   1507 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTAT 1566

Qy   1561 AAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1620

Db   1567 AAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCT 1626

Qy   1621 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1680

Db   1627 GAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1686

Qy   1681 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATA 1740

Db   1687 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATA 1746

Qy   1741 TGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 1800

Db   1747 TGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 1806

Qy   1801 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCT 1860

Db   1807 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCT 1866

Qy   1861 ATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 1920

Db   1867 ATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTAT 1926

Qy   1921 GCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 1980

Db   1927 GCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 1986

Qy   1981 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGT 2040

Db   1987 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGT 2046

Qy   2041 CCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2100

Db   2047 CCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2106

Qy   2101 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATG 2160

Db   2107 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATG 2166

Qy   2161 GTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCA 2220

Db   2167 GTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCA 2226

Qy   2221 CTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2280

Db   2227 CTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2286

Qy   2281 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATG 2340

Db   2287 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATG 2346

Qy   2341 CAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2391

Db   2347 CAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2397
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RESULT   2
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
```

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FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;

  Query Match             86.2%;  Score 2062;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy    1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy    1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy    1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy    1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy    1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy    1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy    1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy    1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy    2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy    2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy    2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy    2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy    2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
           |||||||||||||||||||||||
Db    2901 TACCTCAAACAAGGAAGAGAAA 2922


RESULT   3
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag=  a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


  Query Match             86.2%;  Score 2062;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     861 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 920

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     921 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 980

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 1100

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1101 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1160

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1161 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1220

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1221 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1280

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1281 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1400

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1401 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1460

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1461 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1520

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1521 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1580

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1581 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640

Qy    1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1641 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1700

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1701 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1760

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1761 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1820

Qy    1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1821 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1880

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1881 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 2000

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2001 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 2060

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
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Db    2061 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 2120

Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2121 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2180

Qy    1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2181 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

Qy    1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2300

Qy    1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2301 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2360

Qy    1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2361 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2420

Qy    1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2421 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2480

Qy    1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2481 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

Qy    2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2541 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2600

Qy    2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2601 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2660

Qy    2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2661 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2720

Qy    2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2721 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2780

Qy    2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2781 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2840

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2841 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2900

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
           |||||||||||||||||||||
Db    2901 TACCTCAAACAAGGAAGAGAAA 2922
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RESULT   4
Q72690
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag= a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;
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  Query Match             86.2%;  Score 2062;  DB 1;  Length 3233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 464

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 524

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     525 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 584

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 644

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     645 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 704

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     705 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 764

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     765 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 824

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     825 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 884

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     885 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 944

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     945 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1004

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1005 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1064

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1065 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1124

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
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Db   1125 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1184

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1244

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1304

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1364

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1424

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1484

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1485 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1544

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1545 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1604

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1664

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1665 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1724

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1725 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1784

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1844

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1845 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1904

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1905 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1964

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1965 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2024

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2025 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2084

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2144

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2204

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2205 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2264

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2324

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2325 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2384

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2385 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2444

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db   2445 TACCTCAAACAAGGAAGAGAAA 2466
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RESULT 5
V58447
ID V58447 standard; DNA; 3461 BP.
AC V58447;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2700
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69371.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 188-192; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3461 BP; 1141 A; 675 C; 627 G; 1018 T;

Query Match 86.2%; Score 2062; DB 1; Length 3461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 695

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 755

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 815

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 875

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
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Db    876 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 935

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689

Db    936 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 995

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749

Db    996 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1055

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809

Db   1056 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1115

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869

Db   1116 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1175

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929

Db   1176 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1235

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989

Db   1236 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1295

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049

Db   1296 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1355

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109

Db   1356 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1415

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169

Db   1416 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1475

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229

Db   1476 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1535

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289

Db   1536 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1595

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349

Db   1596 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1655

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409

Db   1656 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1715

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469

Db   1716 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1775

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529

Db   1776 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1835

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589

Db   1836 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1895

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649

Db   1896 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1955

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
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Db   1956 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2015

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769

Db   2016 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2075

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829

Db   2076 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2135

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889

Db   2136 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2195

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949

Db   2196 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2255

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009

Db   2256 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2315

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069

Db   2316 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2375

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129

Db   2376 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2435

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189

Db   2436 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2495

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249

Db   2496 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2555

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309

Db   2556 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2615

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369

Db   2616 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2675

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391

Db   2676 TACCTCAAACAAGGAAGAGAAA 2697
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RESULT   6
V58448
ID   V58448 standard; DNA; 3347 BP.
AC   V58448;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2586
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69372.
PT   Retinoblastoma suppressor protein with N-terminal modification -
```

PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 196-200; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3347 BP; 1096 A; 650 C; 617 G; 984 T;

Query Match 86.2%; Score 2062; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 581

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    582 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 641

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    642 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 701

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    702 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 761

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    762 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 821

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    822 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 881

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    882 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 941

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    942 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1001

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1002 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1061

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1062 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1121

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1122 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1181

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1182 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1241

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1242 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1301

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1302 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1361

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1362 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1421

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1422 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1481

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1482 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1541

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1542 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1601

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1602 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1661

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1662 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1721

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1722 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1781

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1782 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1841

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1842 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1901

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1902 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1961

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1962 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2021

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2022 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2081

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2082 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2141

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2142 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2201

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2202 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2261

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2262 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2321

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2322 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2381

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2382 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2441

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2442 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2501
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Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2502 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2561

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||||
Db   2562 TACCTCAAACAAGGAAGAGAAA 2583


RESULT   7
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


  Query Match             86.2%;  Score 2062;  DB 1;  Length 3554;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 788

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 848

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 908

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 968

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1028

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1088

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1089 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1148

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1208

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1268

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1328

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1388

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1448

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1508

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1568

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1628

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1688

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1748

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1808

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1868

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1928

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1988

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1989 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2048

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2108

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2168

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2228
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Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2288

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2348

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2468

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2528

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2588

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2589 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2648

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2649 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2768

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db   2769 TACCTCAAACAAGGAAGAGAAA 2790
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RESULT   8
V58440
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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  Query Match            86.2%;  Score 2062;  DB 1;  Length 3555;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 788

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 848

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 908

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 968

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1028

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1088

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1148

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1208

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1268

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1328

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1388

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1448

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1508

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1568

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1628

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1688

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1748
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Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1808

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1868

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1928

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1988

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1989 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2048

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2108

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2168

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2228

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2288

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2348

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2468

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2528

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2588

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2589 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2648

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2649 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2768

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db   2769 TACCTCAAACAAGGAAGAGAAA 2790
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RESULT   9
V58441
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;   1153 A;    631 C;    627 G;    1044 T;
```

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  Query Match            86.2%;  Score 2062;  DB 1;  Length 3455;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 689

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 749

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    750 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 809

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    810 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 869

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 929

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    930 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 989

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1049

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1109

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1169
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Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1229

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1289

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1349

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1409

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1469

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1529

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1530 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1589

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1649

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1709

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1769

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1829

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1830 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1889

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1890 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1949

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1950 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2009

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2010 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2069

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2070 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2129

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2130 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2189

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2249
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Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2250 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2309

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2310 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2369

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2370 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2429

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2430 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2489

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2490 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2549

Qy   2250 ATCAGATGAAGCAGATGCAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2550 ATCAGATGAAGCAGATGCAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2609

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2610 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2669

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db   2670 TACCTCAAACAAGGAAGAGAAA 2691
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RESULT 10
V58442
ID V58442 standard; DNA; 3392 BP.
AC V58442;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2641
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69366.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 150-155; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3392 BP; 1137 A; 614 C; 607 G; 1034 T;

Query Match 86.2%; Score 2062; DB 1; Length 3392;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    567 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 626
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Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    627 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 686

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    687 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 746

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    747 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 806

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    807 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 866

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    867 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 926

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    927 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 986

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    987 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1046

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1047 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1106

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1107 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1166

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1167 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1226

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1227 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1286

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1287 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1346

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1347 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1406

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1407 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1466

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1467 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1526

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1527 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1586

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1587 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1646

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1647 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1706
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Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1707 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1766

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1767 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1826

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1827 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1886

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
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Db   1887 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1946

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
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Db   1947 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2006

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2007 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2066

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2067 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2126

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2127 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2186

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2187 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2246

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2247 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2306

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2307 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2366

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2367 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2426

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2427 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2486

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2487 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2546

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2547 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2606

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db   2607 TACCTCAAACAAGGAAGAGAAA 2628
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RESULT 11
V58443
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.

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OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;

  Query Match            86.2%;  Score 2062;  DB 1;  Length 3323;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    498 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 557

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 617

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 677

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 737

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 797

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 857

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 917

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 977

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1037

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1097

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1157

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1217

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1277

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1337

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1397

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1457

Qy   1290 TGCATGGCTCTCAGATTGACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 TGCATGGCTCTCAGATTGACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1517

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1577

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1637

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1697

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
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Db   1698 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1757

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1817

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1877

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1937

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1997

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2057

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2117

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2177

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2237

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
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Db    2238 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2297

Qy    2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
Db    2298 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2357

Qy    2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
Db    2358 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2417

Qy    2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
Db    2418 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2477

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
Db    2478 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2537

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
Db    2538 TACCTCAAACAAGGAAGAGAAA 2559
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RESULT  12
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;
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  Query Match             86.2%;  Score 2062;  DB 1;  Length 3266;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2062;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
Db     441 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 500

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
Db     501 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 560

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
Db     561 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 620

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
Db     621 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 680

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
Db     681 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 740

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
Db     741 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 800

Qy     690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
Db     801 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 860

Qy     750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
Db     861 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 920

Qy     810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
Db     921 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 980

Qy     870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
Db     981 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1040

Qy     930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
Db    1041 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1100

Qy     990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
Db    1101 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1160

Qy    1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
Db    1161 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1220

Qy    1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
Db    1221 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1280

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
Db    1281 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1340

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
Db    1341 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1400

Qy    1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
Db    1401 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1460

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
Db    1461 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1520

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
Db    1521 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1580

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
Db    1581 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1640

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
Db    1641 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1700

Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
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Db   1701 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1760

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1820

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1880

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1940

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2000

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2060

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2120

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2180

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2240

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2300

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2360

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2420

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2480

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391
          |||||||||||||||||||||
Db   2481 TACCTCAAACAAGGAAGAGAAA 2502
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RESULT  13
V58445
ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;
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Query Match 86.2%; Score 2062; DB 1; Length 3113;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    288 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 347

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    348 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 407

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    408 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 467

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    468 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 527

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    528 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 587

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    588 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 647

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    648 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 707

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    708 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 767

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    768 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 827

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    828 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 887

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    888 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 947

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    948 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1007

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1008 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1067

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
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Db    1068 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1127

Qy    1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1128 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1187

Qy    1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1188 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1247

Qy    1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1248 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1307

Qy    1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1308 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1367

Qy    1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1368 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1427

Qy    1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1428 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1487

Qy    1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1488 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1547

Qy    1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1548 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1607

Qy    1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1608 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1667

Qy    1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1668 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1727

Qy    1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1728 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1787

Qy    1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1788 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1847

Qy    1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1848 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1907

Qy    1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1908 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 1967

Qy    2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1968 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2027

Qy    2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2028 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2087

Qy    2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2088 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2147

Qy    2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2148 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2207

Qy    2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2208 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2267

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2268 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2327

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
           |||||||||||||||||||||||
Db    2328 TACCTCAAACAAGGAAGAGAAA 2349
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RESULT 14
V58446
ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

Query Match 86.2%; Score 2062; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     498 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 557

Qy     390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     558 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 617

Qy     450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     618 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 677

Qy     510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     678 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 737

Qy     570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     738 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 797

Qy     630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
```

```
Db    798 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 857

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749

Db    858 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 917

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809

Db    918 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 977

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869

Db    978 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1037

Qy    870 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929

Db   1038 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1097

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989

Db   1098 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1157

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049

Db   1158 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1217

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109

Db   1218 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1277

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169

Db   1278 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1337

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229

Db   1338 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1397

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289

Db   1398 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1457

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349

Db   1458 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1517

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409

Db   1518 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1577

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469

Db   1578 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1637

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529

Db   1638 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1697

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589

Db   1698 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1757

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649

Db   1758 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1817

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709

Db   1818 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1877

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769

Db   1878 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1937

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829

Db   1938 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1997

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889

Db   1998 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2057

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949

Db   2058 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2117

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009

Db   2118 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2177

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069

Db   2178 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2237

Qy   2070 ACCAACAAAAATGACTCGAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129

Db   2238 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2297

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189

Db   2298 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2357

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249

Db   2358 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2417

Qy   2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309

Db   2418 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2477

Qy   2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369

Db   2478 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2537

Qy   2370 TACCTCAAACAAGGAAGAGAAA 2391

Db   2538 TACCTCAAACAAGGAAGAGAAA 2559


RESULT  15
V54990
ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= "a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
```

PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 86.2%; Score 2062; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    330 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGC 788

Qy    390 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACA 848

Qy    450 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 908

Qy    510 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 968

Qy    570 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAA 1028

Qy    630 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAA 1088

Qy    690 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACAC 1148

Qy    750 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1208

Qy    810 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1268

Qy    870 TATAGGATACATCTTTAAAGAGAAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TATAGGATACATCTTTAAAGAGAAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAAT 1328

Qy    930 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 TGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 1388

Qy    990 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 TAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACAT 1448

Qy   1050 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 TTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1508

Qy   1110 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1568

Qy   1170 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1628

Qy   1230 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 CTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCT 1688

Qy   1290 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 TGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGG 1748

Qy   1350 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 ACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1808

Qy   1410 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCG 1868

Qy   1470 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 TGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCC 1928

Qy   1530 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 ATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1988

Qy   1590 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 1649
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Db   1989 GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTG 2048

Qy   1650 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 1709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2108

Qy   1710 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2168

Qy   1770 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 1829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACG 2228

Qy   1830 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 1889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCAT 2288

Qy   1890 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 1949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACC 2348

Qy   1950 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

Qy   2010 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2468

Qy   2070 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGAC 2528

Qy   2130 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 TTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAG 2588

Qy   2190 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2589 AAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGG 2648

Qy    2250 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2649 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708

Qy    2310 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2768

Qy    2370 TACCTCAAACAAGGAAGAGAAA 2391
           |||||||||||||||||||||
Db    2769 TACCTCAAACAAGGAAGAGAAA 2790


Search completed: February 13, 2000, 20:42:52
Job time: 12251 sec
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:42:52 ; Search time 683.56 Seconds
(without alignments)
954.197 Million cell updates/sec

Title: US-09-026-459A-46_COPY_7_2613
Perfect score: 2607
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2607

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2607	100.0	3377	1	V58450	Modified retinobla
2	2061	79.1	2994	1	Q04713	Cancer supressing
3	2061	79.1	2994	1	Q41545	Retinoblastoma gen
4	2061	79.1	3233	1	Q72690	Retinoblastoma 94k
5	2061	79.1	3461	1	V58447	Modified retinobla
6	2061	79.1	3347	1	V58448	Modified retinobla
7	2061	79.1	3161	1	V58449	Modified retinobla
8	2061	79.1	3554	1	V58452	Modified retinobla
9	2061	79.1	3555	1	V58440	Modified retinobla
10	2061	79.1	3455	1	V58441	Modified retinobla
11	2061	79.1	3392	1	V58442	Modified retinobla
12	2061	79.1	3323	1	V58443	Modified retinobla
13	2061	79.1	3266	1	V58444	Modified retinobla
14	2061	79.1	3113	1	V58445	Modified retinobla
15	2061	79.1	3323	1	V58446	Modified retinobla
16	2061	79.1	3555	1	V54990	DNA sequence of th
17	2061	79.1	3218	1	V54991	DNA sequence of th
18	2061	79.1	2994	1	V40004	Retinoblastoma pro
19	2061	79.1	2995	1	X00737	cDNA encoding a re
20	2010	77.1	4597	1	N81369	Human retinoblasto
21	2010	77.1	4597	1	Q70536	Human retinoblasto
22	2010	77.1	2995	1	Q86398	Human Rb110 cDNA.
23	2010	77.1	2995	1	Q90059	Retinoblastoma tum
24	2010	77.1	4597	1	X04501	Human retinoblasto
25	1885	72.3	3383	1	V58451	Modified retinobla
26	1548	59.4	5056	1	N90489	cDNA of human reti
27	1410	54.1	4579	1	N81261	Probe for retinobl
28	198	7.6	18303	1	X04502	Human retinoblasto
29	165	6.3	18177	1	N90490	DNA of human retin
c 30	26	1.0	26	1	V49234	rb gene antisense
c 31	26	1.0	26	1	V49235	rb gene antisense
32	25	1.0	40	1	T12226	Human retinoblasto
33	25	1.0	40	1	V11847	Human Rb PCR prime
34	24	0.9	24	1	V01247	Retinoblastoma 1 P
c 35	24	0.9	24	1	V49224	rb gene antisense
c 36	23	0.9	23	1	V49227	rb gene antisense
c 37	23	0.9	23	1	V49222	rb gene antisense
c 38	23	0.9	23	1	V49225	rb gene antisense
39	22	0.8	52	1	Q27110	PCR primer for the
40	22	0.8	50	1	Q27131	5' PCR primer for
41	22	0.8	50	1	Q99012	Chelating peptide-
c 42	22	0.8	22	1	T11461	Retinoblastoma gen
c 43	22	0.8	22	1	T12860	PCR 3' primer for
c 44	22	0.8	22	1	V49228	rb gene antisense
c 45	22	0.8	22	1	V58453	Primer OMRbAS300 f

ALIGNMENTS

RESULT 1
V58450
ID V58450 standard; DNA; 3377 BP.
AC V58450;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2616
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69374.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 210-215; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3377 BP; 1113 A; 654 C; 626 G; 984 T;

Query Match 100.0%; Score 2607; DB 1; Length 3377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy     181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 246

Qy     241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

Qy     301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 366

Qy     361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
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Db    367 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 426

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Db    427 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 486

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Db    487 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 546

Qy    541 ATGGTCGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGG 600

Db    547 ATGGTCGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGG 606

Qy    601 AGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAA 660

Db    607 AGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAA 666

Qy    661 GAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTT 720

Db    667 GAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTT 726

Qy    721 ATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAA 780

Db    727 ATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAA 786

Qy    781 CGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCAT 840

Db    787 CGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCAT 846

Qy    841 GATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAA 900

Db    847 GATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAA 906

Qy    901 AGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATG 960

Db    907 AGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATG 966

Qy    961 AACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAAT 1020

Db    967 AACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAAT 1026

Qy   1021 CTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1080

Db   1027 CTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTG 1086

Qy   1081 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTC 1140

Db   1087 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTC 1146

Qy   1141 GAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCC 1200

Db   1147 GAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCC 1206

Qy   1201 ATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGAC 1260

Db   1207 ATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGAC 1266

Qy   1261 AACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGC 1320

Db   1267 AACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGC 1326

Qy   1321 AGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1380

Db   1327 AGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAAT 1386

Qy   1381 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 1440

Db   1387 GTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAA 1446

Qy   1441 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAA 1500

Db   1447 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAA 1506

Qy   1501 TCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGA 1560

Db   1507 TCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGA 1566

Qy   1561 GAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAAT 1620

Db   1567 GAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAAT 1626

Qy   1621 CACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1680

Db   1627 CACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACT 1686

Qy   1681 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 1740

Db   1687 ACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAG 1746

Qy   1741 AAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTAT 1800

Db   1747 AAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTAT 1806

Qy   1801 CTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATC 1860

Db   1807 CTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATC 1866

Qy   1861 ATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCAT 1920

Db   1867 ATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCAT 1926

Qy   1921 TTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 1980

Db   1927 TTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTT 1986

Qy   1981 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTC 2040

Db   1987 AAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTC 2046

Qy   2041 AAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTC 2100

Db   2047 AAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTC 2106

Qy   2101 TTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTG 2160

Db   2107 TTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTG 2166

Qy   2161 TCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATT 2220

Db   2167 TCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATT 2226

Qy   2221 CCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2280

Db   2227 CCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTG 2286

Qy   2281 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTC 2340

Db   2287 CCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTC 2346

Qy   2341 GGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTC 2400

Db   2347 GGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTC 2406

Qy   2401 AAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATT 2460

Db   2407 AAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATT 2466

Qy   2461 GAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2520

Db   2467 GAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAG 2526

Qy   2521 AAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2580

Db   2527 AAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGC 2586
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Qy   2581 ATGGATACCTCAAACAAGGAAGAGAAA 2607
          ||||||||||||||||||||||||||
Db   2587 ATGGATACCTCAAACAAGGAAGAGAAA 2613


RESULT   2
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


  Query Match             79.1%;  Score 2061;  DB 1;  Length 2994;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1221

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1222 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1521

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1522 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1641

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1821

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1822 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1881

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1941

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1942 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 2001

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2002 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 2121

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2181

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2241

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2301

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2361

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2421

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2422 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2481

Qy    2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2482 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2541

Qy    2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2542 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2601

Qy    2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2602 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

Qy    2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2662 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2721

Qy    2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2722 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2781

Qy    2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2782 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2841

Qy    2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2842 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2901

Qy    2587 ACCTCAAACAAGGAAGAGAAA 2607
           |||||||||||||||||||||
Db    2902 ACCTCAAACAAGGAAGAGAAA 2922


RESULT   3
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


  Query Match            79.1%;  Score 2061;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 921

Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     922 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 1041

Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1042 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 1101

Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1102 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1221

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1222 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1281

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1341

Qy    1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1342 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1401

Qy    1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1402 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

Qy    1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1521

Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1522 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

Qy    1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1641

Qy    1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1642 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1701

Qy    1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1702 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

Qy    1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1821

Qy    1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
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Db   1822 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1881

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1941

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1942 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 2001

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2002 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 2121

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2181

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2241

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2301

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2361

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2421

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2422 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2481

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2482 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2541

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2542 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2601

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2602 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2662 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2721

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2722 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2781

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2782 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2841

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2842 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2901

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2902 ACCTCAAACAAGGAAGAGAAA 2922
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RESULT 4
Q72690
ID Q72690 standard; DNA; 3233 BP.
AC Q72690;
DT 01-JUN-1995 (first entry)
DE Retinoblastoma 94kD therapeutic protein encoding DNA.
KW Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 19. .2469
FT /*tag= a
PN WO9421115-A.
PD 29-SEP-1994.
PF 24-MAR-1994; U03211.
PR 25-MAR-1993; US-038760.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PI Benedict WF, Xu H, Xu S;
DR WPI; 94-316534/39.
DR P-PSDB; R63564.
PT Broad spectrum tumour suppressor gene - by using retinoblastoma
PT gene product p94RB to suppress abnormal cell proliferation in the
PT treatment of cancer
PS Claim 4; Fig 1; 115pp; English.
CC Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC gene) which encodes the 94kD therapeutic retinoblastoma protein
CC R63564. Expression of this protein in an abnormally proliferating
CC cell causes that cell to enter a senescent-like state, terminating
CC the proliferation. R63564 also has the advantage of engendering a low
CC incidence of tumour suppressor gene resistance in a population of
CC treated cells.
SQ Sequence 3233 BP; 1086 A; 597 C; 567 G; 983 T;

Query Match 79.1%; Score 2061; DB 1; Length 3233;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 465

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 525

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 585

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 645

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 705

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 765

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 825

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 885

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
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Db    886 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 945

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1005

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1065

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1125

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1185

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1245

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1305

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1365

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1425

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1485

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1545

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1605

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1665

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1725

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1785

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1845

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1905

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1906 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 1965

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1966 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2025

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2085

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2145

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2205

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2265

Qy   2407 AGTGCTGAAGGAAGCAAGCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 AGTGCTGAAGGAAGCAAGCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2325

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2385

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2445

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2446 ACCTCAAACAAGGAAGAGAAA 2466
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RESULT 5
V58447
ID V58447 standard; DNA; 3461 BP.
AC V58447;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2700
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69371.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 188-192; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3461 BP; 1141 A; 675 C; 627 G; 1018 T;

Query Match 79.1%; Score 2061; DB 1; Length 3461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
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Db    637 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 696

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    697 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 756

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 816

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 876

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 936

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 996

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1056

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1116

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1176

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1236

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1296

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1356

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1416

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1476

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1536

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1537 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1596

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1597 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1656

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1657 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1716

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1717 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1776

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1777 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1836

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1837 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1896

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1897 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1956

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1957 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2016

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2017 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2076

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2077 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2136

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2137 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2196

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2197 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2256

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2257 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2316

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2317 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2376

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2377 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2436

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2437 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2496

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2497 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2556

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2557 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2616

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2617 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2676

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2677 ACCTCAAACAAGGAAGAGAAA 2697


RESULT   6
V58448
ID   V58448 standard; DNA; 3347 BP.
AC   V58448;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
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KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2586
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69372.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 196-200; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3347 BP;    1096 A;    650 C;    617 G;    984 T;

  Query Match             79.1%;  Score 2061;  DB 1;  Length 3347;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 582

Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 642

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     643 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 702

Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     703 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 762

Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     763 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 822

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     823 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 882

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     883 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 942

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     943 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1002

Qy    1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1003 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1062

Qy    1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1063 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1122

Qy    1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1123 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1182

Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1183 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1242

Qy    1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1243 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1302

Qy    1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1303 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1362

Qy    1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1363 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1422

Qy    1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1423 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1482

Qy    1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1483 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1542

Qy    1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1543 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1602

Qy    1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1603 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1662

Qy    1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1663 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1722

Qy    1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1723 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1782

Qy    1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1783 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1842

Qy    1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1843 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1902

Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1903 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1962

Qy    1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1963 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2022

Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2023 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2082

Qy    2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2083 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2142

Qy    2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2143 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2202

Qy    2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2203 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2262
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Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2263 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2322

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2323 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2382

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2383 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2442

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2443 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2502

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2503 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2562

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2563 ACCTCAAACAAGGAAGAGAAA 2583


RESULT   7
V58449
ID   V58449 standard; DNA; 3161 BP.
AC   V58449;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2400
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69373.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 203-207; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3161 BP;    1037 A;    619 C;    586 G;    919 T;


  Query Match             79.1%;  Score 2061;  DB 1;  Length 3161;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 396

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 456

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    457 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 516

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 576

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 636

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 696

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    697 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 756

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 816

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 876

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 936

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 996

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1056

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1057 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1116

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1117 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1176

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1177 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1236

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1237 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1296

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1297 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1356

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1357 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1416

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1417 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1476

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1477 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1536

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1537 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1596
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Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1597 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1656

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1657 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1716

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1717 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1776

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1777 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1836

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1837 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 1896

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1897 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 1956

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1957 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2016

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2017 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2076

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2077 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2136

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2137 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2196

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2197 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2256

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2257 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2316

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2317 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2376

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2377 ACCTCAAACAAGGAAGAGAAA 2397
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RESULT   8
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;
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  Query Match             79.1%;  Score 2061;  DB 1;  Length 3554;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 789

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 849

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 909

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 969

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1029

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1089

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1149

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1209

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1269

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1329

Qy   1147 GGATCACAGCGATACAAAGTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GGATCACAGCGATACAAAGTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1389

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1449

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1509
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Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1569

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1629

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1689

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1749

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1809

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1869

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1929

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1989

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2049

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2109

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2169

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2229

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2289

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2349

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2409

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2469

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2529

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2589
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Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2649

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2709

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2769

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2770 ACCTCAAACAAGGAAGAGAAA 2790
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RESULT 9
V58440
ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69364.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Disclosure; Page 121-126; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 79.1%; Score 2061; DB 1; Length 3555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 789

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 849

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 909

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 969

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1029
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Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 1089

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1090 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1149

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1150 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1209

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1210 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1269

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1270 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1329

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1330 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1389

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1390 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1449

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1450 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1509

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1510 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1569

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1570 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1629

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1630 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1689

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1690 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1749

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1750 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1809

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1810 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1869

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1870 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1929

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1930 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1989

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2049

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2109

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2110 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2169

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2170 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2229

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2230 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2289

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2290 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2349

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2409

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2469

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2529

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2589

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2649

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2709

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2769

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2770 ACCTCAAACAAGGAAGAGAAA 2790
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RESULT 10
V58441
ID V58441 standard; DNA; 3455 BP.
AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7..2694
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.

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CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


  Query Match            79.1%;  Score 2061;  DB 1;  Length 3455;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     631 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 690

Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 750

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 810

Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 870

Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 930

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 990

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     991 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1050

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1110

Qy    1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1111 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1170

Qy    1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1171 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1230

Qy    1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1231 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1290

Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1291 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1350

Qy    1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1351 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1410

Qy    1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1411 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1470

Qy    1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1471 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1530

Qy    1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1531 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1590

Qy    1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1591 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1650

Qy    1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1651 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1710

Qy    1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1711 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1770

Qy    1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1771 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1830

Qy    1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1831 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1890

Qy    1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1891 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1950

Qy    1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1951 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 2010

Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2011 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2070

Qy    1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2071 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2130

Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2131 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2190

Qy    2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2191 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2250

Qy    2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2251 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2310

Qy    2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2311 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2370

Qy    2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2371 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2430

Qy    2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2431 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2490

Qy    2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2491 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2550

Qy    2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2551 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2610

Qy    2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2611 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2670

Qy    2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db    2671 ACCTCAAACAAGGAAGAGAAA 2691


RESULT  11
V58442
ID    V58442 standard; DNA; 3392 BP.
AC    V58442;
DT    02-DEC-1998  (first entry)
DE    Modified retinoblastoma tumour suppressor gene.
KW    Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW    cellular proliferation inhibitor; ss.
OS    Homo sapiens.
FH    Key             Location/Qualifiers
FT    CDS             7. .2641
FT                    /*tag= a
PN    WO9837091-A2.
PD    27-AUG-1998.
PF    19-FEB-1998; U03041.
PR    20-FEB-1997; US-038118.
PA    (BAYU ) BAYLOR COLLEGE MEDICINE.
PA    (TEXA ) UNIV TEXAS SYSTEM.
PI    Benedict WF, Hu S, Xu H, Zhou Y;
DR    WPI; 98-480788/41.
DR    P-PSDB; W69366.
PT    Retinoblastoma suppressor protein with N-terminal modification -
PT    inhibiting cellular proliferation, particularly cancer
PS    Claim 22; Page 150-155; 249pp; English.
CC    This sequence encodes a modified retinoblastoma tumour suppressor
CC    protein (RTSP) of the invention. The proteins can be used for inhibiting
CC    cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC    can be used for treating diseases characterised by abnormal cellular
CC    proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC    activity than wild type RTSPs.
SQ    Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


  Query Match             79.1%;  Score 2061;  DB 1;  Length 3392;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 627

Qy     607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 687

Qy     667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 747

Qy     727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 807

Qy     787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 867

Qy     847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 927

Qy     907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     928 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 987

Qy     967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     988 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1047

Qy    1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1048 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1107

Qy    1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1108 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1167

Qy    1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1168 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1227

Qy    1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1228 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1287

Qy    1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1288 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1347

Qy    1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1348 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1407

Qy    1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1408 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1467

Qy    1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1468 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1527

Qy    1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1528 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1587

Qy    1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1588 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1647

Qy    1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1648 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1707

Qy    1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1708 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1767

Qy    1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1768 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1827

Qy    1807 CTAAATACACTTTGTGAAGGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1828 CTAAATACACTTTGTGAAGGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1887

Qy    1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1888 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1947

Qy    1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1948 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 2007

Qy    1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2008 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2067

Qy    2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
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Db   2068 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2127

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166

Db   2128 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2187

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226

Db   2188 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2247

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286

Db   2248 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2307

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346

Db   2308 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2367

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406

Db   2368 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2427

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466

Db   2428 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2487

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526

Db   2488 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2547

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586

Db   2548 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2607

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607

Db   2608 ACCTCAAACAAGGAAGAGAAA 2628
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RESULT  12
V58443
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;
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  Query Match             79.1%;  Score 2061;  DB 1;  Length 3323;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606

Db    499 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 558

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666

Db    559 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 618

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726

Db    619 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 678

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786

Db    679 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 738

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846

Db    739 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 798

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906

Db    799 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 858

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966

Db    859 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 918

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026

Db    919 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 978

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086

Db    979 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1038

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146

Db   1039 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1098

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206

Db   1099 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1158

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266

Db   1159 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1218

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326

Db   1219 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1278

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386

Db   1279 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1338

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446

Db   1339 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1398

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506

Db   1399 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1458

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566

Db   1459 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1518

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
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Db   1519 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1578

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1638

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1698

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1758

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1818

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1878

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1938

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1998

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2058

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2118

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2178

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2238

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2298

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2358

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2359 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2418

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2478

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2538

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2539 ACCTCAAACAAGGAAGAGAAA 2559

RESULT 13
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V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


  Query Match             79.1%;  Score 2061;  DB 1;  Length 3266;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 501

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 561

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 621

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    622 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 681

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    682 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 741

Qy    847 ACTCTTCAGACTGATTGTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    742 ACTCTTCAGACTGATTGTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 801

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    802 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 861

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 921

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 981

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
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Db    982 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1041

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1101

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1102 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1161

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1162 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1221

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1222 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1281

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1282 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1341

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1342 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1401

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1402 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1461

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1462 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1521

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1522 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1581

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1582 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1641

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1642 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1701

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1702 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1761

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1762 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1821

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1822 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1881

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1882 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1941

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1942 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2001

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2002 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2061

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2062 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2121

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2181

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2182 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2241

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2301

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2361

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2421

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2422 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2481

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607
          |||||||||||||||||||||
Db   2482 ACCTCAAACAAGGAAGAGAAA 2502
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RESULT 14
V58445
ID V58445 standard; DNA; 3113 BP.
AC V58445;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2352
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69369.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 173-177; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3113 BP; 1039 A; 577 C; 547 G; 950 T;

Query Match 79.1%; Score 2061; DB 1; Length 3113;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 348

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
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Db    349 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 408

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726

Db    409 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 468

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786

Db    469 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 528

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846

Db    529 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 588

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906

Db    589 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 648

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966

Db    649 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 708

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026

Db    709 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 768

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086

Db    769 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 828

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146

Db    829 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 888

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206

Db    889 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 948

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266

Db    949 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1008

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326

Db   1009 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1068

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386

Db   1069 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1128

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446

Db   1129 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1188

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506

Db   1189 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1248

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566

Db   1249 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1308

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626

Db   1309 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1368

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686

Db   1369 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1428

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746

Db   1429 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1488

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806

Db   1489 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1548

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866

Db   1549 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1608

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926

Db   1609 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1668

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986

Db   1669 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1728

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046

Db   1729 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1788

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106

Db   1789 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 1848

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166

Db   1849 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 1908

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226

Db   1909 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 1968

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286

Db   1969 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2028

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346

Db   2029 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2088

Qy   2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406

Db   2089 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2148

Qy   2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466

Db   2149 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2208

Qy   2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526

Db   2209 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2268

Qy   2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586

Db   2269 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2328

Qy   2587 ACCTCAAACAAGGAAGAGAAA 2607

Db   2329 ACCTCAAACAAGGAAGAGAAA 2349


RESULT  15
V58446
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;

  Query Match            79.1%;  Score 2061;  DB 1;  Length 3323;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    547 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCA 558

Qy    607 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 CGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 618

Qy    667 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAT 678

Qy    727 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 TCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATAC 738

Qy    787 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 GAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 798

Qy    847 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAAC 858

Qy    907 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 CTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 918

Qy    967 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATT 978

Qy   1027 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 TCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGAT 1038

Qy   1087 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 ATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1098

Qy   1147 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTT 1158

Qy   1207 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1159 AAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1218

Qy   1267 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGT 1278

Qy   1327 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 ACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTT 1338

Qy   1387 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 AATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1398

Qy   1447 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT 1458

Qy   1507 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 GCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1518

Qy   1567 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACT 1578

Qy   1627 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 GCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGT 1638

Qy   1687 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 GTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1698

Qy   1747 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGG 1758

Qy   1807 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 CTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1818

Qy   1867 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGAC 1878

Qy   1927 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 CAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTC 1938

Qy   1987 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 AAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1998

Qy   2047 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATG 2058

Qy   2107 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2118

Qy   2167 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGA 2178

Qy   2227 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 GGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACA 2238

Qy   2287 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 CCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2298
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Qy    2347 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2299 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGA 2358

Qy    2407 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2359 AGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2418

Qy    2467 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2419 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTG 2478

Qy    2527 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2479 GCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGAT 2538

Qy    2587 ACCTCAAACAAGGAAGAGAAA 2607
           |||||||||||||||||||||
Db    2539 ACCTCAAACAAGGAAGAGAAA 2559
```

Search completed: February 13, 2000, 20:44:58
Job time: 12377 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:44:58 ; Search time 683.56 Seconds
(without alignments)
956.393 Million cell updates/sec

Title: US-09-026-459A-48_COPY_7_2619
Perfect score: 2613
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2613

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2613	100.0	3383	1	V58451	Modified retinobla
2	1885	72.1	2994	1	Q04713	Cancer supressing
3	1885	72.1	2994	1	Q41545	Retinoblastoma gen
4	1885	72.1	3233	1	Q72690	Retinoblastoma 94k
5	1885	72.1	3461	1	V58447	Modified retinobla
6	1885	72.1	3347	1	V58448	Modified retinobla
7	1885	72.1	3161	1	V58449	Modified retinobla
8	1885	72.1	3377	1	V58450	Modified retinobla
9	1885	72.1	3554	1	V58452	Modified retinobla
10	1885	72.1	3555	1	V58440	Modified retinobla
11	1885	72.1	3455	1	V58441	Modified retinobla
12	1885	72.1	3392	1	V58442	Modified retinobla
13	1885	72.1	3323	1	V58443	Modified retinobla
14	1885	72.1	3266	1	V58444	Modified retinobla
15	1885	72.1	3113	1	V58445	Modified retinobla
16	1885	72.1	3323	1	V58446	Modified retinobla
17	1885	72.1	3555	1	V54990	DNA sequence of th
18	1885	72.1	3218	1	V54991	DNA sequence of th
19	1885	72.1	2994	1	V40004	Retinoblastoma pro
20	1885	72.1	2995	1	X00737	cDNA encoding a re
21	1834	70.2	4597	1	N81369	Human retinoblasto
22	1834	70.2	4597	1	Q70536	Human retinoblasto
23	1834	70.2	2995	1	Q86398	Human Rb110 cDNA.
24	1834	70.2	2995	1	Q90059	Retinoblastoma tum
25	1834	70.2	4597	1	X04501	Human retinoblasto
26	1548	59.2	5056	1	N90489	cDNA of human reti
27	1349	51.6	4579	1	N81261	Probe for retinobl
28	198	7.6	18303	1	X04502	Human retinoblasto
29	165	6.3	18177	1	N90490	DNA of human retin
c 30	26	1.0	26	1	V49234	rb gene antisense
c 31	26	1.0	26	1	V49235	rb gene antisense
32	25	1.0	40	1	T12226	Human retinoblasto
33	25	1.0	40	1	V11847	Human Rb PCR prime
34	24	0.9	24	1	V01247	Retinoblastoma 1 P
c 35	24	0.9	24	1	V49224	rb gene antisense
c 36	23	0.9	23	1	V49227	rb gene antisense
c 37	23	0.9	23	1	V49222	rb gene antisense
c 38	23	0.9	23	1	V49225	rb gene antisense
c 39	23	0.9	32	1	V58466	Primer for Modifie
c 40	23	0.9	32	1	V59932	PCR primer used to
41	22	0.8	52	1	Q27110	PCR primer for the
42	22	0.8	50	1	Q27131	5' PCR primer for
43	22	0.8	50	1	Q99012	Chelating peptide-
c 44	22	0.8	22	1	T11461	Retinoblastoma gen
c 45	22	0.8	22	1	T12860	PCR 3' primer for

ALIGNMENTS

RESULT 1
V58451
ID V58451 standard; DNA; 3383 BP.
AC V58451;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2622
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69375.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 218-222; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3383 BP; 1104 A; 657 C; 623 G; 999 T;

Query Match 100.0%; Score 2613; DB 1; Length 3383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy     181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 246

Qy     241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

Qy     301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 366

Qy     361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
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Db    367 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 426

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Db    427 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 486

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Db    487 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 546

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Db    547 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 606

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Db    607 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 666

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Db    667 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 726

Qy    721 ACAGGGTCGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 780

Db    727 ACAGGGTCGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT 786

Qy    781 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 840

Db    787 TCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTG 846

Qy    841 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 900

Db    847 GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 906

Qy    901 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 960

Db    907 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 966

Qy    961 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1020

Db    967 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1026

Qy   1021 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1080

Db   1027 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAA 1086

Qy   1081 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1140

Db   1087 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGT 1146

Qy   1141 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1200

Db   1147 TGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1206

Qy   1201 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1260

Db   1207 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1266

Qy   1261 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1320

Db   1267 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1326

Qy   1321 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1380

Db   1327 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATT 1386

Qy   1381 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1440

Db   1387 CTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAA 1446

Qy   1441 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1500

Db   1447 GCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1506

Qy   1501 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1560

Db   1507 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1566

Qy   1561 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1620

Db   1567 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1626

Qy   1621 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1680

Db   1627 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT 1686

Qy   1681 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1740

Db   1687 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAG 1746

Qy   1741 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1800

Db   1747 ACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1806

Qy   1801 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1860

Db   1807 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1866

Qy   1861 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1920

Db   1867 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1926

Qy   1921 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1980

Db   1927 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 1986

Qy   1981 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2040

Db   1987 GACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAG 2046

Qy   2041 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2100

Db   2047 ACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2106

Qy   2101 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2160

Db   2107 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2166

Qy   2161 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2220

Db   2167 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2226

Qy   2221 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2280

Db   2227 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAA 2286

Qy   2281 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2340

Db   2287 GGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAA 2346

Qy   2341 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2400

Db   2347 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2406

Qy   2401 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2460

Db   2407 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2466

Qy   2461 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2520

Db   2467 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2526

Qy   2521 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2580

Db   2527 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2586
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Qy   2581 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2613
          ||||||||||||||||||||||||||||||||||
Db   2587 GATAGCATGGATACCTCAAACAAGGAAGAGAAA 2619
```

RESULT 2
Q04713
ID Q04713 standard; cDNA; 2994 BP.
AC Q04713;
DT 11-OCT-1990 (first entry)
DE Cancer supressing gene (CSG).
KW Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW RB; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 139. .2922
FT /*tag= a
PN WO9005180-A.
PD 17-MAY-1990.
PF 30-OCT-1989; 004808.
PR 31-OCT-1988; US-265829.
PA (REGC) Univ of Caifornia.
PI Lee WH, Huang HJS;
DR WPI; 90-178822/23.
DR P-PSDB; R05305.
PT Controlling cancer -
PT by replacing ineffective cancer suppressing gene with cloned,
PT active gene.
PS Claim 35; Page 86; 105pp; English.
CC Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC By installing a working CSG, safe and specific treatment and
CC prophylaxis can be given to cancer patients.
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

Query Match 72.1%; Score 1885; DB 1; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 1097

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1157

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1217

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1277

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1337

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1397

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1457

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1517

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1577

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1637

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1697

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1757

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1817

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1877

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1937

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1997

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 2057

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 2117

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2177

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2237

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2238 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2297

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2298 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2357

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2358 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2417

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2418 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2477

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2478 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2537

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2538 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2597

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2598 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2657

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2658 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2717

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2718 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2777

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2778 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2837

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2838 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2897

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2898 GGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   3
Q41545
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


  Query Match            72.1%;  Score 1885;  DB 1;  Length 2994;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 1097

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1157

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1217

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1277

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1337

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1397

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1457

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1517

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1577

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1637

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1697

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1757

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1817

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1877

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1937

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1997

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 2057

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 2117

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2177

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
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Db    2178 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2237

Qy    1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
Db    2238 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2297

Qy    1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
Db    2298 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2357

Qy    2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
Db    2358 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2417

Qy    2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
Db    2418 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2477

Qy    2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
Db    2478 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2537

Qy    2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
Db    2538 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2597

Qy    2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
Db    2598 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2657

Qy    2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
Db    2658 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2717

Qy    2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
Db    2718 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2777

Qy    2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
Db    2778 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2837

Qy    2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
Db    2838 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2897

Qy    2589 GGATACCTCAAACAAGGAAGAGAAA 2613
Db    2898 GGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT   4
Q72690
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;
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  Query Match             72.1%;  Score 1885;  DB 1;  Length 3233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
Db     582 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 641

Qy     789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
Db     642 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 701

Qy     849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
Db     702 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 761

Qy     909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
Db     762 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 821

Qy     969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
Db     822 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 881

Qy    1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
Db     882 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 941

Qy    1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
Db     942 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1001

Qy    1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
Db    1002 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1061

Qy    1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
Db    1062 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1121

Qy    1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
Db    1122 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1181

Qy    1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
Db    1182 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1241

Qy    1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
Db    1242 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1301

Qy    1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
Db    1302 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1361

Qy    1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
Db    1362 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1421

Qy    1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
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Db   1422 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1481

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1482 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1541

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1542 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1601

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1602 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1661

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1662 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1721

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1722 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1781

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1782 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1841

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1842 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1901

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1902 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1961

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1962 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2021

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2022 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2081

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2082 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2141

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2142 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2201

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2202 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2261

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2262 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2321

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2322 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2381

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2382 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2441

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2442 GGATACCTCAAACAAGGAAGAGAAA 2466

RESULT   5
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V58447
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation; when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


  Query Match             72.1%;  Score 1885;  DB 1;  Length 3461;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 872

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 932

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    933 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 992

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1052

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1112

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1113 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1172

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1232

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1292

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1352

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
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Db   1353 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1412

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1472

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1532

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1533 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1592

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1593 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1652

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1653 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1712

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1713 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1772

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1773 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1832

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1833 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1892

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1893 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1952

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1953 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2012

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2013 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2072

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2073 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2132

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2133 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2192

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2193 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2252

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2253 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2312

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2313 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2372

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2373 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2432

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2433 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2492

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2493 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2552

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2553 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2612

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2613 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2672

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2673 GGATACCTCAAACAAGGAAGAGAAA 2697
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RESULT 6
V58448
ID V58448 standard; DNA; 3347 BP.
AC V58448;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2586
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69372.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 196-200; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3347 BP; 1096 A; 650 C; 617 G; 984 T;

Query Match 72.1%; Score 1885; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    699 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 758

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    759 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 818

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    819 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 878

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    879 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 938

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
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Db    939 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 998

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088

Db    999 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1058

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148

Db   1059 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1118

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208

Db   1119 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1178

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268

Db   1179 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1238

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328

Db   1239 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1298

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388

Db   1299 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1358

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448

Db   1359 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1418

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508

Db   1419 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1478

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568

Db   1479 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1538

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628

Db   1539 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1598

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688

Db   1599 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1658

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748

Db   1659 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1718

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808

Db   1719 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1778

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868

Db   1779 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1838

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928

Db   1839 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1898

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988

Db   1899 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1958

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048

Db   1959 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2018

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108

Db   2019 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2078

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168

Db   2079 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2138

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228

Db   2139 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2198

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288

Db   2199 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2258

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348

Db   2259 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2318

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408

Db   2319 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2378

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468

Db   2379 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2438

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528

Db   2439 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2498

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588

Db   2499 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2558

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613

Db   2559 GGATACCTCAAACAAGGAAGAGAAA 2583
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RESULT   7
V58449
ID   V58449 standard; DNA; 3161 BP.
AC   V58449;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2400
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69373.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 203-207; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3161 BP;    1037 A;    619 C;    586 G;    919 T;

  Query Match             72.1%;  Score 1885;  DB 1;  Length 3161;
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 572

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    573 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 632

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 692

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 752

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 812

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 872

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 932

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    933 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 992

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1052

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1112

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1113 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1172

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1232

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1292

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1352

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1353 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1412

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1472

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1532

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1533 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1592

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1593 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1652

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1653 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1712

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1713 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1772

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Db   1773 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1832

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1833 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1892

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1893 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 1952

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1953 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2012

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2013 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2072

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2073 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2132

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2133 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2192

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2193 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2252

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2253 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2312

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2313 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2372

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2373 GGATACCTCAAACAAGGAAGAGAAA 2397


RESULT   8
V58450
ID   V58450 standard; DNA; 3377 BP.
AC   V58450;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2616
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
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PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69374.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 210-215; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3377 BP;    1113 A;    654 C;    626 G;    984 T;

  Query Match           72.1%;  Score 1885;  DB 1;  Length 3377;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
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Db    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
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Db   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
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Db   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Db   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168

Qy   2169 ACCAATACCTCACATTCGTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 ACCAATACCTCACATTCGTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
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Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2589 GGATACCTCAAACAAGGAAGAGAAA 2613


RESULT   9
V58452
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


  Query Match             72.1%;  Score 1885;  DB 1;  Length 3554;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 965

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1025

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1085

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1145

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1205

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1265

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1325

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db   1326 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1385

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1445

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1505

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1565

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1625

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1685

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1745

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1805

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1806 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1865

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1866 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1925

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1926 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1985

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2045

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2046 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2105

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2106 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2165

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2166 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2225

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2226 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2285

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2286 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2345

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2346 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2405

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2406 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2465
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Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2466 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2525

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2526 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2585

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2586 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2645

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2646 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2705

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2706 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2765

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2766 GGATACCTCAAACAAGGAAGAGAAA 2790


RESULT  10
V58440
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


  Query Match             72.1%;  Score 1885;  DB 1;  Length 3555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 965

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 1025

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1026 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 1085

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1145

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1205

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1265

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1325

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
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Db   1326 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1385

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
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Db   1386 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1445

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1505

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1565

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1625

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1685

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1745

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1805

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1806 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1865

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
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Db   1866 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1925

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
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Db   1926 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1985

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 2045

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2046 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2105

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2106 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2165
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Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Db   2166 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2225

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2226 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2285

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2286 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2345

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2346 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2405

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2406 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2465

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2466 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2525

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2526 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2585

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2586 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2645

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2646 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2705

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2706 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2765

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2766 GGATACCTCAAACAAGGAAGAGAAA 2790
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RESULT  11
V58441
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;
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  Query Match             72.1%;  Score 1885;  DB 1;  Length 3455;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    807 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 866

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    867 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 926

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    927 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 986

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    987 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 1046

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1047 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1106

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1107 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1166

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1167 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1226

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1227 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1286

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1287 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1346

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1347 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1406

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1407 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1466

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1467 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1526

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1527 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1586

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1587 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1646

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1647 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1706

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1707 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1766
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Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1767 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1826

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1827 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1886

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1887 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1946

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1947 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2006

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2007 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2066

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2067 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2126

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2127 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2186

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2187 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2246

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2247 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2306

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2307 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2366

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2367 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2426

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2427 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2486

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2487 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2546

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2547 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2606

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2607 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2666

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2667 GGATACCTCAAACAAGGAAGAGAAA 2691
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RESULT  12
V58442
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;   1137 A;    614 C;    607 G;    1034 T;
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Query Match 72.1%; Score 1885; DB 1; Length 3392;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    744 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 803

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    804 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 863

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 923

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 983

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1043

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1103

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1163

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1223

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1283

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1343

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1403
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Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1404 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1463

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1464 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1523

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1524 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1583

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1584 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1643

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1644 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1703

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1704 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1763

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1764 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1823

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1824 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1883

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1884 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1943

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1944 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 2003

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2004 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2063

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2064 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2123

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2124 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2183

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2184 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2243

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2244 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2303

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2304 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2363

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
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Db   2364 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2423

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2424 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2483

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2484 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2543

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2544 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2603

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2604 GGATACCTCAAACAAGGAAGAGAAA 2628
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RESULT 13
V58443
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

Query Match 72.1%; Score 1885; DB 1; Length 3323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 734

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 794

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    795 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 854

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    855 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 914

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    915 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 974

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    975 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1034
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Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1035 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1094

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1095 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1154

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1155 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1214

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1215 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1274

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1275 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1334

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1335 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1394

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1395 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1454

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1455 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1514

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1515 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1574

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1575 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1634

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1635 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1694

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1695 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1754

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1755 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1814

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1815 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1874

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1875 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1934

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1935 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1994

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1995 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2054

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2055 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2114
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Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2115 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2174

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2175 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2234

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2235 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2294

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2295 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2354

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2355 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2414

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2415 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2474

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2475 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2534

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2535 GGATACCTCAAACAAGGAAGAGAAA 2559
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RESULT  14
V58444
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;
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  Query Match           72.1%;  Score 1885;  DB 1;  Length 3266;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 677
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Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 737

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 797

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 857

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 917

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 977

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1037

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1097

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1157

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1217

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1277

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1337

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1397

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1457

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1517

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1577

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1637

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1697

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1757
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Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1817

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1877

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1937

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1997

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2057

Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2117

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2177

Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2237

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2238 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2297

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2298 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2357

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2358 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2417

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2418 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2477

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
          |||||||||||||||||||||||||
Db   2478 GGATACCTCAAACAAGGAAGAGAAA 2502
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RESULT  15
V58445
ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
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DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;

  Query Match            72.1%;  Score 1885;  DB 1;  Length 3113;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1885;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    729 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACG 524

Qy    789 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 ATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGA 584

Qy    849 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 TAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAG 644

Qy    909 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 TAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAA 704

Qy    969 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 CACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCT 764

Qy   1029 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 GATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAA 824

Qy   1089 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 GGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGA 884

Qy   1149 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 AATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT 944

Qy   1209 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 GCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAA 1004

Qy   1269 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 CATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAG 1064

Qy   1329 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGT 1124

Qy   1389 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 GCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGG 1184

Qy   1449 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 CAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATC 1244

Qy   1509 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 CCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGA 1304

Qy   1569 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 AGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCA 1364

Qy   1629 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 CACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTAC 1424

Qy   1689 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425 GCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAA 1484

Qy   1749 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1808
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Db   1485 GCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCT 1544

Qy   1809 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1545 CCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCAT 1604

Qy   1869 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 CTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 1664

Qy   1929 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1988
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Db   1665 GGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAA 1724

Qy   1989 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 2048
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Db   1725 ATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAA 1784

Qy   2049 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1785 ACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTT 1844

Qy   2109 CATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC 2168
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Qy   2169 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2228
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Db   1905 ACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 1964

Qy   2229 TGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC 2288
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Qy   2289 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2348
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Db   2025 AACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGG 2084

Qy   2349 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2085 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAA 2144

Qy   2409 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2145 AAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGA 2204

Qy   2469 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2528
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Db   2205 AGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAA 2264

Qy   2529 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 ACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCAT 2324

Qy   2589 GGATACCTCAAACAAGGAAGAGAAA 2613
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Db   2325 GGATACCTCAAACAAGGAAGAGAAA 2349
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Search completed: February 13, 2000, 20:46:44
Job time: 12483 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2000, 20:46:44 ; Search time 683.56 Seconds
(without alignments)
1018.981 Million cell updates/sec

Title: US-09-026-459A-50_COPY_7_2790
Perfect score: 2784
Sequence: 1 ATGCCGCCCAAAACCCCCCG.....CCTCAAACAAGGAAGAGAAA 2784

Scoring table: OLIGO_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2784	100.0	3554	1	V58452	Modified retinobla
2	2682	96.3	3555	1	V58440	Modified retinobla
3	2682	96.3	3555	1	V54990	DNA sequence of th
4	2682	96.3	2994	1	V40004	Retinoblastoma pro
5	2631	94.5	2994	1	Q41545	Retinoblastoma gen
6	2631	94.5	2995	1	Q90059	Retinoblastoma tum
7	2594	93.2	2994	1	Q04713	Cancer supressing
8	2594	93.2	2995	1	X00737	cDNA encoding a re
9	2581	92.7	3455	1	V58441	Modified retinobla
10	2517	90.4	3392	1	V58442	Modified retinobla
11	2511	90.2	4597	1	Q70536	Human retinoblasto
12	2511	90.2	4597	1	X04501	Human retinoblasto
13	2478	89.0	2995	1	Q86398	Human Rb110 cDNA.
14	2460	88.4	4597	1	N81369	Human retinoblasto
15	2449	88.0	3323	1	V58443	Modified retinobla
16	2448	87.9	3233	1	Q72690	Retinoblastoma 94k
17	2448	87.9	3461	1	V58447	Modified retinobla
18	2448	87.9	3266	1	V58444	Modified retinobla
19	2448	87.9	3323	1	V58446	Modified retinobla
20	2448	87.9	3218	1	V54991	DNA sequence of th
21	2343	84.2	3113	1	V58445	Modified retinobla
22	2242	80.5	3347	1	V58448	Modified retinobla
23	2062	74.1	3161	1	V58449	Modified retinobla
24	2061	74.0	3377	1	V58450	Modified retinobla
25	1885	67.7	3383	1	V58451	Modified retinobla
26	1548	55.6	5056	1	N90489	cDNA of human reti
27	1410	50.6	4579	1	N81261	Probe for retinobl
28	198	7.1	18303	1	X04502	Human retinoblasto
29	165	5.9	18177	1	N90490	DNA of human retin
c 30	26	0.9	26	1	V49234	rb gene antisense
c 31	26	0.9	26	1	V49235	rb gene antisense
32	25	0.9	40	1	T12226	Human retinoblasto
33	25	0.9	40	1	V11847	Human Rb PCR prime
34	24	0.9	24	1	V01247	Retinoblastoma 1 P
c 35	24	0.9	24	1	V49224	rb gene antisense
36	24	0.9	24	1	V58463	Primer OMRbS332 fo
c 37	23	0.8	23	1	V49227	rb gene antisense
c 38	23	0.8	23	1	V49222	rb gene antisense
c 39	23	0.8	23	1	V49225	rb gene antisense
c 40	23	0.8	32	1	V58466	Primer for Modifie
c 41	23	0.8	24	1	V58462	Primer OMRbAS332 f
c 42	23	0.8	32	1	V59932	PCR primer used to
43	22	0.8	52	1	Q27110	PCR primer for the
44	22	0.8	50	1	Q27131	5' PCR primer for
45	22	0.8	50	1	Q99012	Chelating peptide-

ALIGNMENTS

RESULT 1
V58452
ID V58452 standard; DNA; 3554 BP.
AC V58452;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69376.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 226-230; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3554 BP; 1170 A; 683 C; 653 G; 1048 T;

Query Match 100.0%; Score 2784; DB 1; Length 3554;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
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Db       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy      61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy     121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy     181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 246

Qy     241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

Qy     301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 366

Qy     361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
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Db    367 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 426

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Db    427 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 486

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Db    487 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 546

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Db    547 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 606

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Db    607 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 666

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Db    667 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 726

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Db    727 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 786

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Db    787 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 846

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

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Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Db    907 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 966

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Db    967 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1026

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Db   1027 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1086

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Db   1087 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1146

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Db   1147 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1206

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Db   1207 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1266

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Db   1267 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1326

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Db   1327 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1386

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Db   1387 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1446

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
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Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Db   1507 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1566

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Db   1567 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1626

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Db   1627 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1686

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Db   1687 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1746

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Db   1747 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1806

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Db   1807 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1866

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Db   1867 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1926

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Db   1927 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1986

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Db   1987 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2046

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Db   2047 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2106

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Db   2107 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2166

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Db   2167 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2226

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Db   2227 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2286

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Db   2287 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2346

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Db   2347 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2406

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Db   2407 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2466

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Db   2467 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2526

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Db   2527 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2586
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Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
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Db   2587 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2646

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
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Db   2647 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2706

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
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Db   2707 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2766

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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Db   2767 GATACCTCAAACAAGGAAGAGAAA 2790
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RESULT   2
V58440
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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  Query Match             96.3%;  Score 2682;  DB 1;  Length 3555;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2782;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy     61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 246

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    247 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db    307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 366

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 426

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 486

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 546

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 606

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 666

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 726

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 786

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 846

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 906

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 966

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1026

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1086

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1146

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1206

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1266

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1326

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1386
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Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1446

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1506

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1566

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1626

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1686

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1746

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1806

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1866

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1926

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1986

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2046

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2106

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2166

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2226

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2286

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2346

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2406

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2466

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2467 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2526

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2527 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2586

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2587 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2646

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2647 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2706

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2707 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2766

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||
Db   2767 GATACCTCAAACAAGGAAGAGAAA 2790
```

RESULT 3
V54990
ID V54990 standard; DNA; 3555 BP.
AC V54990;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

Query Match 96.3%; Score 2682; DB 1; Length 3555;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2782; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 66

Qy     61 CCGGCACCGCCGCCGCCGCCCCCTCCTCGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CCGGCACCGCCGCCGCCGCCCCCTCCTCGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 126

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 186

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 246

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
        |||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db    307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 366

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 426

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 486

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 546

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 606

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 666

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 726

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 786

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 846

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 906

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
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Db    907 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 966

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
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Db    967 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1026

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
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Db   1027 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1086

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1146

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
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Db   1147 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1206

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1266

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1326

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1386

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1446

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1506

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1566

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1567 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1626

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1686

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1746

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1806

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1807 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1866

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1926

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1986

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2046

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2106

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2166

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2226
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Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2286

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2346

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2406

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2466

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2467 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2526

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2527 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2586

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2587 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2646

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2647 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2706

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2707 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2766

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||
Db   2767 GATACCTCAAACAAGGAAGAGAAA 2790
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RESULT   4
V40004
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;
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  Query Match             96.3%;  Score 2682;  DB 1;  Length 2994;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2782;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCCGCGGAACCC 198

Qy     61 CCGGCACCGCCGCCGCCGCCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 CCGGCACCGCCGCCGCCGCCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 258

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 318

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 378

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 438

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db    439 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 498

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 558

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 618

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 678

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 738

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 798

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 858

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 918

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    919 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 978
Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038
Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 1098
Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1158
Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1218
Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1278
Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338
Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1398
Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1458
Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1518
Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1578
Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638
Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1698
Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1758
Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1818
Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1878
Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938
Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1998
Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 2058

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 2118
Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2178
Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2238
Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2298
Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2358
Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418
Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2478
Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2538
Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2598
Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2599 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2658
Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718
Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2719 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2778
Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2838
Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2839 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898
Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||
Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 5
Q41545
ID Q41545 standard; DNA; 2994 BP.
AC Q41545;
DT 24-AUG-1993 (first entry)
DE Retinoblastoma gene.
KW RB gene product; p56RB portion; cell cycle progression control;
KW combination; therapeutic methods; arrest; tumourigenesis;
KW regulation; physiological processes; blood cell prodn.;
KW gamete prodn.; ss.
OS Homo sapiens SR-40 cell line.

```
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;
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  Query Match             94.5%;  Score 2631;  DB 1;  Length 2994;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2781;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 198

Qy     61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    199 CCGGCACCGCCGCCGCCGCCCCCTCCGGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 258

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 318

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 378

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 438

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db    439 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 498

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 558

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 618

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 678

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    679 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 738

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 798

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 858

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 918

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 978

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 1098

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1158

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1218

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1278

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1398

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1458

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1518

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1578

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1698

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1758

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1818
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Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1878

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1998

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 2058

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 2118

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2178

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2238

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2298

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2358

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2478

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2538

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2598

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2599 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2658

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2719 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2778

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2838

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2839 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898
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Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          ||||||||||||||||||||||||
Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 6
Q90059
ID Q90059 standard; DNA; 2995 BP.
AC Q90059;
DT 28-NOV-1995 (first entry)
DE Retinoblastoma tumour suppressor gene.
KW Recombinant; adenovirus; expression vector; TSG; small lung cancer;
KW hepatocarcinoma; melanoma; retinoblastoma; sarcoma; sickle cell;
KW anaemia; Tay-Sach's disease; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 139. .2925
FT /*tag= a
PN WO9511984-A.
PD 04-MAY-1995.
PF 25-OCT-1994; U12235.
PR 25-OCT-1993; US-142669.
PR 19-MAY-1994; US-246007.
PA (CANJ-) CANJI INC.
PI Gregory RJ, Maneval DC, Wills KN;
DR WPI; 95-178876/23.
DR P-PSDB; R74271.
PT Adenoviral vector with deletion of viral protein IX contains
PT foreign gene - esp. encoding tumour suppressor protein for gene
PT therapy of tumours, reduces contamination by wild type adenovirus
PS Disclosure; Fig 3; 92pp; English.
CC The sequence is that of the DNA sequence encoding a retinoblastoma
CC tumour protein. The gene can be used in a novel method involving a
CC recombinant adenovirus expression vector to treat diseases
CC associated with the ansence of the TSg or the presence of a mutated
CC TSG, e.g. many forms of carcinoma, sickle cell anaemia or Tay-Sach's
CC disease.
CC See also Q90060-5.
SQ Sequence 2995 BP; 975 A; 617 C; 594 G; 809 T;

Query Match 94.5%; Score 2631; DB 1; Length 2995;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2781; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 198

Qy     61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 258

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 318

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 378

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 438

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db    439 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 498

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 558
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Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 618

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 678

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 738

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 798

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 858

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 918

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 978

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 1098

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1158

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 AAAACTCTTCAGAGTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1218

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1278

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1398

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1458

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1518

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1578

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1698

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1758

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1818

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1878

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1998

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 2058

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2059 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 2118

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2119 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2178

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2179 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2238

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2239 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2298

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2299 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2358

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2419 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2478

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2479 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2538

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2598

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2599 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2658

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2719 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2778

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2838

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2839 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||
Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922


RESULT   7
Q04713
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


  Query Match             93.2%;  Score 2594;  DB 1;  Length 2994;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2694;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     89 AGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTG 148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    227 AGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTG 286

Qy    149 AAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATG 208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 AAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATG 346

Qy    209 TCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAG 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    347 TCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAG 406

Qy    269 GTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACC 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    407 GTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACC 466

Qy    329 TAGGTGATATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATA 388
          ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    467 TAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATA 526

Qy    389 AATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAA 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    527 AATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAA 586

Qy    449 GACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTG 508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    587 GACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTG 646

Qy    509 AACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGG 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    647 AACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGG 706

Qy    569 TGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAG 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    707 TGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAG 766

Qy    629 ATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCT 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    767 ATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCT 826

Qy    689 CACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCAC 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    827 CACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCAC 886

Qy    749 CTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATG 808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    887 CTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATG 946

Qy    809 ATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAA 868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    947 ATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAA 1006

Qy    869 ATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATG 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1007 ATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATG 1066

Qy    929 GACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAG 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1067 GACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAG 1126

Qy    989 ATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACA 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1127 ATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACA 1186

Qy   1049 GTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTC 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1187 GTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTC 1246

Qy   1109 CTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAA 1168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1247 CTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAA 1306

Qy   1169 ATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGA 1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1307 ATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGA 1366

Qy   1229 ATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAAT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1367 ATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAAT 1426

Qy   1289 TTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAG 1348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1427 TTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAG 1486

Qy   1349 TTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCA 1408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1487 TTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCA 1546

Qy   1409 TTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCG 1468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1547 TTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCG 1606

Qy   1469 CTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAA 1528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1607 CTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAA 1666

Qy   1529 CAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACA 1588
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Db   1667 CAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACA 1726

Qy   1589 AAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATT 1648

Db   1727 AAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATT 1786

Qy   1649 TAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTAT 1708

Db   1787 TAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTAT 1846

Qy   1709 TTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTT 1768

Db   1847 TTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTT 1906

Qy   1769 GTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTG 1828

Db   1907 GTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTG 1966

Qy   1829 TAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGA 1888

Db   1967 TAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGA 2026

Qy   1889 CACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGT 1948

Db   2027 CACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGT 2086

Qy   1949 TTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTC 2008

Db   2087 TTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTC 2146

Qy   2009 TGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGA 2068

Db   2147 TGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGA 2206

Qy   2069 ATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATG 2128

Db   2207 ATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATG 2266

Qy   2129 GCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGG 2188

Db   2267 GCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGG 2326

Qy   2189 ATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATG 2248

Db   2327 ATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATG 2386

Qy   2249 ATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGC 2308

Db   2387 ATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGC 2446

Qy   2309 AGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTT 2368

Db   2447 AGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTT 2506

Qy   2369 ACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGA 2428

Db   2507 ACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGA 2566

Qy   2429 AGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAA 2488

Db   2567 AGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAA 2626

Qy   2489 GAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATC 2548

Db   2627 GAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATC 2686

Qy   2549 AGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTA 2608

Db   2687 AGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTA 2746

Qy   2609 AACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAAC 2668

Db   2747 AACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAAC 2806

Qy   2669 ATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 2728

Db   2807 ATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 2866

Qy   2729 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784

Db   2867 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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RESULT 8
X00737
ID X00737 standard; cDNA; 2995 BP.
AC X00737;
DT 13-APR-1999 (first entry)
DE cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 139. .2925
FT /*tag= a
FT /product= RB_protein
FT /transl_except= (pos: 226. .228, aa: Glu)
PN US5851991-A.
PD 22-DEC-1998.
PF 13-SEP-1994; 306513.
PR 13-SEP-1994; US-306513.
PR 31-AUG-1987; US-091547.
PR 17-SEP-1987; US-098612.
PR 15-OCT-1987; US-108748.
PR 31-OCT-1988; US-265829.
PR 11-JUL-1990; US-550877.
PR 16-JUL-1990; US-553892.
PR 16-JUL-1990; US-553905.
PR 17-OCT-1991; US-778510.
PR 14-JUL-1992; US-914039.
PR 02-OCT-1992; US-956472.
PR 17-JUN-1993; US-079207.
PR 13-SEP-1993; US-121108.
PR 24-SEP-1993; US-126810.
PA (CANJ-) CANJI INC.
PA (REGC) UNIV CALIFORNIA.
PI Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI Wang NP;
DR WPI; 99-080477/07.
DR P-PSDB; W67801.
PT Inhibition of cancer cell proliferation - with retinoblastoma
PT protein or polypeptide
PS Example 1; Fig 2A-K; 72pp; English.
CC The present sequence encodes a human retinoblastoma (RB) protein
CC designated ppRB-110 or p110-RB. The protein is used in a method
CC for inhibiting proliferation of pathologically proliferating cells
CC lacking endogenous functional retinoblastoma protein. The method
CC comprises contacting the cells with a polypeptide comprising a 56 kD
CC C-terminal fragment of retinoblastoma protein. The method is useful
CC for treating cancers, especially retinoblastoma or secondary
CC osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T;

Query Match 93.2%; Score 2594; DB 1; Length 2995;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy     89 AGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTG 148

Db    227 AGGAGGACCCAGAGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTG 286

Qy    149 AAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATG 208
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Db    287 AAGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATG 346

Qy    209 TCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAG 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    347 TCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAG 406

Qy    269 GTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACC 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    407 GTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACC 466

Qy    329 TAGGTGATATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATA 388
          ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    467 TAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATA 526

Qy    389 AATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAA 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    527 AATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAA 586

Qy    449 GACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTG 508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    587 GACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTG 646

Qy    509 AACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGG 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    647 AACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGG 706

Qy    569 TGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAG 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    707 TGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAG 766

Qy    629 ATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCT 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    767 ATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCT 826

Qy    689 CACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCAC 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    827 CACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCAC 886

Qy    749 CTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATG 808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    887 CTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATG 946

Qy    809 ATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAA 868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    947 ATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAA 1006

Qy    869 ATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATG 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1007 ATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATG 1066

Qy    929 GACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAG 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1067 GACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAG 1126

Qy    989 ATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACA 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1127 ATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACA 1186

Qy   1049 GTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTC 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1187 GTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTC 1246

Qy   1109 CTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAA 1168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1247 CTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAA 1306

Qy   1169 ATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGA 1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1307 ATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGA 1366

Qy   1229 ATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAAT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1367 ATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAAT 1426

Qy   1289 TTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAG 1348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1427 TTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAG 1486

Qy   1349 TTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCA 1408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1487 TTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCA 1546

Qy   1409 TTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCG 1468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1547 TTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCG 1606

Qy   1469 CTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAA 1528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1607 CTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAA 1666

Qy   1529 CAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACA 1588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1667 CAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACA 1726

Qy   1589 AAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATT 1648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1727 AAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATT 1786

Qy   1649 TAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTAT 1708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1787 TAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTAT 1846

Qy   1709 TTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTT 1768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1847 TTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTT 1906

Qy   1769 GTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTG 1828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1907 GTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTG 1966

Qy   1829 TAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGA 1888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1967 TAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGA 2026

Qy   1889 CACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGT 1948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2027 CACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGT 2086

Qy   1949 TTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTC 2008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2087 TTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTC 2146

Qy   2009 TGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGA 2068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2147 TGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGA 2206

Qy   2069 ATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATG 2128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2207 ATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATG 2266

Qy   2129 GCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGG 2188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2267 GCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGG 2326

Qy   2189 ATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATG 2248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2327 ATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATG 2386

Qy   2249 ATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGC 2308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2387 ATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGC 2446

Qy   2309 AGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTT 2368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2447 AGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTT 2506
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Qy   2369 ACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGA 2428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2507 ACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGA 2566

Qy   2429 AGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAA 2488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2567 AGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAA 2626

Qy   2489 GAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATC 2548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2627 GAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATC 2686

Qy   2549 AGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTA 2608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2687 AGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTA 2746

Qy   2609 AACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAAC 2668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2747 AACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAAC 2806

Qy   2669 ATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 2728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2807 ATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACAC 2866

Qy   2729 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2867 GAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922


RESULT   9
V58441
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


  Query Match             92.7%;  Score 2581;  DB 1;  Length 3455;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2681;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    102 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGA 68

Qy    162 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 ACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGC 128

Qy    222 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 TTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 188

Qy    282 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTC 341
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||
Db    189 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 248

Qy    342 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTT 308

Qy    402 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAA 368

Qy    462 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 GTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 428

Qy    522 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 488

Qy    582 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 641
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 548

Qy    642 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 701
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTT 608

Qy    702 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 761
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 GCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAG 668

Qy    762 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 821
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 GCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 728

Qy    822 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 788

Qy    882 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 848

Qy    942 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 1001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAG 908

Qy   1002 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 1061
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 ATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACA 968

Qy   1062 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 GAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1028

Qy   1122 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 1088

Qy   1182 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1148

Qy   1242 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGT 1208
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Qy   1302 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 GGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTA 1268

Qy   1362 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 CCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1328

Qy   1422 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1388

Qy   1482 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1448

Qy   1542 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAG 1508

Qy   1602 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 TTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGA 1568

Qy   1662 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 ACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1628

Qy   1722 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1688

Qy   1782 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1748

Qy   1842 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTC 1808

Qy   1902 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGT 1868

Qy   1962 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 GTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1928

Qy   2022 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 2081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1988

Qy   2082 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1989 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2048

Qy   2142 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGC 2108

Qy   2202 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2109 TGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGT 2168

Qy   2262 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 ATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2228

Qy   2322 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2288

Qy   2382 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2348

Qy   2442 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATC 2408

Qy   2502 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 AATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAA 2468

Qy   2562 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 CAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2528

Qy   2622 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2529 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2588

Qy   2682 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2589 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2648

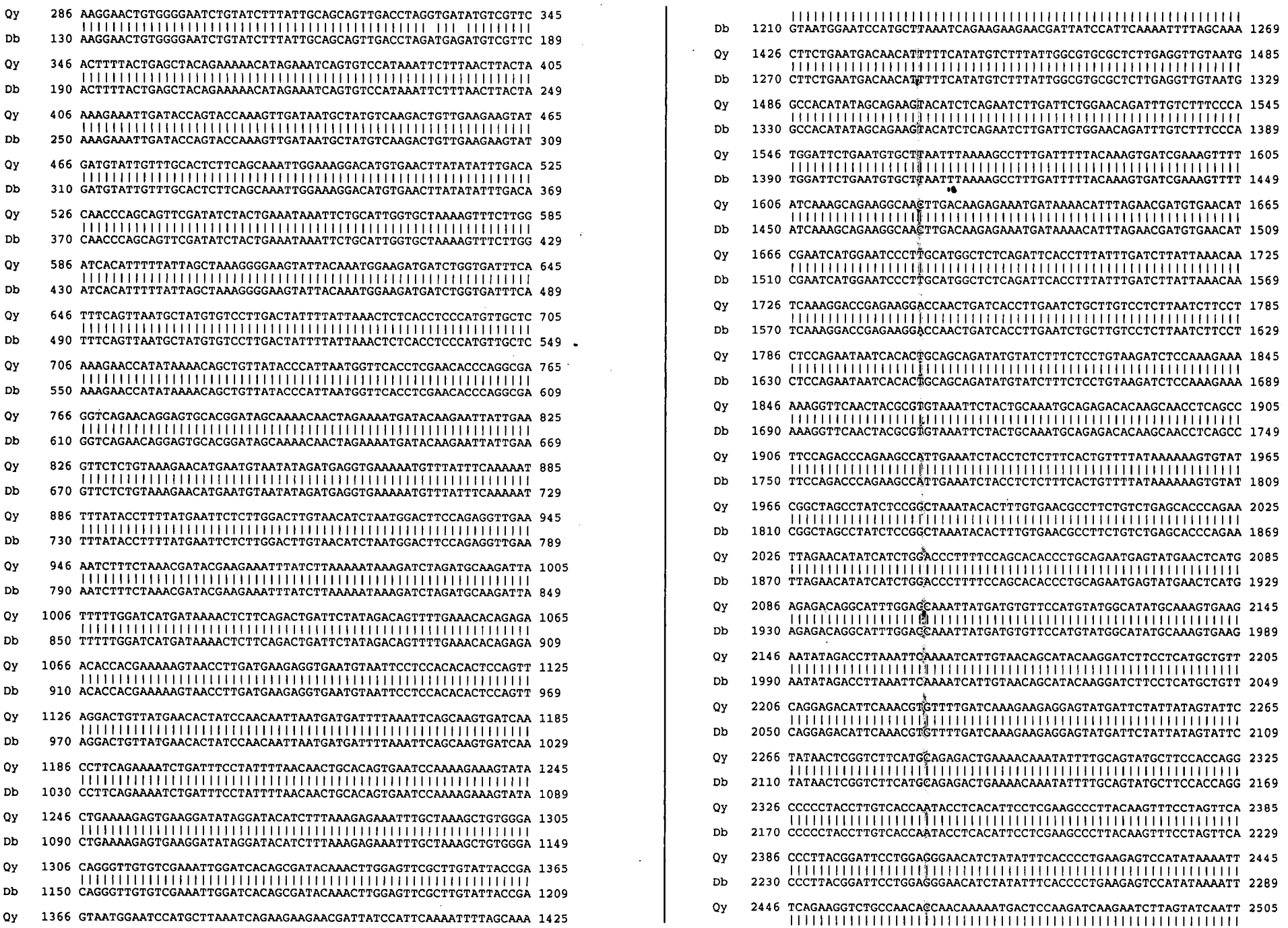
Qy   2742 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||||||||||||||||||||||
Db   2649 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2691
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RESULT 10
V58442
ID V58442 standard; DNA; 3392 BP.
AC V58442;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2641
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69366.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 150-155; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3392 BP; 1137 A; 614 C; 607 G; 1034 T;

Query Match 90.4%; Score 2517; DB 1; Length 3392;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2617; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    166 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGG 69

Qy    226 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 285
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 TTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAA 129
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Qy 286 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTC 345
Db 130 AAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTC 189
Qy 346 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 405
Db 190 ACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTA 249
Qy 406 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 465
Db 250 AAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 309
Qy 466 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 525
Db 310 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACA 369
Qy 526 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 585
Db 370 CAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGG 429
Qy 586 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 645
Db 430 ATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCA 489
Qy 646 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 705
Db 490 TTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTC 549
Qy 706 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 765
Db 550 AAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 609
Qy 766 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 825
Db 610 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAA 669
Qy 826 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 885
Db 670 GTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 729
Qy 886 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 945
Db 730 TTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAA 789
Qy 946 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 1005
Db 790 AATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTA 849
Qy 1006 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1065
Db 850 TTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 909
Qy 1066 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 1125
Db 910 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTT 969
Qy 1126 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1185
Db 970 AGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAA 1029
Qy 1186 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1245
Db 1030 CCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATA 1089
Qy 1246 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1305
Db 1090 CTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1149
Qy 1306 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1365
Db 1150 CAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1209
Qy 1366 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1425
Db 1210 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA 1269
Qy 1426 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1485
Db 1270 CTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG 1329
Qy 1486 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1545
Db 1330 GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA 1389
Qy 1546 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1605
Db 1390 TGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT 1449
Qy 1606 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1665
Db 1450 ATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1509
Qy 1666 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1725
Db 1510 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 1569
Qy 1726 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1785
Db 1570 TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCT 1629
Qy 1786 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1845
Db 1630 CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA 1689
Qy 1846 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1905
Db 1690 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC 1749
Qy 1906 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1965
Db 1750 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1809
Qy 1966 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 2025
Db 1810 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAA 1869
Qy 2026 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 2085
Db 1870 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATG 1929
Qy 2086 AGAGACAGGCATTTGGAGCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 2145
Db 1930 AGAGACAGGCATTTGGAGCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG 1989
Qy 2146 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2205
Db 1990 AATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTT 2049
Qy 2206 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2265
Db 2050 CAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2109
Qy 2266 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2325
Db 2110 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2169
Qy 2326 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2385
Db 2170 CCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCA 2229
Qy 2386 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2445
Db 2230 CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT 2289
Qy 2446 TCAGAAGGTCTGCCAACAGCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2505

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Db   2290 TCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT 2349

Qy   2506 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2350 GGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2409

Qy   2566 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTA 2469

Qy   2626 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 CGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCC 2529

Qy   2686 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 AAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAA 2589

Qy   2746 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||||||||||||||||||
Db   2590 ATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628


RESULT  11
Q70536
ID   Q70536 standard; DNA; 4597 BP.
AC   Q70536;
DT   27-MAR-1995  (first entry)
DE   Human retinoblastoma gene.
KW   Retinoblastoma; cancer; detection; diagnosis; protein; neoplasm;
KW   assay; immune complex; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             337. .2787
FT                   /*tag=  a
PN   EP-608004-A.
PD   27-JUL-1994.
PF   11-AUG-1987; 307095.
PR   11-AUG-1986; US-895163.
PA   (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA   (WHED ) WHITEHEAD INST.
PA   BIOMEDICAL RES.
PI   Dryja TP,  Friend S;
DR   WPI; 94-272746/34.
DR   P-PSDB; R58568.
PT   Diagnosing the presence of defective retinoblastoma alleles -
PT   comprises comparing genetic material corresponding to a normal
PT   human retinoblastoma with DNA from a patient.
PS   Example 2(2); Figure 7; 18pp; English.
CC   A method for detecting the presence, in a tumour sample, of a protein
CC   the absence of which is associated with a neoplasm, comprises
CC   producing an antibody to the protein and then contacting the
CC   antibody with the tumour sample.  Immune complexes indicate the
CC   presence of the protein in the sample.  The method may be used in
CC   the detection and treatment of a defective human gene related to
CC   cancer, in particular retinoblastoma.
SQ   Sequence   4597 BP;    1489 A;    841 C;    812 G;    1455 T;


  Query Match             90.2%;  Score 2511;  DB 1;  Length 4597;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2661;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTTGATCATGAT 1020

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
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Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
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Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||
Db   2761 GATACCTCAAACAAGGAAGAGAAA 2784
```

RESULT 12
X04501
ID X04501 standard; cDNA; 4597 BP.
AC X04501;
DT 05-JUL-1999 (first entry)
DE Human retinoblastoma gene cDNA.
KW Retinoblastoma; Rb gene; human; predisposition; diagnosis; therapy;
KW ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 337. .2787
FT /*tag= a
FT /transl_except= (pos:2632. .2634, aa:Asp)
PN US5853988-A.
PD 29-DEC-1998.
PF 08-OCT-1992; 958290.
PR 08-JUL-1991; US-728756.
PR 11-AUG-1986; US-895163.
PR 21-JAN-1988; US-146525.
PR 23-JAN-1989; US-300667.
PR 25-SEP-1992; US-951342.
PR 08-OCT-1992; US-958290.
PA (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA (WHED) WHITEHEAD INST.
PI Dryja TP, Friend S, Yandell DW;
DR WPI; 99-094898/08.
DR P-PSDB; Y01542.
PT Isolated human retinoblastoma gene - used to develop products for
PT analysing predisposition to retinoblastoma and for the detection and
PT treatment of retinoblastoma
PS Claim 8; Fig 5; 32pp; English.
CC This is the nucleic acid sequence of a cDNA of the normal human
CC retinoblastoma gene Rb. Absence or mutation of the Rb gene (see
CC also X04502) predisposes an individual to retinoblastoma. To
CC isolate Rb cDNA, the human DNA probe pH3-8, isolated from a human
CC chromosome 13 lambda phage library, was used in a chromosome walk
CC to isolate and map 30 kb of genomic DNA surrounding the H3-8
CC sequence. Fragment p7H30.7R (ATCC 97500) was obtained, and was
CC used as a probe to screen a cDNA library that had been constructed
CC from an adenovirus 12-transformed human embryonic retinal cell
CC line. This provided clone p4.7R (ATCC 97383), which in Northern
CC blots cross-reacted with a 4.7 kb transcript in transformed
CC retinal cells which was not present in 4 retinoblastoma and one
CC osteosarcoma cell samples. Rb nucleic acids comprising the Rb
CC gene, cDNA or a fragment of the gene, such as one of the 27 exons
CC or 26 introns, can be used in a claimed method for detecting a
CC deletion or point mutation in the Rb gene of a human patient. The
CC gene can also be used to synthesize Rb polypeptide (see Y01542) for

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CC   use in the treatment of individuals determined to have a defective
CC   Rb allele.
SQ   Sequence   4597 BP;    1489 A;    841 C;    813 G;    1454 T;


  Query Match            90.2%;  Score 2511;  DB 1;  Length 4597;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2661;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
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Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTCATATTGAA 2640

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
Db   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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RESULT  13
Q86398
ID   Q86398 standard; cDNA; 2995 BP.
AC   Q86398;
DT   16-OCT-1995  (first entry)
DE   Human Rb110 cDNA.
KW   Rb110 gene; retinoblastoma; cancer; tumor suppressor protein;
KW   cell cycle; pp110RB; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
PN   WO9507708-A.
PD   23-MAR-1995.
PF   13-SEP-1994; U10357.
PR   13-SEP-1993; US-121108.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW,  Johnson D,  Lee EYP,  Lee W,  Shepard HM;
PI   Wang NP;
DR   WPI; 95-131179/17.
DR   P-PSDB; R71680.
PT   Admin. of a functional retinoblastoma polypeptide or protein  -
PT   used to prevent and inhibit prim. and sec. retinoblastoma-linked
PT   cancers
PS   Disclosure; Fig.2; 163pp; English.
CC   By chromosomal walking from the esterase D gene on chromosome 13,
CC   the retinoblastoma susceptibility gene (RB) was identified on the
CC   basis of chromosomal location, homologous deletion and tumor-specific
CC   alterations in expression.  Screening of cDNA libraries yielded clone
CC   RB-5 incorporating the complete RB cDNA sequence given in Q86398 and
CC   encoding a 110-140 kDa nuclear phosphoprotein named pp110RB (R71680).
CC   Use of recombinant pp110RB will reduce the need for conventional
CC   radiotherapy or chemotherapy.
SQ   Sequence   2995 BP;    975 A;    616 C;    594 G;    810 T;
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  Query Match            89.0%;  Score 2478;  DB 1;  Length 2995;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 2778;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 60
Db    139 ATGCCGCCCAAAACCCCCGCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC 198

Qy     61 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 120
Db    199 CCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAGAGCAGGACAGCGGCCCGGAG 258

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
Db    259 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 318

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
Db    319 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 378

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
Db    379 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 438

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
Db    439 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 498

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
Db    499 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 558

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
Db    559 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 618

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
Db    619 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 678

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
Db    679 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 738

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
Db    739 GCTAAAGGGGAAGTATTAGAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGTTA 798

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
Db    799 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTCCTCAAAGAACCATATAAA 858

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
Db    859 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 918

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
Db    919 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 978

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
Db    979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
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Db   1039 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 1098

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Db   1099 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1158

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Db   1159 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1218

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Db   1219 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1278

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Db   1279 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Db   1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1398

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Db   1399 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1458

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Db   1459 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1518

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Db   1519 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1578

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Db   1579 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Db   1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1698

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Db   1699 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1758

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Db   1759 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1818

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Db   1819 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1878

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Db   1879 GGAGCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

Qy   1801 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Db   1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1998

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920

Db   1999 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 2058

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Db   2059 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 2118

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040

Db   2119 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2178

Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Db   2179 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2238

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Db   2239 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2298

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Db   2299 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2358

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Db   2359 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2418

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Db   2419 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2478

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Db   2479 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2538

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Db   2539 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2598

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Db   2599 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2658

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Db   2659 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2718

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640

Db   2719 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2778

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Db   2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2838

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Db   2839 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2898

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784

Db   2899 GATACCTCAAACAAGGAAGAGAAA 2922
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RESULT  14
N81369
ID   N81369 standard; DNA; 4597 BP.
AC   N81369;
DT   22-OCT-1990  (first entry)
DE   Human retinoblastoma gene
KW   Retinoblastoma; neoplasm; osteocarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             337. .2787
FT                   /*tag= a
PN   EP-259031-A.
PD   09-MAR-1988.
PF   11-AUG-1987; 307095.
PR   11-AUG-1986; US-895163.
PA   (MASS-) Massachusets Eye; (WHIT-) Whitehead Inst Biomed Re.
PI   Dryja TP, Friend S;
DR   WPI; 88-065827/10.
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DR   P-PSDB; P82112.
PT   Diagnosis of retinoblastoma - using genetic material corresp. to a normal
PT   human retinoblastoma gene or a unique sub-region
PS   Disclosure; p; English.
CC   This gene encodes a protein, the absence of which is associated with a
CC   neoplasm.  It is used to produce an antibody to the protein, contacting
CC   this with the tumour sample and detecting immune complexes as indication
CC   of the presence in the tumour sample of the protein. Whole sequence or
CC   a unique sub-region can be used.  The method identifies patients lacking
CC   the defective retinoblastoma (Rb) allele and thus are not at risk of
CC   developing the disease.
SQ   Sequence   4597 BP;   1489 A;   839 C;   815 G;   1454 T;

  Query Match             88.4%;  Score 2460;  DB 1;  Length 4597;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2660;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA 180

Qy    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA 240

Qy    241 GTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTTTCATGTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 300

Qy    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTACTGAGCTA 360
          |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db    301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 360

Qy    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

Qy    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCA 480

Qy    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG 540

Qy    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 600

Qy    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTA 660

Qy    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

Qy    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGT 780

Qy    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAA 840

Qy    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG 900

Qy    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGA 960

Qy    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT 1020

Qy   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGT 1080

Qy   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1140

Qy   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1200

Qy   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG 1260

Qy   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAA 1320

Qy   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG 1380

Qy   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAAC 1440

Qy   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1500

Qy   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG 1560

Qy   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC 1620

Qy   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC 1680

Qy   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA 1740

Qy   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1800

Qy   1801 ACTGCAGCAGATATGTATGTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ACTGCAGCAGATATGTATGTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG 1860

Qy   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   1861 CGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCGAGAAG 1920

Qy   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC 1980

Qy   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC 2040
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Qy   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2100

Qy   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA 2160

Qy   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAA 2220

Qy   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC 2280

Qy   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCA 2340

Qy   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2400

Qy   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCA 2460

Qy   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGG 2520

Qy   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA 2580

Qy   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA 2640

Qy   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2700

Qy   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2760

Qy   2761 GATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||
Db   2761 GATACCTCAAACAAGGAAGAGAAA 2784
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RESULT  15
V58443
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;
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  Query Match           88.0%;  Score 2449;  DB 1;  Length 3323;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2549;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    234 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACT 68

Qy    294 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTTTAC 353
          |||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Db     69 GTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTAC 128

Qy    354 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 TGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAAT 188

Qy    414 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 TGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATT 248

Qy    474 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 GTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAG 308

Qy    534 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 CAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 368

Qy    594 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTT 428

Qy    654 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 AATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACC 488

Qy    714 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 ATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 548

Qy    774 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTG 608

Qy    834 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 TAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 668

Qy    894 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC 728

Qy    954 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 1013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 TAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGA 788

Qy   1014 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 TCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 848
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Qy   1074 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 1133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGT 908

Qy   1134 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 TATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 968

Qy   1194 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAG 1028

Qy   1254 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTG 1088

Qy   1314 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 TGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1148

Qy   1374 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAA 1208

Qy   1434 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 TGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1268

Qy   1494 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCT 1328

Qy   1554 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 GAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGC 1388

Qy   1614 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 AGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1448

Qy   1674 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGA 1508

Qy   1734 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 CCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1568

Qy   1794 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTC 1628

Qy   1854 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 AACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGAC 1688

Qy   1914 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 CCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1748

Qy   1974 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 2033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACA 1808

Qy   2034 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1809 TATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1868

Qy   2094 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 2153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1869 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGA 1928

Qy   2154 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 2213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1929 CCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAC 1988

Qy   2214 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2273
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Db   1989 ATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2048

Qy   2274 GGTCTTCATGCAGAGAGTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2049 GGTCTTCATGCAGAGAGTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTAC 2108

Qy   2334 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2393
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Db   2109 CTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2168

Qy   2394 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2169 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGG 2228

Qy   2454 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2229 TCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATC 2288

Qy   2514 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2289 ATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2348

Qy   2574 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2349 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGA 2408

Qy   2634 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2409 TATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2468

Qy   2694 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2469 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGA 2528

Qy   2754 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2784
          |||||||||||||||||||||||||||||||
Db   2529 TAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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Search completed: February 13, 2000, 20:49:32
Job time: 12651 sec

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OM of: US-09-026-459A-29 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 13, 2000  2:22 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
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 -THREADS=1

Search information block:
Query: US-09-026-459A-29
Query length: 895
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence            Strd Orig    ZScore    EScore Len   ! Documentation  ..
N_Geneseq_36:V58441  +  895.00 16439.67  0.0       3455  ! Modified retinoblastoma tumou
N_Geneseq_36:Q04713  +  894.00 16422.32  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545  +  894.00 16422.32  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:V58440  +  894.00 16421.05  0.0       3555  ! Modified retinoblastoma tumou
N_Geneseq_36:V54990  +  894.00 16421.05  0.0       3555  ! DNA sequence of the specifica
N_Geneseq_36:V40004  +  894.00 16422.32  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737  +  894.00 16422.32  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:V58442  +  873.00 16034.72  0.0       3392  ! Modified retinoblastoma tumou
N_Geneseq_36:V58443  +  850.00 15611.38  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:X04501  +  837.00 15369.60  0.0       4597  ! Human retinoblastoma gene cDN
N_Geneseq_36:V58444  +  831.00 15261.66  0.0       3266  ! Modified retinoblastoma tumou
N_Geneseq_36:V58447  +  821.00 15077.10  0.0       3461  ! Modified retinoblastoma tumou
N_Geneseq_36:V58446  +  821.00 15077.40  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:Q72690  +  820.00 15059.19  0.0       3233  ! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58452  +  816.00 14984.84  0.0       3554  ! Modified retinoblastoma tumou
N_Geneseq_36:V54991  +  816.00 14985.57  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:Q70536  +  801.00 14706.74  0.0       4597  ! Human retinoblastoma gene. Di
N_Geneseq_36:Q90059  +  793.00 14562.61  0.0       2995  ! Retinoblastoma tumour suppres
N_Geneseq_36:V58445  +  781.00 14341.37  0.0       3113  ! Modified retinoblastoma tumou
N_Geneseq_36:V58448  +  747.00 13714.79  0.0       3347  ! Modified retinoblastoma tumou
N_Geneseq_36:N81369  +  744.00 13657.20  0.0       4597  ! Human retinoblastoma gene Dia
N_Geneseq_36:V58449  +  687.00 12610.43  0.0       3161  ! Modified retinoblastoma tumou
N_Geneseq_36:V58450  +  687.00 12609.94  0.0       3377  ! Modified retinoblastoma tumou
N_Geneseq_36:V58451  +  628.00 11523.57  0.0       3383  ! Modified retinoblastoma tumou
N_Geneseq_36:Q86398  +  593.00 10880.01  0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489  +  474.00 8684.99   0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261  +  286.00 5224.09   2.2e-283  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502  +   65.00 1144.56   3.7e-56   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490  +   55.00  960.48   6.7e-46   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:T18371  -    9.00  134.20   7.10      1110  ! Human pituitary G-protein coup
N_Geneseq_36:T18373  -    9.00  138.54   4.07      618  ! Mouse pancreas G-protein couple
N_Geneseq_36:T87884  -    9.00  133.92   7.35      1152  ! Consensus human hypothalamic r
N_Geneseq_36:T87886  -    9.00  133.79   7.48      1173  ! Human hypothalamic receptor DN
N_Geneseq_36:T87887  -    9.00  133.78   7.48      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87888  -    9.00  133.78   7.48      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87889  -    9.00  133.78   7.48      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87885  -    9.00  137.60   4.59      701  ! Human hypothalamic receptor DNA
N_Geneseq_36:V02402  -    9.00  134.20   7.10      1110  ! Human G protein-coupled recept
N_Geneseq_36:V02403  -    9.00  138.54   4.07      618  ! Mouse MIN6-derived G protein-cd
N_Geneseq_36:V81232  -    9.00  134.20   7.10      1110  ! Human pituitary-derived G-p
N_Geneseq_36:V81233  -    9.00  138.54   4.07      618  ! Mouse MIN6-derived G-protein
N_Geneseq_36:X15507  -    9.00  134.20   7.10      1110  ! Human pituitary-derived G p
N_Geneseq_36:X15508  -    9.00  138.54   4.07      618  ! MIN6-derived G protein-coupl
N_Geneseq_36:Q48043  -    8.00  109.23  174.63     2691  ! TGF-beta induced gene betaI
N_Geneseq_36:V81234  -    8.00  123.77  27.05      378  ! Mouse MIN6-derived G-protein

seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x V58441   ..

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       7 ATGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGA 56

      17 uGluThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleP 34
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      57 AGAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATAC 106

      34 roAspHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerSer 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     107 CAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCT 156

      51 ValAspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGl 67
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGG 206

      67 yIleCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrP 84
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     207 AATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTT 256

      84 heThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsn 100
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 257 TTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAAC 306

 101 LeuLeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerAr 117
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 307 TTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAG 356

 117 gLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluA 134
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 357 ACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAA 406

 134 rgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThr 150
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 407 GGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACT 456

 151 GluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLe 167
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 457 GAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATT 506

 167 uAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheG 184
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 184 lnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMet 200
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 201 LeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerPr 217
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 217 oArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnL 234
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 234 euGluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCys 250
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 317 rPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValA 334
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 334 snValIleProProHisThrProValArgThrValMetAsnThrIleGln 350
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1007 ATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAA 1056

 351 GlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLe 367
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 434 rgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHis 450
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 467 gSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpI 484
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1407 AAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGA 1456

 484 leLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGlu 500
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 551 AspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHi 567
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 567 sThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysG 584
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 584 lySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThr 600
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 601 SerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPh 617
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 617 eTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysG 634
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 651 PheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLe 667
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1957 TTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTT 2006

 667 uAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnI 684
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 684 leAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHis 700
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     717 pSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrA 734
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     734 snIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIlePro 750
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     751 HisIleProArgSerProTyrLysPheProSerSerProLeuArgIlePr 767
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    2257 CACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCC 2306

     767 oGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerG 784
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     784 luGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuVal 800
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     801 SerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGl 817
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     867 sLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetA 884
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     884 snAspSerMetAspThrSerAsnLysGluGluLys 895
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seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of California.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.

CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


alignment_scores:
            Quality:  894.00              Length:    894
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seq 1/1  to: Q04713  from: 1  to: 2994

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      18 uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
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     291 AACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAG 340

      35 spHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerSerVal 51
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     341 ATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTG 390

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     391 GATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAAT 440

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     102 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLe 118
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     541 CTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACT 590

     118 uLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgT 135
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     591 GTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGA 640

     135 hrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGlu 151
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     152 IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAl 168
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     168 aLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnL 185
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     202 LeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerProAr 218
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     891 AACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAG 940

     235 luAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsn 251
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     852 AlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLe 868
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     868 uAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnA 885
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seq_name: N_Geneseq_36:Q41545

seq_documentation_block:
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  894.00              Length:    894
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x Q41545   ..

 Align seg 1/1  to: Q41545  from: 1  to: 2994

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      18 uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
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     341 ATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTG 390

      52 AspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIl 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     391 GATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAAT 440

      68 eCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrPheT 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     441 CTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTA 490

      85 hrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeu 101
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     168 aLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnL 185
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     741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGT 790

     185 euMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeu 201
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     202 LeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerProAr 218
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     218 gThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuG 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     891 AACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAG 940

     235 luAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsn 251
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     252 IleAspGluValLysAsnValTyrPheLysAsnPheIleProPheMetAs 268
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     268 nSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuS 285
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     285 erLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArg 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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 352 LeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIl 368
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 368 eSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysA 385
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 385 rgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaVal 401
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 602 AlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTy 618
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 618 rLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluA 635
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 685 spLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAla 701
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 702 ValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSe 718
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 718 rIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnI 735
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 735 leLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHis 751
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 752 IleProArgSerProTyrLysPheProSerSerProLeuArgIleProGl 768
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 768 yGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluG 785
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 785 lyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSer 801
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 802 IleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMe 818
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2641 ATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGAT 2690

 818 tValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnP 835
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 835 roProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGlu 851
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 868 uAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnA 885
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 885 spSerMetAspThrSerAsnLysGluGluLys 895
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seq_name: N_Geneseq_36:V58440

seq_documentation_block:
ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.

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FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  894.00              Length:    894
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x V58440   ..

 Align seg 1/1  to: V58440  from: 1  to: 3555

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     109 CAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGA 158

      18 uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     159 AACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAG 208

      35 spHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerServal 51
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     209 ATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTG 258

      52 AspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIl 68
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     259 GATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAAT 308

      68 eCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrPheT 85
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     309 CTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTA 358

      85 hrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeu 101
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     102 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLe 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     409 CTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACT 458

     118 uLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgT 135
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     459 GTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGA 508

     135 hrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGlu 151
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     509 CATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 558

     152 IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAl 168
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     559 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 608

     168 aLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnL 185
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     185 euMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeu 201
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     302 LeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPh 318
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 602 AlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTy 618
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 618 rLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluA 635
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 635 rgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPhe 651
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     ||||||||||||||||||||||||||||||||||||||||||||||||||
2159 ACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCT 2208

 702 ValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSe 718
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2209 GTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTC 2258

 718 rIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnI 735
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2259 TATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATA 2308

 735 leLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHis 751
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2309 TTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2358

 752 IleProArgSerProTyrLysPheProSerSerProLeuArgIleProGl 768
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2359 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

 768 yGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluG 785
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAG 2458

 785 lyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSer 801
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2459 GTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCA 2508

 802 IleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMe 818
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2509 ATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGAT 2558

 818 tValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnP 835
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2559 GGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACC 2608

 835 roProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGlu 851
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2609 CTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2658

 852 AlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLe 868
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2659 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708

 868 uAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnA 885
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATG 2758

 885 spSerMetAspThrSerAsnLysGluGluLys 895
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2759 ATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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seq_name: N_Geneseq_36:V54990

seq_documentation_block:

ID V54990 standard; DNA; 3555 BP.
AC V54990;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

```
alignment_scores:
           Quality:  894.00              Length:    894
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x V54990   ..

 Align seg 1/1  to: V54990  from: 1  to: 3555

       2 GlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGluGl 18
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     109 CAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGA 158

      18 uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     159 AACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAG 208

      35 spHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerSerVal 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     209 ATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTG 258

      52 AspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIl 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     259 GATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAAT 308

      68 eCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrPheT 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     309 CTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTA 358

      85 hrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeu 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     359 CTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTA 408

     102 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLe 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     409 CTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACT 458

     118 uLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgT 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     459 GTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGA 508

     135 hrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGlu 151
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     509 CATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 558

     152 IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAl 168
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     559 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 608

     168 aLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnL 185
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     609 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGT 658

     185 euMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeu 201
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     659 TAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTG 708

     202 LeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerProAr 218
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     709 CTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCG 758

     218 gThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuG 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     759 AACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAG 808

     235 luAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsn 251
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     809 AAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 858

     252 IleAspGluValLysAsnValTyrPheLysAsnPheIleProPheMetAs 268
         ||||||||||||||||||||||||||||||||||||||||||||||||||

     859 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 908

     268 nSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuS 285
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     909 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTT 958

     285 erLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArg 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     959 CTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGA 1008

     302 LeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPh 318
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1009 TTATTTTTGGATCATGATAAAAGTCTTCAGACTGATTCTATAGACAGTTT 1058

     318 eGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsnV 335
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1059 TGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATG 1108

     335 alIleProProHisThrProValArgThrValMetAsnThrIleGlnGln 351
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1109 TAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1158

     352 LeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIl 368
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1159 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1208

     368 eSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysA 385
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1209 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAA 1258

     385 rgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaVal 401
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1259 GAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTG 1308

     402 GlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValAr 418
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1309 GGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCG 1358

     418 gLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgL 435
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1359 CTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGAT 1408

     435 euSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMet 451
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1409 TATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1458

     452 SerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSe 468
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1459 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1508

     468 rThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleL 485
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1509 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTC 1558

     485 euAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSer 501
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1559 TGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGT 1608

     502 PheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGl 518
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1609 TTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGA 1658

     518 uArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerP 535
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1659 ACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCAC 1708

     535 roLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAsp 551
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1709 CTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1758

     552 HisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisTh 568
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1759 CACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1808
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 568 rAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGlyS 585
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1809 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTT 1858

 585 erThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 601
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1859 CAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCA 1908

 602 AlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTy 618
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1909 GCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTA 1958

 618 rLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluA 635
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1959 TAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAAC 2008

 635 rgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPhe 651
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2009 GCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTC 2058

 652 GlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAs 668
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2059 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2108

 668 pGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleA 685
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2109 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAG 2158

 685 spLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAla 701
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2159 ACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCT 2208

 702 ValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSe 718
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2209 GTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTC 2258

 718 rIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnI 735
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2259 TATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATA 2308

 735 leLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHis 751
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2309 TTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCAC 2358

 752 IleProArgSerProTyrLysPheProSerSerProLeuArgIleProGl 768
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2359 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2408

 768 yGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluG 785
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2409 AGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAG 2458

 785 lyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSer 801
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2459 GTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCA 2508

 802 IleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMe 818
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2509 ATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGAT 2558

 818 tValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnP 835
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2559 GGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACC 2608

 835 roProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGlu 851
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2609 CTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATGAA 2658

 852 AlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLe 868
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2659 GCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACT 2708

 868 uAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnA 885
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2709 GGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATG 2758

 885 spSerMetAspThrSerAsnLysGluGluLys 895
     |||||||||||||||||||||||||||||||
2759 ATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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seq_name: N_Geneseq_36:V40004

seq_documentation_block:

ID	V40004 standard; DNA; 2994 BP.	
AC	V40004;	
DT	15-FEB-1999 (first entry)	
DE	Retinoblastoma protein RB.	
KW	Retinoblastoma protein RB; E2F; transcription factor; human;	
KW	bladder cancer; restenosis; angioplasty; diabetic retinopathy;	
KW	thyroid hyperplasia; Grave's disease; psoriasis;	
KW	benign prostatic hypertrophy; Li-Fraumeni syndrome;	
KW	peripheral vascular disease; therapy; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	139. .2925
FT		/*tag= a
PN	WO9821228-A1.	
PD	22-MAY-1998.	
PF	13-NOV-1997; U21821.	
PR	14-FEB-1997; US-801092.	
PR	15-NOV-1996; US-751517.	
PA	(CANJ-) CANJI INC.	
PI	Antelman D, Gregory RJ, Wills KN;	
DR	WPI; 98-297858/26.	
DR	P-PSDB; W62465.	
PT	New fusion polypeptide of, e.g. transcription factor - used to	
PT	treat, e.g. hyper-proliferative disease such as cancer and	
PT	restenosis	
PS	Example 1; Fig 2A; 91pp; English.	

CC This nucleotide sequence includes a coding region for retinoblastoma
CC protein RB (see W62465). A new claimed polypeptide is a fusion of:
CC (i) a transcription factor (TF) comprising a DNA binding domain,
CC and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC suppression domain. Also new are: (1) a nucleic acid encoding the
CC fusion protein, and (2) expression vectors containing such DNA.
CC The fusion protein, particularly expressed from gene therapy
CC vectors (especially adenovirus vectors), is used to treat
CC hyperproliferative conditions, specifically cancer (particularly of
CC the bladder) or restenosis (after angioplasty), but also diabetic
CC retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC vascular disease. Tissue-specific expression of E2F-RB fusions is
CC provided. The fusion proteins are more effective in repressing
CC transcription of the E2F promoter than Rb alone and cause cell-cycle
CC arrest in a variety of cells.

SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

alignment_scores:

Quality:	894.00	Length:	894
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:
US-09-026-459A-29 x V40004 ..

Align seg 1/1 to: V40004 from: 1 to: 2994

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   2 GlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGluGl 18
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 241 CAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGA 290

  18 uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 291 AACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAG 340
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```
 35 spHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerSerVal 51
    ||||||||||||||||||||||||||||||||||||||||||||||||||
341 ATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTG 390

 52 AspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIl 68
    ||||||||||||||||||||||||||||||||||||||||||||||||||
391 GATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAAT 440

 68 eCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrPheT 85
    ||||||||||||||||||||||||||||||||||||||||||||||||||
441 CTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTA 490

 85 hrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeu 101
    ||||||||||||||||||||||||||||||||||||||||||||||||||
491 CTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTA 540

102 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLe 118
    ||||||||||||||||||||||||||||||||||||||||||||||||||
541 CTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACT 590

118 uLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgT 135
    ||||||||||||||||||||||||||||||||||||||||||||||||||
591 GTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGA 640

135 hrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGlu 151
    ||||||||||||||||||||||||||||||||||||||||||||||||||
641 CATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690

152 IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAl 168
    ||||||||||||||||||||||||||||||||||||||||||||||||||
691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740

168 aLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnL 185
    ||||||||||||||||||||||||||||||||||||||||||||||||||
741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGT 790

185 euMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeu 201
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791 TAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTG 840

202 LeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerProAr 218
    ||||||||||||||||||||||||||||||||||||||||||||||||||
841 CTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCG 890

218 gThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuG 235
    ||||||||||||||||||||||||||||||||||||||||||||||||||
891 AACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAG 940

235 luAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsn 251
    ||||||||||||||||||||||||||||||||||||||||||||||||||
941 AAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990

252 IleAspGluValLysAsnValTyrPheLysAsnPheIleProPheMetAs 268
    ||||||||||||||||||||||||||||||||||||||||||||||||||
991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040

268 nSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuS 285
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1041 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTT 1090

285 erLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArg 301
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1091 CTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGA 1140

302 LeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPh 318
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1141 TTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTT 1190

318 eGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsnV 335
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1191 TGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATG 1240

335 alIleProProHisThrProValArgThrValMetAsnThrIleGlnGln 351
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352 LeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIl 368
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1291 TTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGAT 1340

368 eSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysA 385
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1341 TTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAA 1390

385 rgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaVal 401
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418 gLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluArgL 435
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1541 TATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATG 1590

452 SerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSe 468
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468 rThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleL 485
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518 uArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerP 535
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1791 ACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCAC 1840

535 roLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAsp 551
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1841 CTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGAT 1890

552 HisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisTh 568
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1891 CACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACAC 1940

568 rAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGlyS 585
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1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTT 1990

585 erThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 601
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602 AlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTy 618
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618 rLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluA 635
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    2191 CAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGA 2240

     668 pGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleA 685
    2241 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAG 2290

     685 spLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAla 701
    2291 ACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCT 2340

     702 ValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSe 718
    2341 GTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTC 2390

     718 rIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnI 735
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     752 IleProArgSerProTyrLysPheProSerSerProLeuArgIleProGl 768
    2491 ATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG 2540

     768 yGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluG 785
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    2591 GTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCA 2640

     802 IleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMe 818
    2641 ATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGAT 2690

     818 tValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnP 835
    2691 GGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACC 2740

     835 roProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGlu 851
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     852 AlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLysLe 868
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     868 uAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnA 885
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seq_name: N_Geneseq_36:X00737

seq_documentation_block:
ID   X00737 standard; cDNA; 2995 BP.
AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens:
FH   Key             Location/Qualifiers
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FT                   /*tag= a
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FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;

alignment_scores:
           Quality:  894.00              Length:    894
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x X00737  ..

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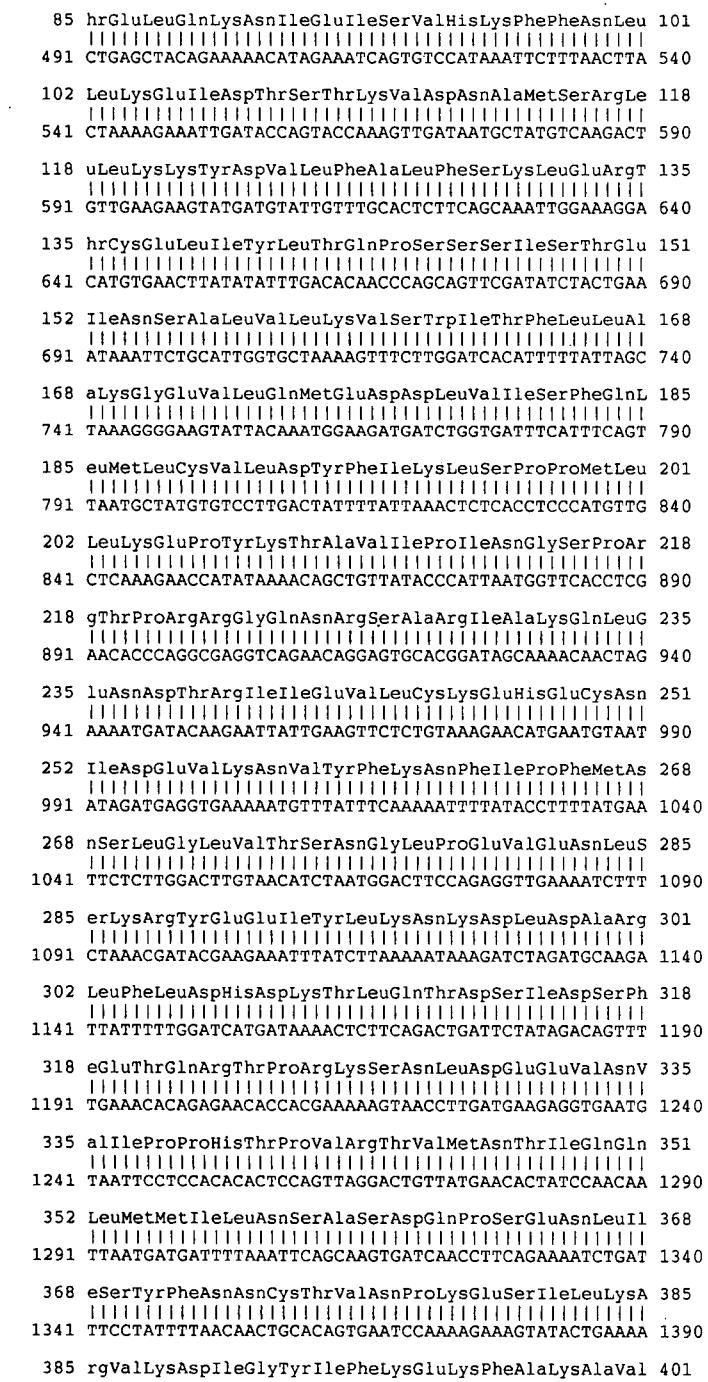
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     291 AACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAG 340

      35 spHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerSerVal 51
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85 hrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeu 101
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102 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLe 118
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118 uLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgT 135
591 GTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGA 640
135 hrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGlu 151
641 CATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTGAA 690
152 IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAl 168
691 ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC 740
168 aLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnL 185
741 TAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGT 790
185 euMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeu 201
791 TAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTG 840
202 LeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerProAr 218
841 CTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCG 890
218 gThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuG 235
891 AACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAG 940
235 luAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsn 251
941 AAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAAT 990
252 IleAspGluValLysAsnValTyrPheLysAsnPheIleProPheMetAs 268
991 ATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 1040
268 nSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuS 285
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285 erLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArg 301
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302 LeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPh 318
1141 TTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTT 1190
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1241 TAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAA 1290
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452 SerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArgSe 468
1591 TCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAG 1640
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485 euAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSer 501
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1941 TGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTT 1990
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618 rLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluA 635
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seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
           Quality:  873.00              Length:    873
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58442  from: 1  to: 3392

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      39 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 56
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      60 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 109

      56 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 72
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     110 GAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATT 159

      73 AlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLy 89
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     160 GCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAA 209

      89 sAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleA 106
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     210 AAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTG 259

     106 spThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 122
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     260 ATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 309

     123 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 139
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     139 eTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaL 156
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     360 ATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCAT 409

     156 euValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluVal 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     410 TGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTA 459

     173 LeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysVa 189
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     189 lLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProT 206
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     223 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrAr 239
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 256 ysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeu 272
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 706 heLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValPhe 722
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seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

alignment_scores:
Quality: 850.00 Length: 850
Ratio: 1.000 Gaps: 0
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alignment_block:
US-09-026-459A-29 x V58443 ..

Align seg 1/1 to: V58443 from: 1 to: 3323

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     129 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 145
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 529 laTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAsp 545
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 579 erProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 595
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1610 CTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1659

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1660 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTAC 1709

 612 rSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgL 629
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1710 CTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGC 1759

 629 euAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHis 645
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 646 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 662
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 679 ysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyr 695
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 712 sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG 729
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2010 AGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGC 2059

 729 lnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThr 745
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DT   05-JUL-1999  (first entry)
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KW   Retinoblastoma; Rb gene; human; predisposition; diagnosis; therapy;
KW   ss.
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FT                   /transl_except= (pos:2632. .2634, aa:Asp)
PN   US5853988-A.
PD   29-DEC-1998.
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PR   08-JUL-1991; US-728756.
PR   11-AUG-1986; US-895163.
PR   21-JAN-1988; US-146525.
PR   23-JAN-1989; US-300667.
PR   25-SEP-1992; US-951342.
PR   08-OCT-1992; US-958290.
PA   (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA   (WHED ) WHITEHEAD INST.
PI   Dryja TP, Friend S, Yandell DW;
DR   WPI; 99-094898/08.
DR   P-PSDB; Y01542.
PT   Isolated human retinoblastoma gene - used to develop products for
PT   analysing predisposition to retinoblastoma and for the detection and
```

```
PT   treatment of retinoblastoma
PS   Claim 8; Fig 5; 32pp; English.
CC   This is the nucleic acid sequence of a cDNA of the normal human
CC   retinoblastoma gene Rb.  Absence or mutation of the Rb gene (see
CC   also X04502) predisposes an individual to retinoblastoma.  To
CC   isolate Rb cDNA, the human DNA probe pH3-8, isolated from a human
CC   chromosome 13 lambda phage library, was used in a chromosome walk
CC   to isolate and map 30 kb of genomic DNA surrounding the H3-8
CC   sequence.  Fragment p7H30.7R (ATCC 97500) was obtained, and was
CC   used as a probe to screen a cDNA library that had been constructed
CC   from an adenovirus 12-transformed human embryonic retinal cell
CC   line.  This provided clone p4.7R (ATCC 97383), which in Northern
CC   blots cross-reacted with a 4.7 kb transcript in transformed
CC   retinal cells which was not present in 4 retinoblastoma and one
CC   osteosarcoma cell samples.  Rb nucleic acids comprising the Rb
CC   gene, cDNA or a fragment of the gene, such as one of the 27 exons
CC   or 26 introns, can be used in a claimed method for detecting a
CC   deletion or point mutation in the Rb gene of a human patient.  The
CC   gene can also be used to synthesize Rb polypeptide (see Y01542) for
CC   use in the treatment of individuals determined to have a defective
CC   Rb allele.
SQ   Sequence   4597 BP;    1489 A;    841 C;    813 G;    1454 T;


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     371 TAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACC 420

     108 SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVa 124
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     191 spTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLys 207
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     671 ACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA 720

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     721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCA 770

     224 nAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleI 241
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     308 LysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPr 324
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 558 ProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLe 574
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1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCT 1970

 624 uAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisP 641
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AC V58444;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2505
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69368.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 166-170; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T;

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Ratio: 1.000 Gaps: 0
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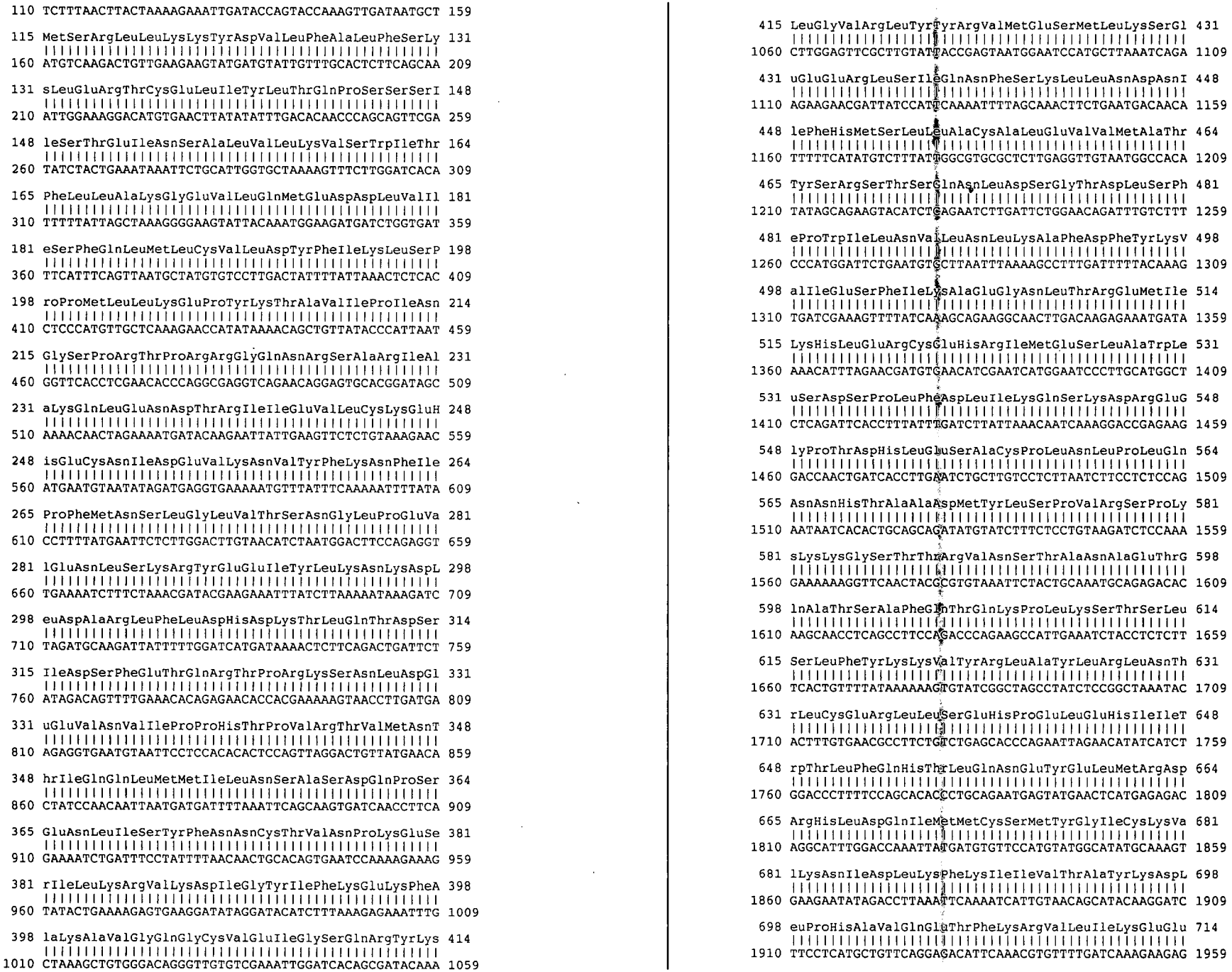
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Align seg 1/1 to: V58444 from: 1 to: 3266

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131 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 148
210 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 259
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260 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 309
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215 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 231
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
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PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


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seq_documentation_block:
ID   V58446 standard; DNA; 3323 BP.
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AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
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PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;


alignment_scores:
            Quality:  821.00              Length:    821
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      97 GTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 146

      91 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 108
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     147 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 196

     108 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 124
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     197 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 246

     125 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 141
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     247 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 296

     141 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 158
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     297 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 346

     158 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 174
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     347 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 396

     175 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 191
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     397 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 446

     191 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 208
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     208 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 224
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     225 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 241
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     241 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 258
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 791 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 808
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 808 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 824
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 841 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 858
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 858 euProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 874
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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag= a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
            Quality:  820.00              Length:    820
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x Q72690   ..

 Align seg 1/1  to: Q72690  from: 1  to: 3233

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      92 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 109
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109 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 125
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107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

126 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 142
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157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

142 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 159
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207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

159 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 175
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257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

176 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 192
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192 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 209
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407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

226 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 242
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457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

242 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 259
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259 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 275
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359 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 375
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 642 uLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluT 659
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1707 ATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGT 1756

 659 yrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMet 675
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1757 ATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

 676 TyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleVa 692
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGT 1856

 692 lThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArgV 709
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1857 AACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTG 1906

 709 alLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSer 725
     ||||||||||||||||||||||||||||||||||||||||||||||||||
```

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    1907 TTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCG 1956

     726 ValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrAr 742
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1957 GTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAG 2006

     742 gProProThrLeuSerProIleProHisIleProArgSerProTyrLysP 759
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2007 GCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGT 2056

     759 heProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 775
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2057 TTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

     776 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 792
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAAT 2156

     792 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 809
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2157 GACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTT 2206

     809 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 825
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2207 CTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTG 2256

     826 LeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysLe 842
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    2257 CTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACT 2306

     842 uArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuP 859
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2307 ACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCC 2356

     859 roGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArg 875
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    2357 CAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

     876 ThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLy 892
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     892 sGluGluLys 895
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    2457 GGAAGAGAAA 2466

seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;   1170 A;    683 C;    653 G;    1048 T;


alignment_scores:
            Quality:  816.00              Length:    816
              Ratio:  1.000               Gaps:        0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-29 x V58452   ..

 Align seg 1/1  to: V58452  from: 1  to: 3554

      80 MetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHi 96
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 392

      96 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 113
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442

     113 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 129
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492

     130 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 146
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     493 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 542

     146 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 163
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592

     163 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 179
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     593 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

     180 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 196
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 692

     196 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 213
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     693 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 742

     213 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 229
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     743 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 792

     230 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 246
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     246 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 263
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     843 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 892

     263 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 279
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     893 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 942

     280 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 296
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     943 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 992

     296 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 313
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     993 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 1042
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 313 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 329
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1043 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 1092

 330 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 346
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1093 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 1142

 346 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 363
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1143 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1192

 363 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 379
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1193 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242

 380 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 396
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1292

 396 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 413
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1293 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1342

 413 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 429
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1343 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1392

 430 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 446
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1393 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1442

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1443 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1492

 463 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 479
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 496 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 513
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1593 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1642

 513 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 529
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 530 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 546
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 546 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 563
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1743 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1792

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1793 TCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1842

 580 ProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGl 596
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1843 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1892

 596 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 613
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1893 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1942

 613 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 629
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     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1943 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1992

 630 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 646
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1993 AATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATAT 2042

 646 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 663
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 663 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 679
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 680 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 696
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2143 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAA 2192

 696 sAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysG 713
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2193 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 2242

 713 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 729
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2243 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 2292

 730 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 746
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 746 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 763
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 763 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 779
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 796 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 813
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2493 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2542

 813 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 829
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2543 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2592

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2593 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2642

 846 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 863
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 863 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 879
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OM of: US-09-026-459A-31 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 13, 2000  2:25 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=oligo.rng -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-31
Query length: 874
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence           Strd Orig    ZScore    EScore Len  ! Documentation  ..
N_Geneseq_36:V58442  +  874.00 16132.08  0.0       3392  ! Modified retinoblastoma tumou
N_Geneseq_36:Q04713  +  873.00 16114.50  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545  +  873.00 16114.50  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:V58440  +  873.00 16113.23  0.0       3555  ! Modified retinoblastoma tumou
N_Geneseq_36:V58441  +  873.00 16113.44  0.0       3455  ! Modified retinoblastoma tumou
N_Geneseq_36:V54990  +  873.00 16113.23  0.0       3555  ! DNA sequence of the specifica
N_Geneseq_36:V40004  +  873.00 16114.50  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737  +  873.00 16114.50  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:V58443  +  850.00 15688.15  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:V58444  +  831.00 15336.71  0.0       3266  ! Modified retinoblastoma tumou
N_Geneseq_36:X04501  +  822.00 15167.63  0.0       4597  ! Human retinoblastoma gene cDN
N_Geneseq_36:V58447  +  821.00 15151.24  0.0       3461  ! Modified retinoblastoma tumou
N_Geneseq_36:V58446  +  821.00 15151.54  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:Q72690  +  820.00 15133.24  0.0       3233  ! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58452  +  816.00 15058.53  0.0       3554  ! Modified retinoblastoma tumou
N_Geneseq_36:V54991  +  816.00 15059.26  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:Q70536  +  786.00 14501.51  0.0       4597  ! Human retinoblastoma gene. Di
N_Geneseq_36:V58445  +  781.00 14411.89  0.0       3113  ! Modified retinoblastoma tumou
N_Geneseq_36:Q90059  +  772.00 14245.64  0.0       2995  ! Retinoblastoma tumour suppres
N_Geneseq_36:V58448  +  747.00 13782.23  0.0       3347  ! Modified retinoblastoma tumou
N_Geneseq_36:N81369  +  744.00 13724.36  0.0       4597  ! Human retinoblastoma gene Dia
N_Geneseq_36:V58449  +  687.00 12672.44  0.0       3161  ! Modified retinoblastoma tumou
N_Geneseq_36:V58450  +  687.00 12671.95  0.0       3377  ! Modified retinoblastoma tumou
N_Geneseq_36:V58451  +  628.00 11580.22  0.0       3383  ! Modified retinoblastoma tumou
N_Geneseq_36:Q86398  +  593.00 10933.50  0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489  +  474.00 8727.69   0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261  +  286.00 5249.76   8.2e-285  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502  +   65.00 1150.17   1.8e-56   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490  +   55.00  965.19   3.7e-46   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:T18371  -    9.00  134.81   6.57      1110  ! Human pituitary G-protein coup
N_Geneseq_36:T18373  -    9.00  139.16   3.76      618  ! Mouse pancreas G-protein couple
N_Geneseq_36:T87884  -    9.00  134.53   6.80      1152  ! Consensus human hypothalamic r
N_Geneseq_36:T87886  -    9.00  134.39   6.92      1173  ! Human hypothalamic receptor DN
N_Geneseq_36:T87887  -    9.00  134.39   6.93      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87888  -    9.00  134.39   6.93      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87889  -    9.00  134.39   6.93      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87885  -    9.00  138.22   4.24      701  ! Human hypothalamic receptor DNA
N_Geneseq_36:V02402  -    9.00  134.81   6.57      1110  ! Human G protein-coupled recept
N_Geneseq_36:V02403  -    9.00  139.16   3.76      618  ! Mouse MIN6-derived G protein-cd
N_Geneseq_36:V81232  -    9.00  134.81   6.57      1110  ! Human pituitary-derived G-p
N_Geneseq_36:V81233  -    9.00  139.16   3.76      618  ! Mouse MIN6-derived G-protein
N_Geneseq_36:X15507  -    9.00  134.81   6.57      1110  ! Human pituitary-derived G p
N_Geneseq_36:X15508  -    9.00  139.16   3.76      618  ! MIN6-derived G protein-coupl
N_Geneseq_36:Q48043  -    8.00  109.72  163.91     2691  ! TGF-beta induced gene betaI
N_Geneseq_36:V81234  -    8.00  124.31   25.23     378  ! Mouse MIN6-derived G-protein

seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
            Quality:  874.00              Length:    874
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x V58442   ..

 Align seg 1/1  to: V58442  from: 1  to: 3392

       1 MetAspPheThrAlaLeuCysGlnLysLeuLysIleProAspHisValAr 17
         |||||||||||!|||||||||||||||||||||||||||||||||||||||
       7 ATGGATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAG 56

      17 gGluArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValL 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 AGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTAT 106

      34 euGlyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePhe 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 TGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTT 156

      51 IleAlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 ATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACA 206

      67 nLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluI 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 GAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAA 256

      84 leAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLys 100
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257 TTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAG 306

101 TyrAspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLe 117
    ||||||||||||||||||||||||||||||||||||||||||||||||||
307 TATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACT 356

117 uIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerA 134
    ||||||||||||||||||||||||||||||||||||||||||||||||||
357 TATATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTG 406

134 laLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGlu 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
407 CATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAA 456

151 ValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeuCy 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||
457 GTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATG 506

167 sValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluP 184
    ||||||||||||||||||||||||||||||||||||||||||||||||||
507 TGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAAC 556

184 roTyrLysThrAlaValIleProIleAsnGlySerProArgThrProArg 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
557 CATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGG 606

201 ArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspTh 217
    ||||||||||||||||||||||||||||||||||||||||||||||||||
607 CGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATAC 656

217 rArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGluV 234
    ||||||||||||||||||||||||||||||||||||||||||||||||||
657 AAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGG 706

234 alLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGly 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
707 TGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGA 756

251 LeuValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTy 267
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757 CTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATA 806

267 rGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuA 284
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807 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGG 856

284 spHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGln 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
857 ATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAG 906

301 ArgThrProArgLysSerAsnLeuAspGluGluValAsnValIleProPr 317
    ||||||||||||||||||||||||||||||||||||||||||||||||||
907 AGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCC 956

317 oHisThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetI 334
    ||||||||||||||||||||||||||||||||||||||||||||||||||
957 ACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGA 1006

334 leLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPhe 350
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1007 TTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTT 1056

351 AsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAs 367
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1057 AACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGA 1106

367 pIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyC 384
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1107 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTT 1156

384 ysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyr 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1157 GTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTAC 1206

401 ArgValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGl 417
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1207 CGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCA 1256

417 nAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuA 434
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1257 AAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGG 1306

434 laCysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGln 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1307 CGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAG 1356

451 AsnLeuAspSerGlyThrAspLeuSerProProTrpIleLeuAsnValLe 467
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1357 AATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1406

467 uAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysA 484
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1407 TAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAG 1456

484 laGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGlu 500
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1457 CAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAA 1506

501 HisArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAs 517
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1507 CATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGA 1556

517 pLeuIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluS 534
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1557 TCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAAT 1606

534 erAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAsp 550
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1607 CTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGAT 1656

551 MetTyrLeuSerProValArgSerProLysLysLysGlySerThrThrAr 567
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567 gValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnT 584
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584 hrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysVal 600
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1757 CCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTG 1806

601 TyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSe 617
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1807 TATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTC 1856

617 rGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrL 634
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1857 TGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCC 1906

634 euGlnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMet 650
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1907 TGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATG 1956

651 MetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPh 667
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1957 ATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 2006

667 eLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluT 684
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2007 CAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGA 2056

684 hrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleVal 700
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2057 CATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTA 2106
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     701 PheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTy 717
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    2107 TTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTA 2156

     717 rAlaSerThrArgProProThrLeuSerProIleProHisIleProArgS 734
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    2157 TGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAA 2206

     734 erProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIle 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2207 GCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATC 2256

     751 TyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProTh 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2257 TATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAC 2306

     767 rProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluS 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2307 ACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAAT 2356

     784 erPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsn 800
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    2357 CATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAAC 2406

     801 SerAspArgValLeuLysArgSerAlaGluGlySerAsnProProLysPr 817
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     817 oLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGlyS 834
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    2507 GTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATG 2556

     851 ThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAs 867
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    2557 ACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGA 2606

     867 pThrSerAsnLysGluGluLys 874
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    2607 TACCTCAAACAAGGAAGAGAAA 2628

seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;

alignment_scores:
           Quality:  873.00   •          Length:    873
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x Q04713   ..

 Align seg 1/1  to: Q04713  from: 1  to: 2994

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     304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGA 353

      18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     354 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 403

      35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     404 GAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATT 453

      52 AlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     454 GCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAA 503

      68 sAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleA 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     504 AAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTG 553

      85 spThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     554 ATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

     102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTAT 653

     118 eTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaL 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     654 ATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCAT 703

     135 euValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluVal 151
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     704 TGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTA 753

     152 LeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysVa 168
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     754 TTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 803

     168 lLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProT 185
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     804 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCAT 853

     185 yrLysThrAlaValIleProIleAsnGlySerProArgThrProArgArg 201
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     854 ATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 903

     202 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrAr 218
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     904 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAG 953

     218 gIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGluValL 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     954 AATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGA 1003

     235 ysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeu 251
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1004 AAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTT 1053

     252 ValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGl 268
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1054 GTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGA 1103

 268 uGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspH 285
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1104 AGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATC 1153

 285 isAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 301
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1154 ATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1203

 302 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHi 318
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1204 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACA 1253

 318 sThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleL 335
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1254 CACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTT 1303

 335 euAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsn 351
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1304 TAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAAC 1353

 352 AsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspIl 368
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1354 AACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATAT 1403

 368 eGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysV 385
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1404 AGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTG 1453

 385 alGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
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1754 AAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1803

 502 ArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLe 518
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DT   24-AUG-1993  (first entry)
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KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
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FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  873.00            Length:    873
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x Q41545   ..

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      18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 35
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     354 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 403

      35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
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     404 GAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATT 453

      52 AlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     454 GCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAA 503

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seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
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PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Disclosure; Page 121-126; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

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Percent Similarity: 100.000 Percent Identity: 100.000

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     102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 118
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seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;   1153 A;   631 C;   627 G;   1044 T;


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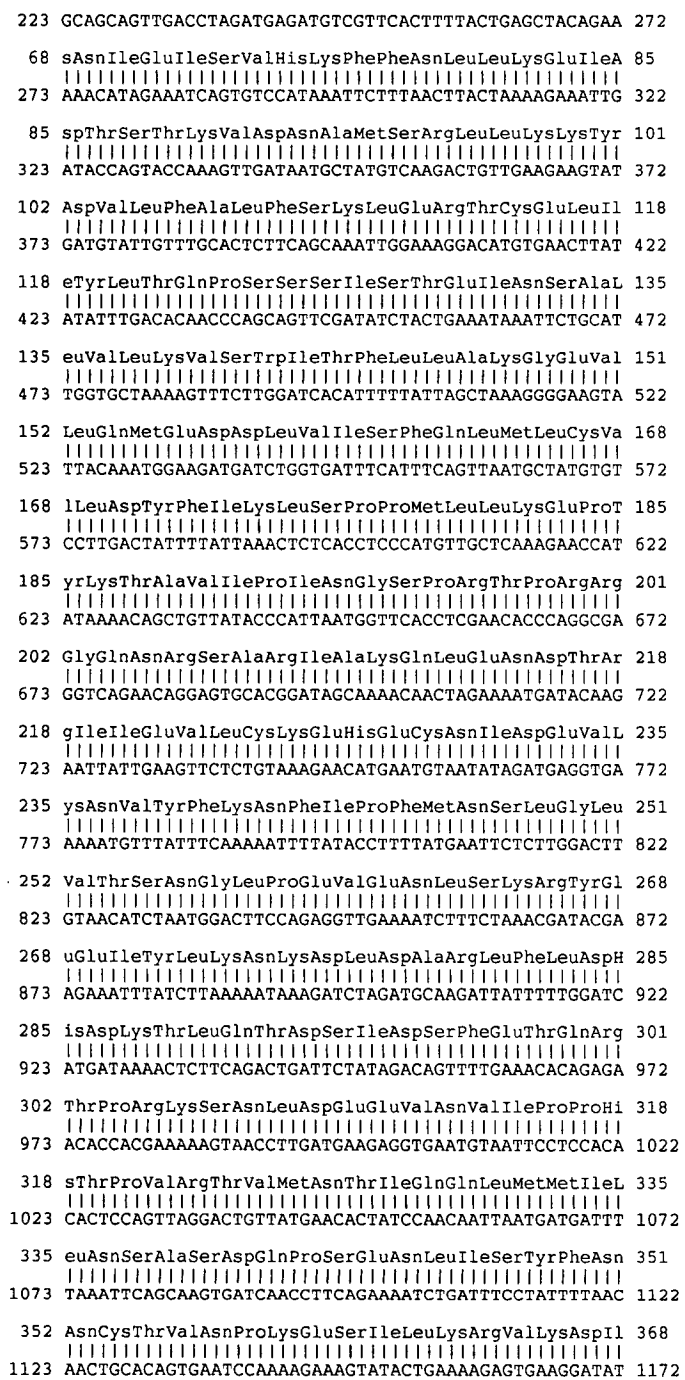
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102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 118
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     685 heLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValPhe 701
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    2123 TCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2172

     702 TyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAl 718
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2173 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGC 2222

     718 aSerThrArgProProThrLeuSerProIleProHisIleProArgSerP 735
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2223 TTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCC 2272

     735 roTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyr 751
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2273 CTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTAT 2322

     752 IleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThrPr 768
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2323 ATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACC 2372

     768 oThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerP 785
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2373 AACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCAT 2422

     785 heGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSer 801
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2423 TCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2472

     802 AspArgValLeuLysArgSerAlaGluGlySerAsnProProLysProLe 818
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2473 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACT 2522

     818 uLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerL 835
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2523 GAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTA 2572

     835 ysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThr 851
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2573 AACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACT 2622

     852 SerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspTh 868
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2623 TCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATAC 2672

     868 rSerAsnLysGluGluLys 874
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    2673 CTCAAACAAGGAAGAGAAA 2691

seq_name: N_Geneseq_36:V54990

seq_documentation_block:
ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  873.00              Length:    873
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x V54990   ..

 Align seg 1/1  to: V54990  from: 1  to: 3555

       2 AspPheThrAlaLeuCysGlnLysLeuLysIleProAspHisValArgGl 18
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     172 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGA 221

      18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     222 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 271

      35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     272 GAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATT 321

      52 AlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     322 GCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAA 371

      68 sAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleA 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     372 AAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTG 421

      85 spThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     422 ATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 471

     102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     472 GATGTATTGTTTGCACTGTTCAGCAAATTGGAAAGGACATGTGAACTTAT 521

     118 eTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaL 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     522 ATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCAT 571

     135 euValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluVal 151
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     572 TGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTA 621

     152 LeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysVa 168
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     622 TTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGT 671

     168 lLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProT 185
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    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
672 CCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCAT 721

185 yrLysThrAlaValIleProIleAsnGlySerProArgThrProArgArg 201
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
722 ATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGA 771

202 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrAr 218
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
772 GGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAG 821

218 gIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGluValL 235
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
822 AATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGA 871

235 ysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeu 251
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
872 AAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTT 921

252 ValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGl 268
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
922 GTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGA 971

268 uGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspH 285
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
972 AGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATC 1021

285 isAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 301
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1022 ATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGA 1071

302 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHi 318
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1072 ACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACA 1121

318 sThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleL 335
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1122 CACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTT 1171

335 euAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsn 351
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1172 TAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAAC 1221

352 AsnCysThrValAsnProLysGluSerIleLeuLysArgValLysAspIl 368
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1222 AACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATAT 1271

368 eGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysV 385
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1272 AGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTG 1321

385 alGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1322 TCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA 1371

402 ValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAs 418
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1372 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAA 1421

418 nPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaC 435
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1422 TTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGT 1471

435 ysAlaLeuGluValValMetAlaThrTyrSerArgSerThrSerGlnAsn 451
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1472 GCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAAT 1521

452 LeuAspSerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAs 468
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1522 CTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAA 1571

468 nLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaG 485
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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1572 TTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAG 1621

485 luGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHis 501
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1622 AAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT 1671

502 ArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLe 518
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1672 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCT 1721

518 uIleLysGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerA 535
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1722 TATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTG 1771

535 laCysProLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMet 551
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1772 CTTGTCCTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATG 1821

552 TyrLeuSerProValArgSerProLysLysLysGlySerThrThrArgVa 568
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1822 TATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGT 1871

568 lAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrG 585
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1872 AAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCC 1921

585 lnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyr 601
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1922 AGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTAT 1971

602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGl 618
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1972 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGA 2021

618 uHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuG 635
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2022 GCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGC 2071

635 lnAsnGluTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMet 651
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2072 AGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATG 2121

652 CysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLy 668
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2122 TGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAA 2171

668 sIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrP 685
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2172 AATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACAT 2221

685 heLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValPhe 701
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2222 TCAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTC 2271

702 TyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAl 718
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2272 TATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGC 2321

718 aSerThrArgProProThrLeuSerProIleProHisIleProArgSerP 735
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2322 TTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCC 2371

735 roTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyr 751
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2372 CTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTAT 2421

752 IleSerProLeuLysSerProTyrLysIleSerGluGlyLeuProThrPr 768
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2422 ATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACC 2471

768 oThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerP 785
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2472 AACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCAT 2521
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     785 heGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSer 801
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    2522 TCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGC 2571

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2572 GACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACT 2621

     818 uLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerL 835
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2622 GAAAAAACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTA 2671

     835 ysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThr 851
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2672 AACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACT 2721

     852 SerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspTh 868
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2722 TCTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATAC 2771

     868 rSerAsnLysGluGluLys 874
         ||||||||||||||||||
    2772 CTCAAACAAGGAAGAGAAA 2790

seq_name: N_Geneseq_36:V40004

seq_documentation_block:
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;

alignment_scores:
           Quality:  873.00              Length:    873
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x V40004   ..

 Align seg 1/1  to: V40004  from: 1  to: 2994

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
     304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGA 353

      18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     354 GAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTGTGGATGGAGTATTGG 403

      35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     404 GAGGTTATATTCAAAAGAAAAGGAACTGTGGGGAATCTGTATCTTTATT 453

      52 AlaAlaValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     454 GCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAA 503

      68 sAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleA 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     504 AAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTG 553

      85 spThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     554 ATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 603

     102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIl 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     604 GATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTAT 653

     118 eTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaL 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     654 ATATTTGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCAT 703

     135 euValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluVal 151
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     704 TGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTA 753

     152 LeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysVa 168
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    2904 CTCAAACAAGGAAGAGAAA 2922

seq_name: N_Geneseq_36:X00737

seq_documentation_block:
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AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;


alignment_scores:
            Quality:  873.00              Length:    873
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x X00737   ..

 Align seg 1/1  to: X00737  from: 1  to: 2995

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      18 uArgAlaTrpLeuThrTrpGluLysValSerSerValAspGlyValLeuG 35
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      35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
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 852 SerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspTh 868
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seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
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PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

alignment_scores:
Quality: 850.00 Length: 850
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: V58443 from: 1 to: 3323

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  41 sLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspG 58
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  58 luMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerVal 74
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 110 AGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 159

  75 HisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAs 91
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  91 pAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuP 108
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 125 SerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTr 141
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 141 pIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspL 158
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 275 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 291
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 358 ysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGlu 374
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1010 AAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1059

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seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID V58444 standard; DNA; 3266 BP.
AC V58444;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2505
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69368.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 166-170; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T;

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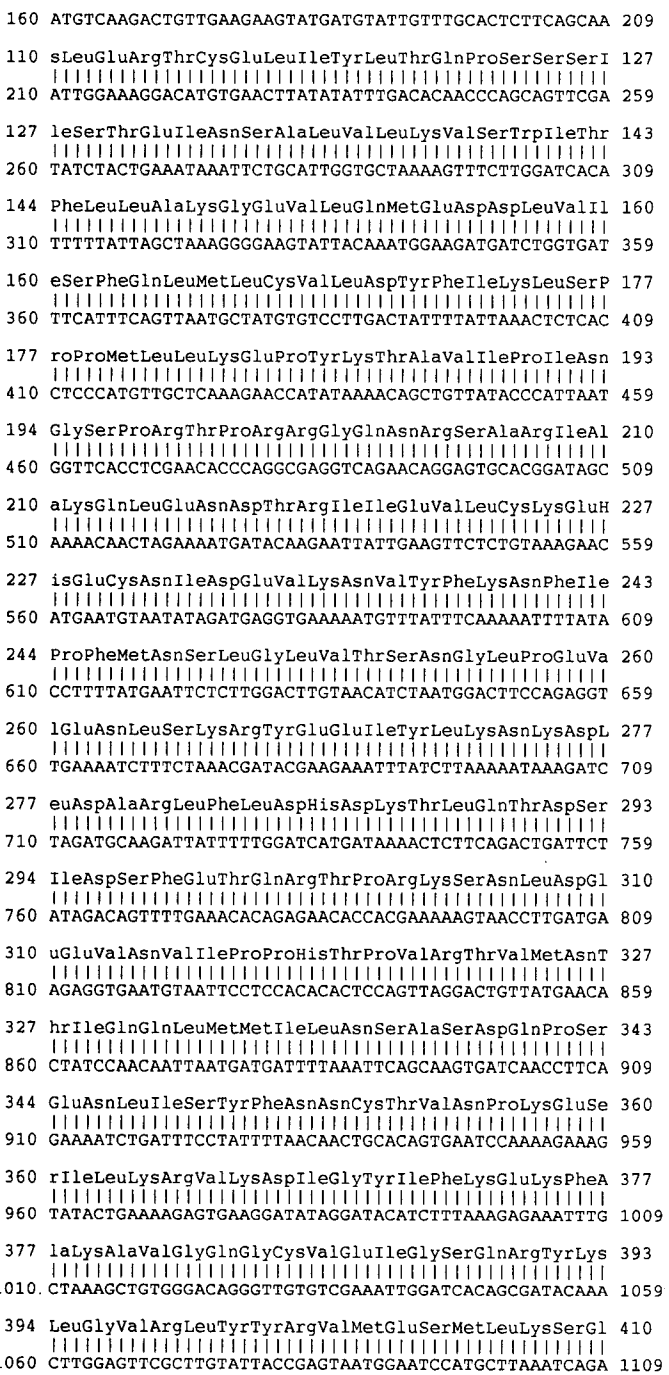
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210 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 259
127 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 143
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144 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 160
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160 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 177
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410 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 459
194 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 210
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     710 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 727
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     827 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 843
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seq_name: N_Geneseq_36:X04501

seq_documentation_block:

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ID   X04501 standard; cDNA; 4597 BP.
AC   X04501;
DT   05-JUL-1999  (first entry)
DE   Human retinoblastoma gene cDNA.
KW   Retinoblastoma; Rb gene; human; predisposition; diagnosis; therapy;
KW   ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             337. .2787
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PN   US5853988-A.
PD   29-DEC-1998.
PF   08-OCT-1992; 958290.
PR   08-JUL-1991; US-728756.
PR   11-AUG-1986; US-895163.
PR   21-JAN-1988; US-146525.
PR   23-JAN-1989; US-300667.
PR   25-SEP-1992; US-951342.
PR   08-OCT-1992; US-958290.
PA   (MASS-) MASSACHUSETTS EYE & EAR INFIRMARY.
PA   (WHED ) WHITEHEAD INST.
PI   Dryja TP, Friend S, Yandell DW;
DR   WPI; 99-094898/08.
DR   P-PSDB; Y01542.
PT   Isolated human retinoblastoma gene - used to develop products for
PT   analysing predisposition to retinoblastoma and for the detection and
PT   treatment of retinoblastoma
PS   Claim 8; Fig 5; 32pp; English.
CC   This is the nucleic acid sequence of a cDNA of the normal human
CC   retinoblastoma gene Rb.  Absence or mutation of the Rb gene (see
CC   also X04502) predisposes an individual to retinoblastoma.  To
CC   isolate Rb cDNA, the human DNA probe pH3-8, isolated from a human
CC   chromosome 13 lambda phage library, was used in a chromosome walk
CC   to isolate and map 30 kb of genomic DNA surrounding the H3-8
CC   sequence.  Fragment p7H30.7R (ATCC 97500) was obtained, and was
CC   used as a probe to screen a cDNA library that had been constructed
CC   from an adenovirus 12-transformed human embryonic retinal cell
CC   line.  This provided clone p4.7R (ATCC 97383), which in Northern
CC   blots cross-reacted with a 4.7 kb transcript in transformed
CC   retinal cells which was not present in 4 retinoblastoma and one
CC   osteosarcoma cell samples.  Rb nucleic acids comprising the Rb
CC   gene, cDNA or a fragment of the gene, such as one of the 27 exons
CC   or 26 introns, can be used in a claimed method for detecting a
CC   deletion or point mutation in the Rb gene of a human patient.  The
CC   gene can also be used to synthesize Rb polypeptide (see Y01542) for
CC   use in the treatment of individuals determined to have a defective
CC   Rb allele.
SQ   Sequence   4597 BP;    1489 A;    841 C;    813 G;    1454 T;
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              Ratio:  1.000                 Gaps:      0
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alignment_block:

US-09-026-459A-31 x X04501 ..

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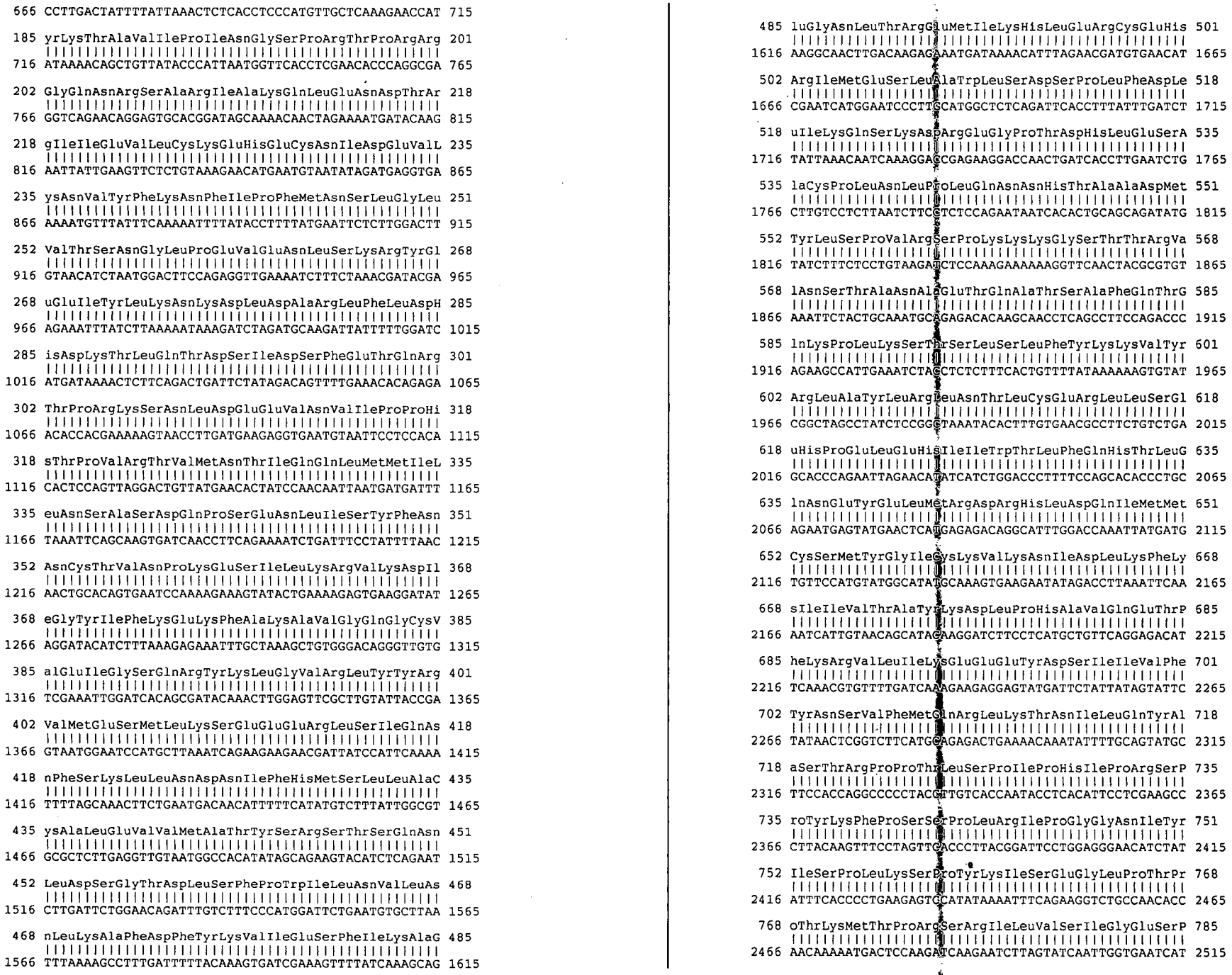
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


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              Ratio:  1.000                 Gaps:      0
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 470 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 487
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1485 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1534

 487 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 503
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 504 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 520
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1585 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1634

 520 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 537
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1635 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1684

 537 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 553
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1685 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1734

 554 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 570
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 570 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 587
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1785 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1834

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1835 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1884

 604 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 620
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1885 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1934

 620 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 637
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1935 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 1984

 637 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 653
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1985 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2034

 654 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 670
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 670 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 687
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 687 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 703
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 704 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 720
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 720 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 737
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 737 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 753
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 754 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 770
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 770 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 787
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 820 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 837
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 854 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 870
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seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

alignment_scores:
Quality: 821.00 Length: 821

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            Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x V58446   ..

 Align seg 1/1  to: V58446  from: 1  to: 3323

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      70 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 87
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     147 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 196

      87 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 103
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     104 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 120
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     120 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 137
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     137 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 153
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     154 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 170
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     337 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 353
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     354 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 370
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     370 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 387
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     487 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 503
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 1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1946

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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag= a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF, Xu H, Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;

alignment_scores:
           Quality:  820.00              Length:    820
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x Q72690    ..

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      71 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 88
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      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

      88 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 104
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     105 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 121
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     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

     121 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 138
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     207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

     138 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 154
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     257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

     155 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 171
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     171 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 188
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     188 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 204
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     205 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 221
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 221 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 238
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 238 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 254
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 455 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 471
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 771 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 788
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 788 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 804
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


alignment_scores:
            Quality:  816.00              Length:    816
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-31 x V58452   ..

 Align seg 1/1  to: V58452  from: 1  to: 3554

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      75 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 92
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     393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442

      92 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 108
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492

     109 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 125
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     493 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 542

     125 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 142
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     543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592

     142 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 158
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     593 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

     159 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 175
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     743 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 792

     209 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 225
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2443 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATC 2492

 775 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 792
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2493 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2542

 792 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 808
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2543 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2592

 809 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 825
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2593 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2642

 825 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 842
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2643 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2692

 842 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 858
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2693 AATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2742

 859 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 874
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2743 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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OM of: US-09-026-459A-33 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 13, 2000  2:27 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=oligo.rng -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-33
Query length: 851
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence           Strd Orig    ZScore    EScore Len  ! Documentation  ..
N_Geneseq_36:V58443  +  851.00 15698.00  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:Q04713  +  850.00 15680.28  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545  +  850.00 15680.28  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:V58440  +  850.00 15679.00  0.0       3555  ! Modified retinoblastoma tumou
N_Geneseq_36:V58441  +  850.00 15679.21  0.0       3455  ! Modified retinoblastoma tumou
N_Geneseq_36:V58442  +  850.00 15679.35  0.0       3392  ! Modified retinoblastoma tumou
N_Geneseq_36:V54990  +  850.00 15679.00  0.0       3555  ! DNA sequence of the specifica
N_Geneseq_36:V40004  +  850.00 15680.28  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737  +  850.00 15680.28  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:V58444  +  831.00 15328.26  0.0       3266  ! Modified retinoblastoma tumou
N_Geneseq_36:V58447  +  821.00 15142.90  0.0       3461  ! Modified retinoblastoma tumou
N_Geneseq_36:V58446  +  821.00 15143.20  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:Q72690  +  820.00 15124.91  0.0       3233  ! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58452  +  816.00 15050.23  0.0       3554  ! Modified retinoblastoma tumou
N_Geneseq_36:V54991  +  816.00 15050.97  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:X04501  +  799.00 14733.93  0.0       4597  ! Human retinoblastoma gene cDN
N_Geneseq_36:V58445  +  781.00 14403.96  0.0       3113  ! Modified retinoblastoma tumou
N_Geneseq_36:Q70536  +  763.00 14068.18  0.0       4597  ! Human retinoblastoma gene. Di
N_Geneseq_36:Q90059  +  749.00 13812.46  0.0       2995  ! Retinoblastoma tumour suppres
N_Geneseq_36:V58448  +  747.00 13774.65  0.0       3347  ! Modified retinoblastoma tumou
N_Geneseq_36:N81369  +  744.00 13716.80  0.0       4597  ! Human retinoblastoma gene Dia
N_Geneseq_36:V58449  +  687.00 12665.48  0.0       3161  ! Modified retinoblastoma tumou
N_Geneseq_36:V58450  +  687.00 12664.98  0.0       3377  ! Modified retinoblastoma tumou
N_Geneseq_36:V58451  +  628.00 11573.87  0.0       3383  ! Modified retinoblastoma tumou
N_Geneseq_36:Q86398  +  593.00 10927.51  0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489  +  474.00 8722.92   0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261  +  286.00 5246.92   1.2e-284  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502  +   65.00 1149.60   2.0e-56   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490  +   55.00  964.72   3.9e-46   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:T18371  -    9.00  134.84   6.53      1110  ! Human pituitary G-protein coup
N_Geneseq_36:T18373  -    9.00  139.20   3.74      618  ! Mouse pancreas G-protein couple
N_Geneseq_36:T87884  -    9.00  134.57   6.77      1152  ! Consensus human hypothalamic r
N_Geneseq_36:T87886  -    9.00  134.43   6.89      1173  ! Human hypothalamic receptor DN
N_Geneseq_36:T87887  -    9.00  134.43   6.89      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87888  -    9.00  134.43   6.89      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87889  -    9.00  134.43   6.89      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87885  -    9.00  138.26   4.21      701  ! Human hypothalamic receptor DNA
N_Geneseq_36:V02402  -    9.00  134.84   6.53      1110  ! Human G protein-coupled recept
N_Geneseq_36:V02403  -    9.00  139.20   3.74      618  ! Mouse MIN6-derived G protein-cd
N_Geneseq_36:V81232  -    9.00  134.84   6.53      1110  ! Human pituitary-derived G-p
N_Geneseq_36:V81233  -    9.00  139.20   3.74      618  ! Mouse MIN6-derived G-protein
N_Geneseq_36:X15507  -    9.00  134.84   6.53      1110  ! Human pituitary-derived G p
N_Geneseq_36:X15508  -    9.00  139.20   3.74      618  ! MIN6-derived G protein-coupl
N_Geneseq_36:Q48043  -    8.00  109.76  163.10     2691  ! TGF-beta induced gene betaI
N_Geneseq_36:V81234  -    8.00  124.37  25.04      378  ! Mouse MIN6-derived G-protein

seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;


alignment_scores:
           Quality:  851.00              Length:    851
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x V58443   ..

 Align seg 1/1  to: V58443  from: 1  to: 3323

       1 MetGluLysValSerSerValAspGlyValLeuGlyGlyTyrIleGlnLy 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       7 ATGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAA 56

      17 sLysLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 GAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAG 106

      34 spGluMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSer 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 ATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGT 156

      51 ValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysVa 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGT 206

      67 lAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaL 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 TGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCAC 256

      84 euPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnPro 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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257 TCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 306

101 SerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSe 117
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
307 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 356

117 rTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspA 134
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
357 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATG 406

134 spLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
407 ATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 456

151 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIl 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
457 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTAT 506

167 eProIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerA 184
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
507 ACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTG 556

184 laArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeu 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
557 CACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 606

201 CysLysGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLy 217
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
607 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 656

217 sAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyL 234
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
657 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGAC 706

234 euProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
707 TTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 756

251 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGl 267
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
757 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCA 806

267 nThrAspSerIleAspSerPheGluThrGlnArgThrProArgLysSerA 284
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807 GACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTA 856

284 snLeuAspGluGluValAsnValIleProProHisThrProValArgThr 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
857 ACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 906

301 ValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAs 317
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
907 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 956

317 pGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnP 334
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
957 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATC 1006

334 roLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1007 CAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1056

351 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGl 367
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1057 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACA 1106

367 nArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetL 384
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1107 GCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGC 1156

384 euLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeu 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1157 TTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1206

401 AsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValVa 417
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1207 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1256

417 lMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrA 434
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1257 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAG 1306

434 spLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1307 ATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1356

451 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrAr 467
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1357 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAG 1406

467 gGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSerL 484
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1407 AGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCC 1456

484 euAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLys 500
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1457 TTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1506

501 AspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLe 517
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1507 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1556

517 uProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValA 534
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1557 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAA 1606

534 rgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 550
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1607 GATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1656

551 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSe 567
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1657 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATC 1706

567 rThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuA 584
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1707 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCC 1756

584 rgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGlu 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1757 GGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1806

601 HisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLe 617
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1807 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1856

617 uMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyI 634
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1857 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCA 1906

634 leCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1907 TATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1956

651 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIl 667
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1957 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGAT 2006

667 eLysGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheM 684
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
2007 CAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCA 2056

684 etGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProPro 700
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
2057 TGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2106
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     701 ThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSe 717
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    2107 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2156

     717 rSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysS 734
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2157 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGA 2206

     734 erProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2207 GTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2256

     751 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLy 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2257 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAA 2306

     767 sPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysA 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2307 GTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAA 2356

     784 rgSerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPhe 800
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2357 GAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2406

     801 AspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGl 817
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2407 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2456

     817 uSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgM 834
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2457 GTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAA 2506

     834 etGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 850
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2507 TGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAG 2556

     851 Lys 851
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    2557 AAA 2559
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seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


alignment_scores:
          Quality:  850.00            Length:    850
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              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: Q04713  from: 1  to: 2994

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     373 GAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAA 422

      18 sLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspG 35
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     423 AAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATG 472

      35 luMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerVal 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     473 AGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

      52 HisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAs 68
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     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGA 572

      68 pAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuP 85
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     573 TAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCT 622

      85 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 101
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     623 TCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGC 672

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     118 pIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspL 135
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     135 euValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys 151
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     152 LeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIlePr 168
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     235 roGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsn 251
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    1073 CAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

     252 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 268
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 535 erProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 551
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 552 GluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerTh 568
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 602 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 618
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2173 ATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCAT 2222

 618 tArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleC 635
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 668 sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG 685
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 718 rProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerP 735
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2523 ACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTC 2572

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seq_name: N_Geneseq_36:Q41545

seq_documentation_block:
ID Q41545 standard; DNA; 2994 BP.
AC Q41545;
DT 24-AUG-1993 (first entry)
DE Retinoblastoma gene.

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KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  850.00              Length:    850
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x Q41545   ..

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1923 TCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGAT 1972

 535 erProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 551
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1973 CTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

 552 GluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerTh 568
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2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTAC 2072

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 602 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 618
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2173 ATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCAT 2222

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 652 LysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLy 668
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2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAA 2372

 668 sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG 685
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2373 AGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGC 2422

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2423 AGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACC 2472

 702 LeuSerProIleProHisIleProArgSerProTyrLysPheProSerSe 718
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 735 roTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 751
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 752 SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPh 768
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seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


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alignment_block:
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    591 GATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATC 640

    135 euValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys 151
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    235 roGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsn 251
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    352 LysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnAr 368
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    452 TyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGl 468
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seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a

PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


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     85 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 101
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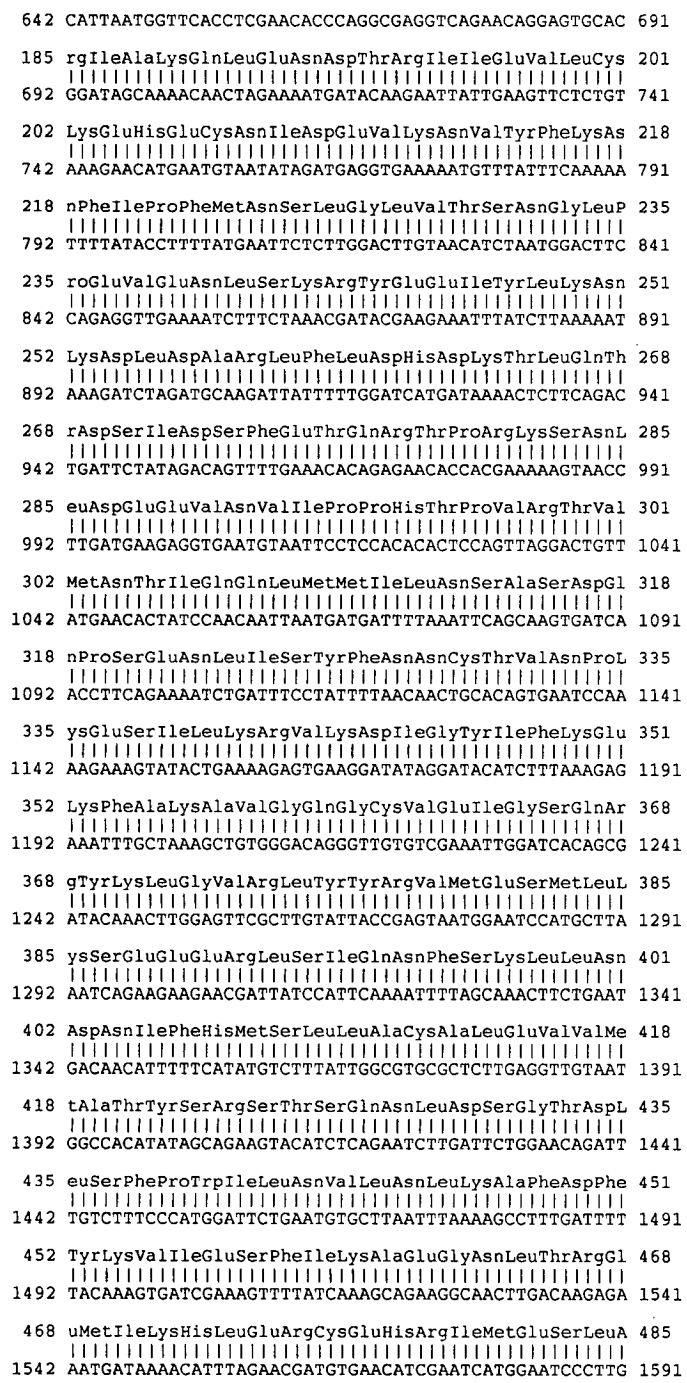
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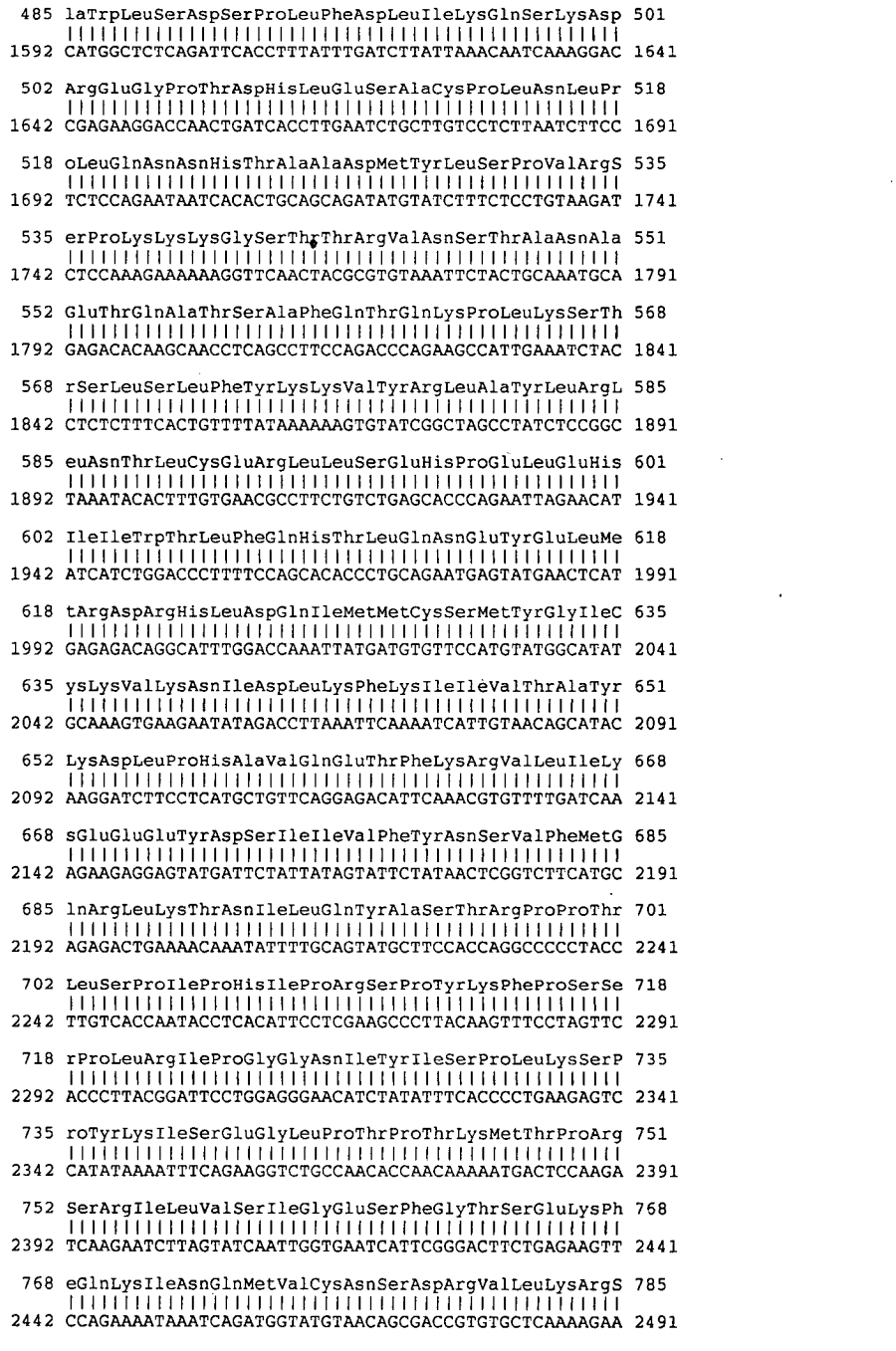
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    492 GATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATC 541

    135 euValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys 151
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    152 LeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIlePr 168
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    168 oIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaA 185
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692 GGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGT 741
202 LysGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAs 218
742 AAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAA 791
218 nPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuP 235
792 TTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTC 841
235 roGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsn 251
842 CAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 891
252 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 268
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268 rAspSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnL 285
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
           Quality:  850.00             Length:    850
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
```

```
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  850.00              Length:    850
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x V54990    ..

 Align seg 1/1  to: V54990  from: 1  to: 3555

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     241 GAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAA 290

      18 sLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspG 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     291 AAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATG 340

      35 luMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerVal 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     341 AGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 390

      52 HisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAs 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     391 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGA 440

      68 pAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuP 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     441 TAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCT 490

      85 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     491 TCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGC 540

     102 SerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTr 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     541 AGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTG 590

     118 pIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspL 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     591 GATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATC 640

     135 euValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys 151
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     641 TGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 690

     152 LeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIlePr 168
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     691 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACC 740

     168 oIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaA 185
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     185 rgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCys 201
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     218 nPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuP 235
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     235 roGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsn 251
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     252 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     268 rAspSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnL 285
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     318 nProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProL 335
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     335 ysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGlu 351
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     368 gTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuL 385
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1341 ATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTA 1390

     385 ysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsn 401
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     402 AspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMe 418
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     418 tAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspL 435
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     435 euSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPhe 451
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 518 oLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgS 535
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1791 TCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGAT 1840

 535 erProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 551
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1841 CTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 1890

 552 GluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerTh 568
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 568 rSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgL 585
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1941 CTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGC 1990

 585 euAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHis 601
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 602 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 618
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 618 tArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleC 635
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 685 lnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThr 701
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 702 LeuSerProIleProHisIleProArgSerProTyrLysPheProSerSe 718
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 718 rProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerP 735
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2391 ACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTC 2440

 735 roTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 751
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 752 SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPh 768
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2491 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTT 2540

 768 eGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgS 785
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 802 IleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSe 818
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 818 rLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetG 835
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2691 CAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGC 2740

 835 lnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 851
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2741 AAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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seq_name: N_Geneseq_36:V40004

seq_documentation_block:
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;


alignment_scores:
            Quality:  850.00              Length:    850
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x V40004   ..

 Align seg 1/1  to: V40004  from: 1  to: 2994

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      18 sLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspG 35
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423 AAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATG 472

 35 luMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerVal 51
473 AGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

 52 HisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAs 68
523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGA 572

 68 pAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuP 85
573 TAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCT 622

 85 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 101
623 TCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGC 672

102 SerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTr 118
673 AGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTG 722

118 pIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspL 135
723 GATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATC 772

135 euValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys 151
773 TGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAA 822

152 LeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIlePr 168
823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACC 872

168 oIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaA 185
873 CATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCAC 922

185 rgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCys 201
923 GGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGT 972

202 LysGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAs 218
973 AAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAA 1022

218 nPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuP 235
1023 TTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTC 1072

235 roGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsn 251
1073 CAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 1122

252 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 268
1123 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGAC 1172

268 rAspSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnL 285
1173 TGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACC 1222

285 euAspGluGluValAsnValIleProProHisThrProValArgThrVal 301
1223 TTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTT 1272

302 MetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGl 318
1273 ATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCA 1322

318 nProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProL 335

1323 ACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAA 1372

335 ysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGlu 351
1373 AAGAAAGTATACTGAAAACAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

352 LysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnAr 368
1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCG 1472

368 gTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuL 385
1473 ATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTA 1522

385 ysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsn 401
1523 AATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAAT 1572

402 AspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMe 418
1573 GACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAAT 1622

418 tAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspL 435
1623 GGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATT 1672

435 euSerProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPhe 451
1673 TGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

452 TyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGl 468
1723 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGA 1772

468 uMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuA 485
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485 laTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAsp 501
1823 CATGGCTCTCAGATTCACGTTTATTTGATCTTATTAAACAATCAAAGGAC 1872

502 ArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuPr 518
1873 CGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCC 1922

518 oLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgS 535
1923 TCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGAT 1972

535 erProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 551
1973 CTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

552 GluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerTh 568
2023 GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTAC 2072

568 rSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgL 585
2073 CTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGC 2122

585 euAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHis 601
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602 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 618
2173 ATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCAT 2222

618 tArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleC 635
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     635 ysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyr 651
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    2273 GCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

     652 LysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLy 668
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2323 AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAA 2372

     668 sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG 685
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2373 AGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGC 2422

     685 lnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThr 701
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2423 AGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACC 2472

     702 LeuSerProIleProHisIleProArgSerProTyrLysPheProSerSe 718
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2473 TTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTC 2522

     718 rProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerP 735
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2523 ACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTC 2572

     735 roTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 751
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2573 CATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGA 2622

     752 SerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPh 768
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2623 TCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTT 2672

     768 eGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgS 785
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    2673 CCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAA 2722

     785 erAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAsp 801
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    2723 GTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGAT 2772

     802 IleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSe 818
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    2773 ATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTC 2822

     818 rLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetG 835
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     835 lnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 851
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seq_name: N_Geneseq_36:X00737

seq_documentation_block:

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ID   X00737 standard; cDNA; 2995 BP.
AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;
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alignment_scores:

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            Quality:  850.00              Length:   850
              Ratio:  1.000                 Gaps:     0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

US-09-026-459A-33 x X00737 ..

Align seg 1/1 to: X00737 from: 1 to: 2995

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     373 GAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAA 422

      18 sLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspG 35
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     423 AAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATG 472

      35 luMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerVal 51
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     473 AGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTC 522

      52 HisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAs 68
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     523 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGA 572

      68 pAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuP 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     573 TAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCT 622

      85 heSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSer 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     623 TCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGC 672

     102 SerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTr 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     673 AGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTG 722

     118 pIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspL 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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 135 euValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLys 151
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 152 LeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIlePr 168
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 823 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACC 872

 168 oIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaA 185
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 873 CATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCAC 922

 185 rgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCys 201
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 923 GGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGT 972

 202 LysGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAs 218
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 973 AAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAA 1022

 218 nPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuP 235
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1023 TTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTC 1072

 235 roGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsn 251
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 252 LysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnTh 268
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 268 rAspSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnL 285
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 285 euAspGluGluValAsnValIleProProHisThrProValArgThrVal 301
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 302 MetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGl 318
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 318 nProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProL 335
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1323 ACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAA 1372

 335 ysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGlu 351
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1373 AAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 1422

 352 LysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnAr 368
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1423 AAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCG 1472

 368 gTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuL 385
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 385 ysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsn 401
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 402 AspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMe 418
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1573 GACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAAT 1622

 418 tAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspL 435
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 435 euSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPhe 451
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1673 TGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT 1722

 452 TyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGl 468
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 468 uMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuA 485
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 485 laTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAsp 501
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 502 ArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuPr 518
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1873 CGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCC 1922

 518 oLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgS 535
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1923 TCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGAT 1972

 535 erProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 551
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1973 CTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA 2022

 552 GluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerTh 568
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 568 rSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgL 585
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
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 585 euAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHis 601
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2123 TAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACAT 2172

 602 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe 618
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2173 ATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCAT 2222

 618 tArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleC 635
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2223 GAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATAT 2272

 635 ysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyr 651
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2273 GCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC 2322

 652 LysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLy 668
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 668 sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG 685
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 702 LeuSerProIleProHisIleProArgSerProTyrLysPheProSerSe 718
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 718 rProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerP 735
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   2673 CCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAA 2722

    785 erAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAsp 801
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        ||||||||||||||||||||||||||||||||||||||||||||||||||
   2773 ATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTC 2822

    818 rLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetG 835
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   2823 CAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGC 2872

    835 lnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 851
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seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


alignment_scores:
            Quality:  831.00             Length:    831
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x V58444   ..

 Align seg 1/1  to: V58444  from: 1  to: 3266

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      10 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 59

      37 rPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysP 54
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      60 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAAT 109

      54 hePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 70
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     110 TCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 159

      71 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 87
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     160 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 209

      87 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 104
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 259

     104 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 309

     121 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 137
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 359

     137 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 154
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 409

     154 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 170
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 459

     171 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 187
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     460 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 509

     187 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 204
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     510 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 559

     204 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 220
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     560 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 609

     221 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 237
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     610 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 659

     237 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 254
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     271 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 287
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     287 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 304
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     810 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 859

     304 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 320
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     860 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 909

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 910 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 959

 337 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 354
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 737 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 754
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2160 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2209

 754 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 770
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
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DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


alignment_scores:
           Quality:  821.00              Length:    821
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x V58447   ..

 Align seg 1/1  to: V58447  from: 1  to: 3461

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     235 GTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 284

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     285 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 334

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     335 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 384

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     385 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 434

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
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     435 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 484

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
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     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
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 764 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
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    2685 CAAGGAAGAGAAA 2697
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seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x V58446   ..

 Align seq 1/1 to: V58446 from: 1  to: 3323

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      97 GTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 146

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     147 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 196

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     197 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 246

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     247 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 296

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
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     297 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 346

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
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     347 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 396
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 131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
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 147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
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 447 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 496

 164 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 180
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 181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
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 597 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 614
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     764 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
            Quality:  820.00            Length:    820
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x Q72690   ..

 Align seg 1/1  to: Q72690  from: 1  to: 3233

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     48 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 65
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     57 AATCAGTGTCCATAAATTGTTTAACTTACTAAAAGAAATTGATACCAGTA 106

     65 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 81
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     82 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 98
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    157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

     98 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 115
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    207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

    115 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 131
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    257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

    132 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 148
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    307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 356

    148 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 165
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    357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

    165 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 181
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    407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

    182 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 198
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    457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

    198 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 215
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    215 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 231
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    557 ATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

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    607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 656

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    265 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 281
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    282 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVa 298
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1107 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 1156

 415 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 431
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 432 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 448
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 498 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 515
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 532 ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerTh 548
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1507 CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTAC 1556

 548 rAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProL 565
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1557 TGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCAT 1606

 565 euLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 581
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1607 TGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCC 1656

 582 TyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGl 598
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1657 TATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGA 1706

 598 uLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluT 615
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1707 ATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGT 1756

 615 yrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMet 631
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1757 ATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATG 1806

 632 TyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleVa 648
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGT 1856

  648 lThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArgV 665
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1857 AACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTG 1906

  665 alLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSer 681
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1907 TTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCG 1956

  682 ValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrAr 698
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1957 GTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAG 2006

  698 gProProThrLeuSerProIleProHisIleProArgSerProTyrLysP 715
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2007 GCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGT 2056

  715 heProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 731
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2057 TTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

  732 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 748
      ||||||||||||||||||||||||||||||||||||||||||||||||||
2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAAT 2156

  748 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 765
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2157 GACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTT 2206

  765 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 781
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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  782 LeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysLe 798
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2257 CTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACT 2306

  798 uArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuP 815
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2307 ACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCC 2356

  815 roGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArg 831
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2357 CAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

  832 ThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLy 848
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2407 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAA 2456

  848 sGluGluLys 851
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2457 GGAAGAGAAA 2466
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
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PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69376.
PT Retinoblastoma suppressor protein with N-terminal modification - inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 226-230; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor protein (RTSP) of the invention. The proteins can be used for inhibiting cellular proliferation, when coadministered with a p53 protein. The RTSPs can be used for treating diseases characterised by abnormal cellular proliferation, particularly cancers. The RTSPs have a broader spectrum of activity than wild type RTSPs.
SQ Sequence 3554 BP; 1170 A; 683 C; 653 G; 1048 T;

alignment_scores:
Quality: 816.00 Length: 816
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-33 x V58452 ..

Align seg 1/1 to: V58452 from: 1 to: 3554

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    343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 392

     52 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 69
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442

     69 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 85
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492

     86 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 102
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    493 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 542

    102 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 119
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592

    119 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 135
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    593 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

    136 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 152
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 692

    152 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 169
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    693 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 742

    169 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 185
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    743 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 792

    186 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 202
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    793 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 842

    202 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 219
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    843 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 892

    219 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 235
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    893 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 942

    236 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 252
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    943 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 992

    252 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 269
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    993 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 1042

    269 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 285
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   1043 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 1092

    286 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 302
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   1093 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 1142

    302 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 319
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1143 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1192

    319 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 335
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1193 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242

    336 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 352
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1292

    352 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 369
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1293 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1342

    369 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 385
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1343 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1392

    386 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 402
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1393 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1442

    402 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 419
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    419 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 435
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   1493 CCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1542

    436 SerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 452
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1543 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1592

    452 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 469
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1593 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1642

    469 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 485
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   1643 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 1692

    486 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 502
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   1693 TGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCG 1742

    502 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 519
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   1743 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1792

    519 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 535
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 536 ProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGl 552
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1843 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1892

 552 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 569
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1893 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1942

 569 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 585
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1943 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1992

 586 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 602
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1993 AATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATAT 2042

 602 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 619
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2043 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 2092

 619 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 635
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2093 GAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2142

 636 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 652
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2143 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAA 2192

 652 sAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysG 669
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2193 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 2242

 669 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 685
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2243 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 2292

 686 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 702
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2293 AGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTT 2342

 702 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 719
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2343 GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCAC 2392

 719 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 735
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2393 CCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2442

 736 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSe 752
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2443 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATC 2492

 752 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 769
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2493 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2542

 769 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 785
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2543 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2592

 786 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 802
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2593 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2642

 802 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 819
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2643 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2692

 819 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 835
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 836 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 851
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seq_documentation_block:
ID   V54991 standard; DNA; 3218 BP.
AC   V54991;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2457
FT                   /*tag= a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71355.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 153-157; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3218 BP;    1080 A;    595 C;    561 G;    982 T;


alignment_scores:
            Quality:  816.00              Length:    816
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-33 x V54991  ..

 Align seg 1/1  to: V54991  from: 1  to: 3218

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       7 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 56

      52 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 69
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 106

      69 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 156

      86 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 102
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 206

     102 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 119
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    ||||||||||||||||||||||||||||||||||||||||||||||||||
207 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 256

119 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 135
    ||||||||||||||||||||||||||||||||||||||||||||||||||
257 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 306

136 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 152
    ||||||||||||||||||||||||||||||||||||||||||||||||||
307 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 356

152 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 169
    ||||||||||||||||||||||||||||||||||||||||||||||||||
357 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 406

169 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 185
    ||||||||||||||||||||||||||||||||||||||||||||||||||
407 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 456

186 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 202
    ||||||||||||||||||||||||||||||||||||||||||||||||||
457 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 506

202 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 219
    ||||||||||||||||||||||||||||||||||||||||||||||||||
507 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 556

219 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 235
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557 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 606

236 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 252
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607 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 656

252 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 269
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657 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 706

269 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 285
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286 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 302
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757 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 806

302 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 319
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807 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 856

319 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 335
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857 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 906

336 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 352
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907 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 956

352 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 369
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957 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1006

369 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 385
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1007 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1056

386 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 402
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1057 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1106

402 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 419
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 452 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 469
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 469 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 485
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 519 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 535
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 819 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 835
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 836 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 851
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Date: Feb 13, 2000  2:29 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
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 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
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Query length: 832
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence            Strd Orig    ZScore    EScore Len   ! Documentation  ..
N_Geneseq_36:V58444  +  832.00 15355.47  0.0       3266  ! Modified retinoblastoma tumou
N_Geneseq_36:Q04713  +  831.00 15337.62  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545  +  831.00 15337.62  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:V58440  +  831.00 15336.34  0.0       3555  ! Modified retinoblastoma tumou
N_Geneseq_36:V58441  +  831.00 15336.55  0.0       3455  ! Modified retinoblastoma tumou
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N_Geneseq_36:V40004  +  831.00 15337.62  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737  +  831.00 15337.61  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:V58447  +  821.00 15151.50  0.0       3461  ! Modified retinoblastoma tumou
N_Geneseq_36:V58446  +  821.00 15151.81  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:Q72690  +  820.00 15133.51  0.0       3233  ! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58452  +  816.00 15058.79  0.0       3554  ! Modified retinoblastoma tumou
N_Geneseq_36:V54991  +  816.00 15059.53  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:V58445  +  781.00 14412.15  0.0       3113  ! Modified retinoblastoma tumou
N_Geneseq_36:X04501  +  780.00 14390.75  0.0       4597  ! Human retinoblastoma gene cDN
N_Geneseq_36:V58448  +  747.00 13782.50  0.0       3347  ! Modified retinoblastoma tumou
N_Geneseq_36:Q70536  +  744.00 13724.63  0.0       4597  ! Human retinoblastoma gene. Di
N_Geneseq_36:N81369  +  730.00 13465.58  0.0       4597  ! Human retinoblastoma gene Dia
N_Geneseq_36:Q90059  +  730.00 13468.76  0.0       2995  ! Retinoblastoma tumour suppres
N_Geneseq_36:V58449  +  687.00 12672.71  0.0       3161  ! Modified retinoblastoma tumou
N_Geneseq_36:V58450  +  687.00 12672.22  0.0       3377  ! Modified retinoblastoma tumou
N_Geneseq_36:V58451  +  628.00 11580.50  0.0       3383  ! Modified retinoblastoma tumou
N_Geneseq_36:Q86398  +  593.00 10933.79  0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489  +  474.00 8727.98   0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261  +  286.00 5250.06   7.9e-285  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502  +   65.00 1150.50   1.7e-56   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490  +   55.00  965.52   3.5e-46   18177  ! DNA of human retinoblastoma g
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N_Geneseq_36:T18373  -    9.00  139.48   3.60      618  ! Mouse pancreas G-protein couple
N_Geneseq_36:T87884  -    9.00  134.86   6.52      1152  ! Consensus human hypothalamic r
N_Geneseq_36:T87886  -    9.00  134.72   6.64      1173  ! Human hypothalamic receptor DN
N_Geneseq_36:T87887  -    9.00  134.72   6.64      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87888  -    9.00  134.72   6.64      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87889  -    9.00  134.72   6.64      1174  ! Human hypothalamic receptor DN
N_Geneseq_36:T87885  -    9.00  138.55   4.06      701  ! Human hypothalamic receptor DNA
N_Geneseq_36:V02402  -    9.00  135.13   6.30      1110  ! Human G protein-coupled recept
N_Geneseq_36:V02403  -    9.00  139.48   3.60      618  ! Mouse MIN6-derived G protein-cd
N_Geneseq_36:V81232  -    9.00  135.13   6.30      1110  ! Human pituitary-derived G-p
N_Geneseq_36:V81233  -    9.00  139.48   3.60      618  ! Mouse MIN6-derived G-protein
N_Geneseq_36:X15507  -    9.00  135.13   6.30      1110  ! Human pituitary-derived G p
N_Geneseq_36:X15508  -    9.00  139.48   3.60      618  ! MIN6-derived G protein-coupl
N_Geneseq_36:Q48043  -    8.00  110.05  157.17     2691  ! TGF-beta induced gene betaI
N_Geneseq_36:V81234  -    8.00  124.63   24.20     378  ! Mouse MIN6-derived G-protein

seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x V58444   ..

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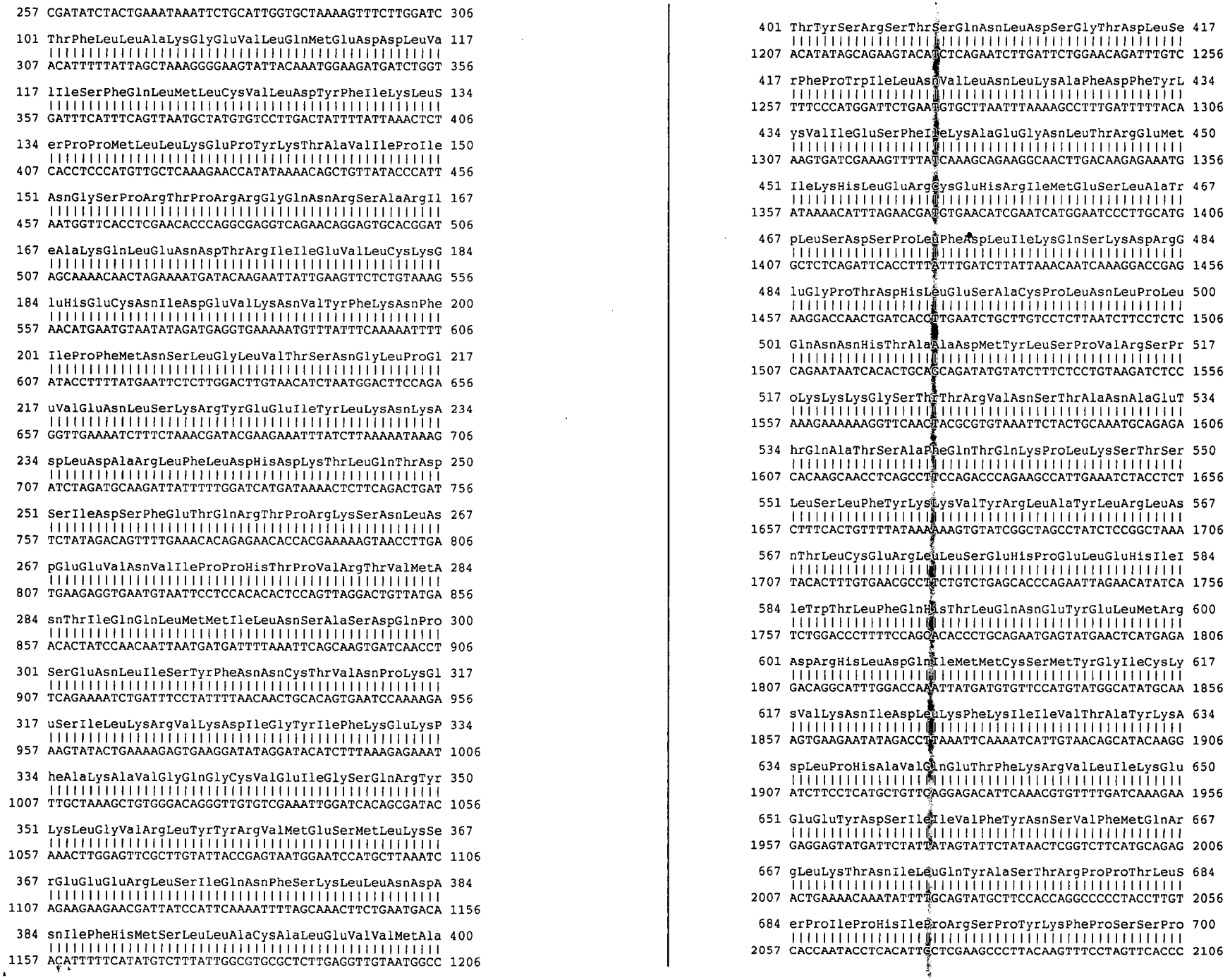
      17 tSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisL 34
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      57 GTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATA 106

      34 ysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsn 50
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     107 AATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAAT 156

      51 AlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSe 67
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     157 GCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAG 206

      67 rLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerS 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 CAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTT 256

      84 erIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIle 100
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101 ThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuVa 117
307 ACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGT 356
117 lIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuS 134
357 GATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCT 406
134 erProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIle 150
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151 AsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIl 167
457 AATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGAT 506
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234 spLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAsp 250
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251 SerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAs 267
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401 ThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSe 417
1207 ACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTC 1256
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1407 GCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAG 1456
484 luGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeu 500
1457 AAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTC 1506
501 GlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerPr 517
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517 oLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluT 534
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534 hrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSer 550
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551 LeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAs 567
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567 nThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleI 584
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601 AspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLy 617
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617 sValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysA 634
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634 spLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGlu 650
1907 ATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAA 1956
651 GluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnAr 667
1957 GAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAG 2006
667 gLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuS 684
2007 ACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGT 2056
684 erProIleProHisIleProArgSerProTyrLysPheProSerSerPro 700
2057 CACCAATACCTCACATTGCTCGAAGCCCTTACAAGTTTCCTAGTTCACCC 2106

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     734 rgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGln 750
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seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


alignment_scores:
            Quality:  831.00              Length:    831
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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      18 rPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysP 35
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     480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAAT 529

      35 hePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 51
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      52 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 68
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      68 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 85
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      85 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
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     102 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 118
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     730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

     118 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 135
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     235 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 251
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     252 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 268
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 352 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 368
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 418 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 435
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 468 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 485
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1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

 518 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 535
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 535 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 551
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 552 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 568
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ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
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PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  831.00              Length:    831
              Ratio:  1.000                 Gaps:      0
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 US-09-026-459A-35 x Q41545   ..

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     202 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 218
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    1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

     218 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 235
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    1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 1129

     235 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 251
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     252 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 268
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 1229

     268 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 285
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    1230 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1279

     285 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 301
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     318 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 335
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     335 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 351
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     352 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 368
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 468 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 485
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 502 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 518
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 518 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 535
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 718 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 735
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 752 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 768
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 768 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 785
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seq_name: N_Geneseq_36:V58440

seq_documentation_block:

ID V58440 standard; DNA; 3555 BP.
AC V58440;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	7. .2793
FT		/*tag= a

PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69364.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Disclosure; Page 121-126; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

alignment_scores:

Quality:	831.00	Length:	831
Ratio:	1.000	Gaps:	0
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alignment_block:
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Align seg 1/1 to: V58440 from: 1 to: 3555

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  18 rPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysP 35
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 348 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAAT 397

  35 hePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 51
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 398 TCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 447

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68 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 85
498 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 547
85 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
548 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 597
102 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 118
598 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 647
118 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 135
648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 697
135 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 151
698 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747
152 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 168
748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 797
168 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 185
798 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 847
185 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 201
848 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 897
202 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 218
898 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 947
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235 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 251
998 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1047
252 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 268
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1198 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1247
318 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 335
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1898 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1947
552 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 568
1948 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1997
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1998 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 2047
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seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;
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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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     399 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 448

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     118 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 135
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 702 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 718
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 735 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 751
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 802 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 818
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
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KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
            Quality:  831.00              Length:    831
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x V58442   ..

 Align seg 1/1  to: V58442  from: 1  to: 3392

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      18 rPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysP 35
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     186 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAAT 235

      35 hePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 51
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     236 TCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 285

      52 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 68
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      68 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 85
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     336 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 385

      85 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
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 668 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 685
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2136 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2185

 685 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 701
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2186 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2235

 702 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 718
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2236 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2285

 718 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 735
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2286 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2335

 735 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 751
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2336 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2385

 752 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 768
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2386 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2435

 768 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 785
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2436 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2485

 785 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 801
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2486 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2535

 802 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 818
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2536 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2585

 818 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 832
     |||||||||||||||||||||||||||||||||||||||||||
2586 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628
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seq_name: N_Geneseq_36:V58443

seq_documentation_block:

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ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;
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alignment_scores:

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           Quality:  831.00              Length:    831
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

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 US-09-026-459A-35 x V58443   ..

 Align seg 1/1  to: V58443  from: 1  to: 3323

       2 LeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspGluMetSe 18
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      67 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 116

      18 rPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysP 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     117 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAAT 166

      35 hePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     167 TCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 216
```

```
 52 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 68
    ||||||||||||||||||||||||||||||||||||||||||||||||||
217 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 266

 68 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 85
    ||||||||||||||||||||||||||||||||||||||||||||||||||
267 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 316

 85 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
    ||||||||||||||||||||||||||||||||||||||||||||||||||
317 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 366

102 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 118
    ||||||||||||||||||||||||||||||||||||||||||||||||||
367 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 416

118 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 135
    ||||||||||||||||||||||||||||||||||||||||||||||||||
417 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 466

135 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 151
    ||||||||||||||||||||||||||||||||||||||||||||||||||
467 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 516

152 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 168
    ||||||||||||||||||||||||||||||||||||||||||||||||||
517 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 566

168 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 185
    ||||||||||||||||||||||||||||||||||||||||||||||||||
567 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 616

185 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 201
    ||||||||||||||||||||||||||||||||||||||||||||||||||
617 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 666

202 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 218
    ||||||||||||||||||||||||||||||||||||||||||||||||||
667 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 716

218 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 235
    ||||||||||||||||||||||||||||||||||||||||||||||||||
717 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 766

235 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 251
    ||||||||||||||||||||||||||||||||||||||||||||||||||
767 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 816

252 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 268
    ||||||||||||||||||||||||||||||||||||||||||||||||||
817 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 866

268 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 285
    ||||||||||||||||||||||||||||||||||||||||||||||||||
867 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 916

285 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 301
    ||||||||||||||||||||||||||||||||||||||||||||||||||
917 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 966

302 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 318
    ||||||||||||||||||||||||||||||||||||||||||||||||||
967 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1016

318 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 335
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1017 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1066

335 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 351
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1067 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1116

352 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 368
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1117 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1166

368 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 385
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1167 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1216

385 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 401
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1217 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1266

402 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 418
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1267 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1316

418 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 435
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1317 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1366

435 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 451
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1367 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1416

452 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 468
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1417 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCT 1466

468 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 485
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1467 CTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAG 1516

485 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 501
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1517 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1566

502 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 518
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1567 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1616

518 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 535
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1617 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 1666

535 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 551
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1667 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1716

552 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 568
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1717 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1766

568 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 585
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1767 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1816

585 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 601
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1817 GGACCCTTTTCCAGCACAGCCTGCAGAATGAGTATGAACTCATGAGAGAC 1866

602 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 618
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1867 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 1916

618 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 635
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1917 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 1966

635 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 651
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1967 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2016

652 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 668
    ||||||||||||||||||||||||||||||||||||||||||||||||||
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    2017 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 2066

     668 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 685
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2067 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2116

     685 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 701
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2117 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2166

     702 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 718
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2167 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2216

     718 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 735
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2217 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2266

     735 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 751
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2267 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2316

     752 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 768
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2317 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2366

     768 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 785
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2367 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2416

     785 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 801
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2417 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2466

     802 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 818
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2467 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2516

     818 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 832
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seq_name: N_Geneseq_36:V54990

seq_documentation_block:
ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  831.00              Length:    831
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x V54990   ..

 Align seg 1/1  to: V54990  from: 1  to: 3555

       2 LeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspGluMetSe 18
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     298 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 347

      18 rPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysP 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     348 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAAT 397

      35 hePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     398 TCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 447

      52 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     448 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 497

      68 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     498 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 547

      85 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     548 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 597

     102 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 118
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     598 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 647

     118 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 135
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 697

     135 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 151
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     698 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747

     152 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 168
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 797

     168 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 185
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     798 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 847

     185 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 201
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     848 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 897

     202 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 218
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     898 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 947
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 218 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 235
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 948 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 997

 235 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 251
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 998 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1047

 252 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 268
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1048 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 1097

 268 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 285
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1098 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1147

 285 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 301
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1148 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1197

 302 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 318
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1198 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1247

 318 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 335
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1248 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1297

 335 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 351
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1298 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1347

 352 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 368
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1348 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1397

 368 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 385
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1398 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1447

 385 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 401
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 402 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 418
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1498 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1547

 418 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 435
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 435 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 451
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 452 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 468
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 468 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 485
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1748 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1797

 502 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 518
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 535 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 551
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 552 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 568
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 568 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 585
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 635 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 651
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 652 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 668
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 718 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 735
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 785 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 801
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2648 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2697

 802 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 818
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
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 818 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 832
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seq_name: N_Geneseq_36:V40004

seq_documentation_block:
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;


alignment_scores:
            Quality:  831.00            Length:    831
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x V40004   ..

 Align seg 1/1  to: V40004  from: 1  to: 2994

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     430 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTC 479

      18 rPheThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysP 35
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     480 GTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAAT 529

      35 hePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAla 51
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     530 TCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCT 579

      52 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 68
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 629

      68 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 85
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     630 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 679

      85 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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      102 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 118
          ||||||||||||||||||||||||||||||||||||||||||||||||||
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      118 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||
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     830 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

      152 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 168
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     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 929

      168 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 185
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     930 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 979

      185 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 201
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     980 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

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      218 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 235
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    1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 1129

      235 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 251
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    1130 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

      252 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||
    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 1229

      268 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||
    1230 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1279

      285 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 301
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      302 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||
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      318 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||
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 418 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 435
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seq_name: N_Geneseq_36:X00737

seq_documentation_block:
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AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
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PR 13-SEP-1993; US-121108.
PR 24-SEP-1993; US-126810.
PA (CANJ-) CANJI INC.
PA (REGC) UNIV CALIFORNIA.
PI Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI Wang NP;
DR WPI; 99-080477/07.
DR P-PSDB; W67801.
PT Inhibition of cancer cell proliferation - with retinoblastoma
PT protein or polypeptide
PS Example 1; Fig 2A-K; 72pp; English.
CC The present sequence encodes a human retinoblastoma (RB) protein
CC designated ppRB-110 or p110-RB. The protein is used in a method
CC for inhibiting proliferation of pathologically proliferating cells
CC lacking endogenous functional retinoblastoma protein. The method
CC comprises contacting the cells with a polypeptide comprising a 56 kD
CC C-terminal fragment of retinoblastoma protein. The method is useful
CC for treating cancers, especially retinoblastoma or secondary
CC osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T;

alignment_scores:
Quality: 831.00 Length: 831
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: X00737 from: 1 to: 2995

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seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


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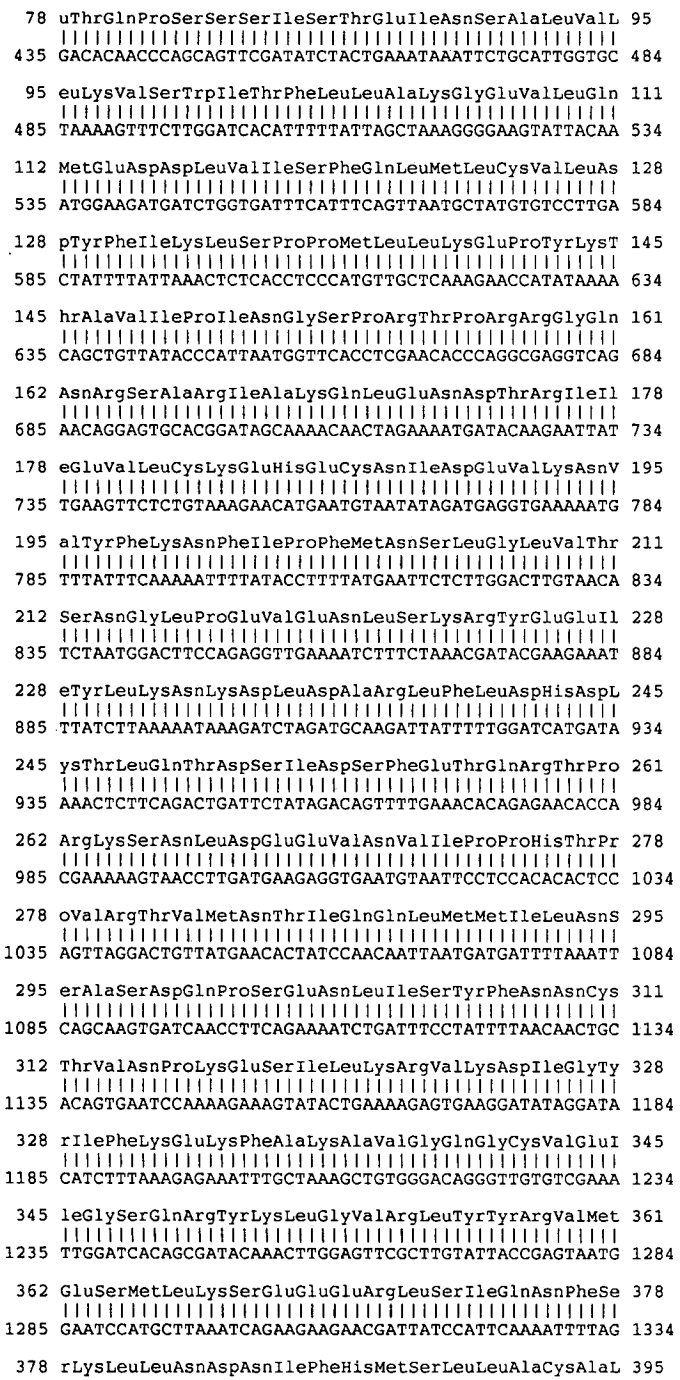
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95 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 111
485 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 534
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685 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 734
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678 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 695

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    2235 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACA 2284

     695 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 711
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2285 AGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2334

     712 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 728
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2335 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2384

     728 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 745
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2385 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2434

     745 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 761
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2435 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2484

     762 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 778
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2485 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2534

     778 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 795
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2535 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATC 2584

     795 euProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 811
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2585 TCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2634

     812 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 828
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2635 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2684

     828 nLysGluGluLys 832
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    2685 CAAGGAAGAGAAA 2697

seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;

alignment_scores:
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            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x V58446  ..

 Align seg 1/1  to: V58446  from: 1  to: 3323

      12 ValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIl 28
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      97 GTCGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 146

      28 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 45
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     147 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 196

      45 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 61
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     197 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 246

      62 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 78
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     247 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 296

      78 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 95
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     297 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 346

      95 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 111
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     347 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 396

     112 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 128
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     397 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 446

     128 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 145
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     447 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 496

     145 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 161
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     497 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 546

     162 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 178
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     547 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 596

     178 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 195
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     597 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 646

     195 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 211
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     647 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 696

     212 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 228
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     697 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 746

     228 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 245
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     747 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 796

     245 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 261
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     797 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 846

     262 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 278
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     847 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 896
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 278 oValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnS 295
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 897 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 946

 295 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 311
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 947 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 996

 312 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 328
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 997 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1046

 328 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 345
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1047 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1096

 345 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 361
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1097 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1146

 362 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 378
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1147 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1196

 378 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 395
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1197 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1246

 395 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 411
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1247 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1296

 412 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 428
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1297 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1346

 428 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 445
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1347 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1396

 445 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 461
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1397 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1446

 462 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 478
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1447 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1496

 478 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 495
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1497 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1546

 495 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 511
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1547 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1596

 512 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 528
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1597 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 1646

 528 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 545
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1647 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1696

 545 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 561
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1697 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1746

 562 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 578
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1747 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1796

 578 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 595
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1797 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 1846

 595 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 611
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1847 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1896

 612 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 628
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1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1946

 628 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 645
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1947 TGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAAC 1996

 645 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 661
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1997 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2046

 662 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 678
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 678 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 695
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 695 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 711
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2147 AGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2196

 712 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 728
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2197 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2246

 728 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 745
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2247 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2296

 745 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 761
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2297 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2346

 762 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 778
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2347 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2396

 778 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 795
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 812 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 828
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2497 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2546

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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:

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ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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FT   cds             19. .2469
FT                   /*tag= a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
            Quality:  820.00              Length:    820
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-35 x Q72690   ..

 Align seg 1/1  to: Q72690  from: 1  to: 3233

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       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGA 56

      29 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 46
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

      46 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 62
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

      63 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

      79 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 96
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

      96 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 112
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

     113 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 129
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     129 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

     146 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

     163 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

     179 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 196
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     196 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     557 ATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

     213 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 229
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     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 656

     229 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 246
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     657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

     246 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 262
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     263 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVa 279
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     279 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACAT 956

     329 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 346
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     957 CTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTG 1006

     346 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1007 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 1056

     363 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1057 TCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAA 1106

     379 sLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuG 396
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1107 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 1156

     396 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 412
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1157 AGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

     413 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 429
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1207 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGC 1256

     429 aPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnL 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1257 CTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACT 1306

     446 euThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 462
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    1307 TGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATG 1356

     463 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGl 479
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    1357 GAATCCCTTGCATGGCTCTGAGATTCACCTTTATTTGATCTTATTAAACA 1406
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 479 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 496
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1407 ATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTC 1456

 496 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 512
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1457 TTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCT 1506

 513 ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerTh 529
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 529 rAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProL 546
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 546 euLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 562
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1657 TATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGA 1706

 579 uLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluT 596
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1707 ATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGT 1756

 596 yrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMet 612
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 613 TyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleVa 629
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1807 TATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGT 1856

 629 lThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArgV 646
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1857 AACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTG 1906

 646 alLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSer 662
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1907 TTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCG 1956

 663 ValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrAr 679
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1957 GTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAG 2006

 679 gProProThrLeuSerProIleProHisIleProArgSerProTyrLysP 696
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2007 GCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGT 2056

 696 heProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 712
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2057 TTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCC 2106

 713 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 729
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2107 CTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAAT 2156

 729 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 746
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2157 GACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTT 2206

 746 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 762
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2207 CTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTG 2256

 763 LeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysLe 779
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2257 CTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACT 2306

 779 uArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuP 796
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 796 roGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArg 812
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2357 CAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGA 2406

 813 ThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLy 829
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2457 GGAAGAGAAA 2466
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID V58452 standard; DNA; 3554 BP.
AC V58452;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69376.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 226-230; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3554 BP; 1170 A; 683 C; 653 G; 1048 T;

alignment_scores:
Quality: 816.00 Length: 816
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-35 x V58452

Align seg 1/1 to: V58452 from: 1 to: 3554

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 343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 392

  33 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442

  50 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 66
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492

  67 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 83
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 493 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 542

  83 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592

 100 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 116
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 593 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

 117 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 133
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 692

 133 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 150
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 693 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 742

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 743 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 792

 167 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 183
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 183 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 217 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 233
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 233 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 250
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 267 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 283
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1093 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 1142

 283 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 300
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 300 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 316
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1193 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242

 317 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 333
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1292

 333 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1293 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1342

 350 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 366
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1343 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1392

 367 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 383
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     ||||||||||||||||||||||||||||||||||||||||||||||||||
1493 CCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1542

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1543 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1592

 433 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 450
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1593 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1642

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 467 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 483
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1743 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1792

 500 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 516
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1843 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1892

 533 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 550
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1893 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1942

 550 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 566
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1943 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1992

 567 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 583
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1993 AATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATAT 2042

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2193 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 2242

 650 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 666
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2243 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 2292

 667 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 683
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    2593 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2642

     783 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 800
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     800 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 816
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     817 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 832
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seq_name: N_Geneseq_36:V54991

seq_documentation_block:

ID V54991 standard; DNA; 3218 BP.
AC V54991;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2457
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71355.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 153-157; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T;

alignment_scores:
Quality: 816.00 Length: 816
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-35 x V54991 ..

Align seg 1/1 to: V54991 from: 1 to: 3218

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      33 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 106

      50 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 66
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 156

      67 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 83
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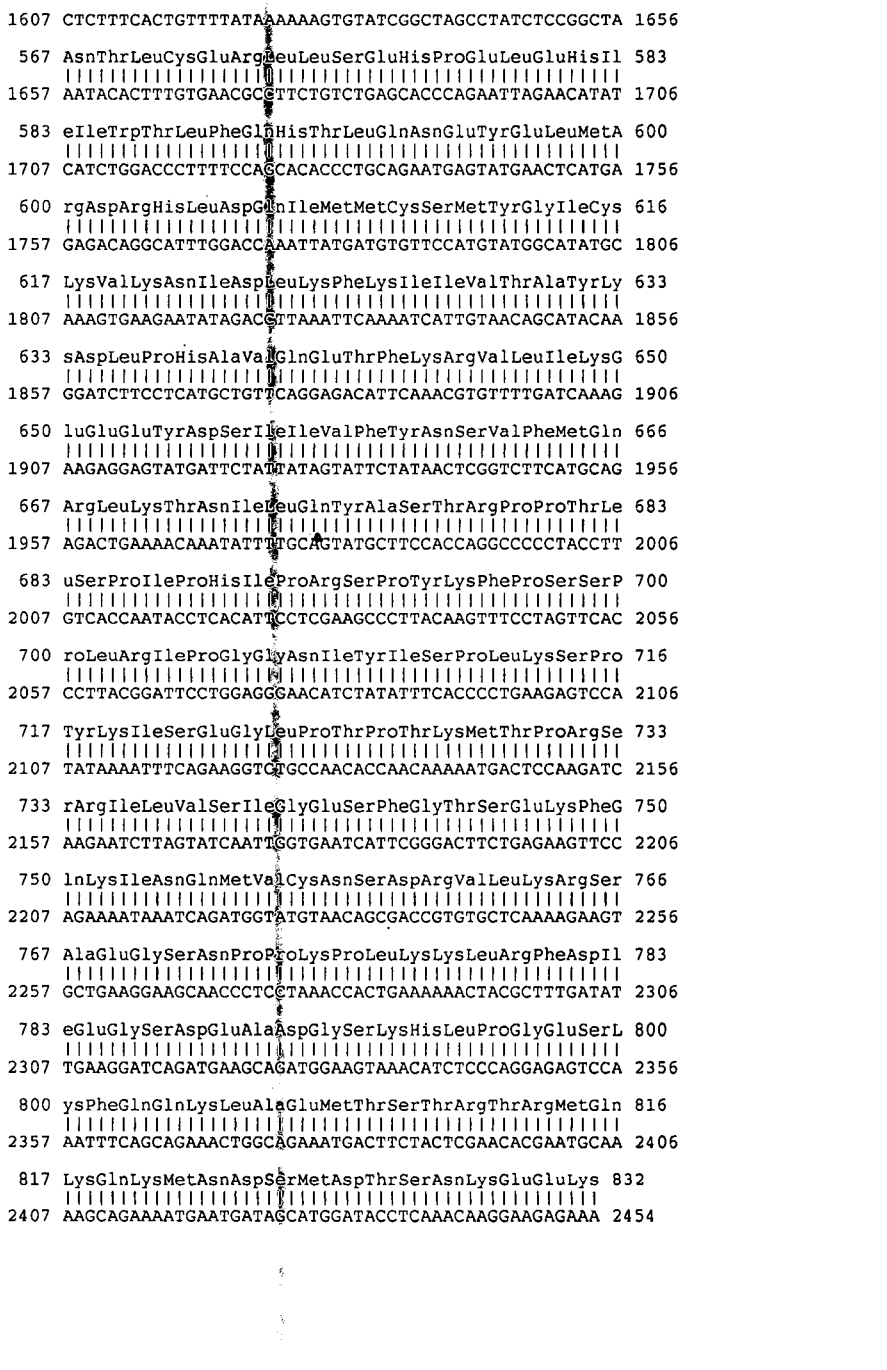
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Date: Feb 13, 2000  2:31 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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N_Geneseq_36:V54990   +  781.00 14377.26  0.0       3555  ! DNA sequence of the specifica
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N_Geneseq_36:X00737   +  781.00 14378.53  0.0       2995  ! cDNA encoding a retinoblastom
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DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
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FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


alignment_scores:
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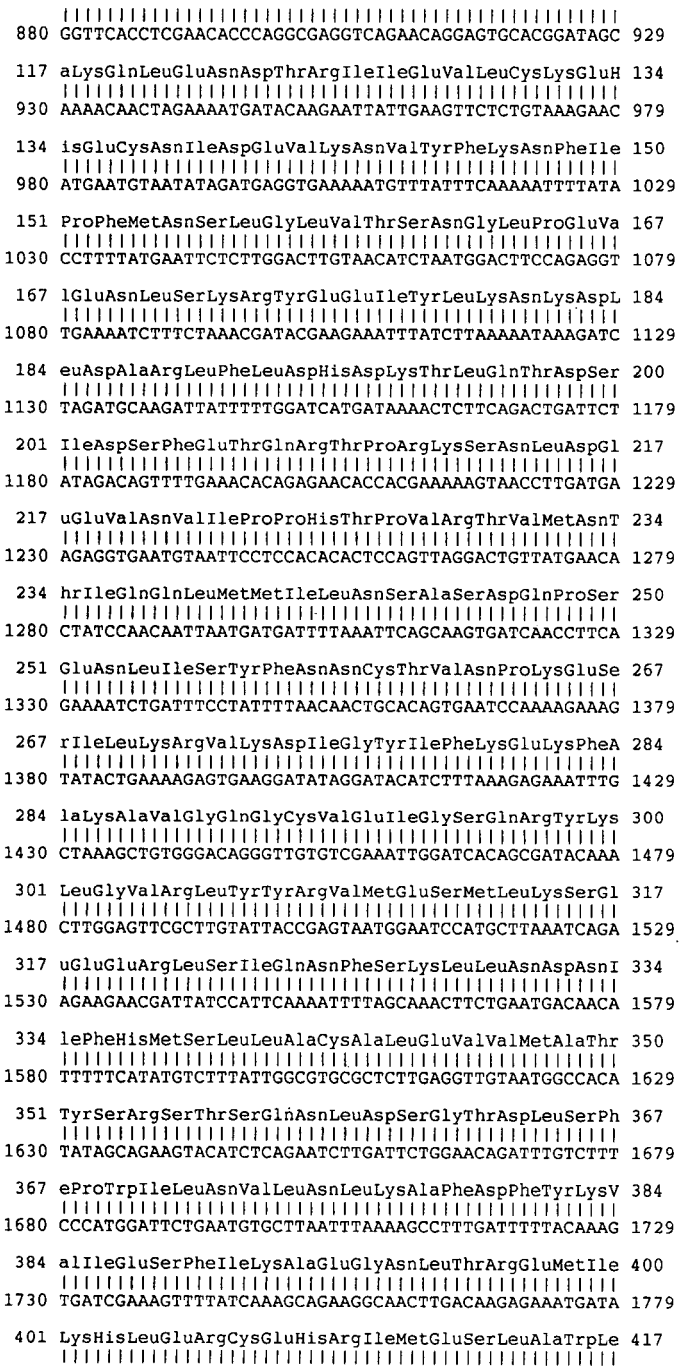
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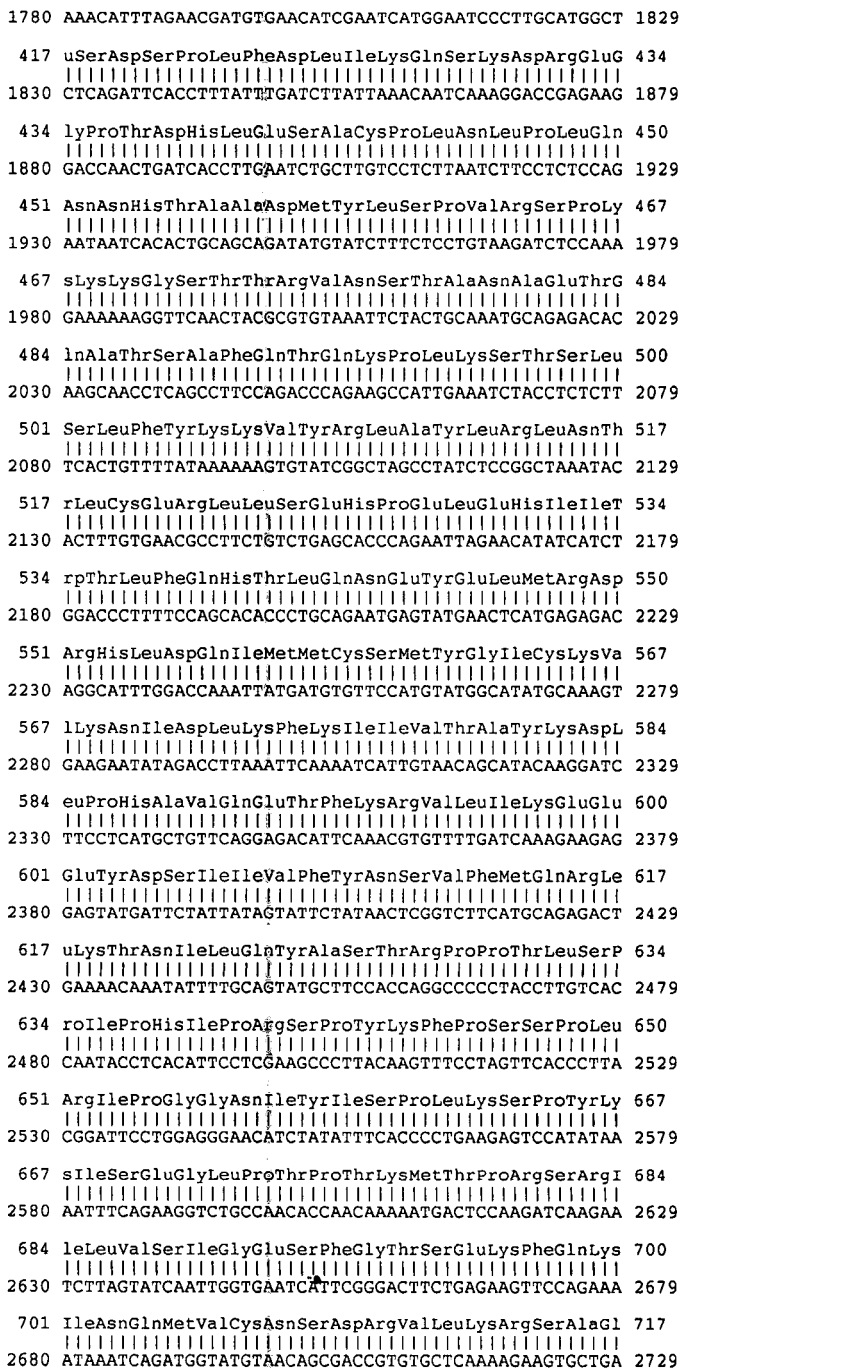
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2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 2129
517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
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534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
2180 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229
551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279
567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 2329
584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
2330 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379
601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 2429
617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
2430 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2479
634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
2480 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529
651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579
667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2629
684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2729

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     717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
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     734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
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     751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
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    2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

     767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
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seq_documentation_block:
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  781.00              Length:    781
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 629

      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     630 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 679

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     680 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
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     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
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     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 929

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     930 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 979

     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     980 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
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     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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    1230 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1279

     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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     251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
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    1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

     267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
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     284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
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    1430 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
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 317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
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 334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
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1580 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

 351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

 367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
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 434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
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 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
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1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

 467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
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 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
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 534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
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 551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
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2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:

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ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;
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alignment_scores:
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              Ratio:  1.000                 Gaps:      0
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alignment_block:
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      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
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      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
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     224 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 273

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
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      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
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      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
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     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
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     424 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 473

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
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     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
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     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
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     184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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     674 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 723

     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
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     724 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 773

     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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     774 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 823

     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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     251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
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     874 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 923

     267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
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     924 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 973

     284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
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     974 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1023

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1024 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1073

     317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1074 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1123

     334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1124 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1173

     351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1174 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1223

     367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1224 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1273

     384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1274 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1323

     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
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    1324 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCT 1373

     417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
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    1374 CTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAG 1423

     434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
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    1424 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1473

     451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
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    1474 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1523

     467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
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    1524 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 1573

     484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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    1574 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1623

     501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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    1624 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1673

     517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1674 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1723

     534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1724 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1773

     551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
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    1774 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 1823
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     567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
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    1824 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 1873

     584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
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    1874 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1923

     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
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    1924 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 1973

     617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
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    1974 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2023

     634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
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     651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
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    2074 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2123

     667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2124 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2173

     684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2174 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2223

     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
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    2224 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2273

     717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
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    2274 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2323

     734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
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     751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
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    2374 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2423

     767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


alignment_scores:
           Quality:  781.00              Length:    781
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V58447  ..

 Align seg 1/1  to: V58447  from: 1  to: 3461

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     355 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 404

      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     405 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 454

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     455 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 504

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     505 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 554

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     555 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 604

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     605 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 654

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     655 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 704

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     705 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 754

     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     755 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 804

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     805 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 854

     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
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     855 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 904

     184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     905 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 954

     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
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 955 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 1004

 217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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1005 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1054

 234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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1055 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1104

 251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1105 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1154

 267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
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1155 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1204

 284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1205 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1254

 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1255 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1304

 317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
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1305 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1354

 334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
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1355 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1404

 351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
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1405 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1454

 367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
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 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
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 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
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1705 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1754

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 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
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1905 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1954

 534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
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 551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
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 567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
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2105 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2154

 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
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2205 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2254

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 651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
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2555 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2604

 751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID V58452 standard; DNA; 3554 BP.
AC V58452;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;

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KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


alignment_scores:
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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V58452   ..

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      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     498 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 547

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     548 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 597

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     598 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 647

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
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     648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 697

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     698 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
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     748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 797

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
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     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
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     848 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 897

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
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     898 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 947

     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
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     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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     251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
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    1348 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1397

     317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
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 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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1948 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1997

 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
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 617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
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 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
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 684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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seq_name: N_Geneseq_36:V58440

seq_documentation_block:

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ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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alignment_scores:

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           Quality:  781.00              Length:    781
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

US-09-026-459A-37 x V58440 ..

Align seg 1/1 to: V58440 from: 1 to: 3555

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 448 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 497

  17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
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 498 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 547

  34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
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 548 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 597

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 648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 697

  84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
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 698 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747
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 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
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 748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 797

 117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
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 134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
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 184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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1048 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 1097

 217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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 234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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 267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
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 317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
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1448 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1497

 351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
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 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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1948 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1997

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 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
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     734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
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    2648 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2697

     751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
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    2698 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2747

     767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
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    2748 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790

seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


alignment_scores:
            Quality:  781.00              Length:    781
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V58441   ..

 Align seg 1/1  to: V58441  from: 1  to: 3455

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     349 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 398

      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     399 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 448

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     449 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 498

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     499 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 548

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     549 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 598

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     599 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 648

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     649 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 698

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
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     699 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 748

     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     749 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 798

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     799 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 848

     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
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     849 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 898

     184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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     899 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 948

     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
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     949 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 998

     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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     999 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1048

     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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    1049 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1098

     251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
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    1099 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1148

     267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
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    1149 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1198

     284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
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    1199 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1248

     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
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    1249 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1298

     317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
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    1299 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1348

     334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
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    1349 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1398
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 351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
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1399 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1448

 367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
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1449 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1498

 384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
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1499 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1548

 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
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 417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
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1599 CTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAG 1648

 434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
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1649 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1698

 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
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1699 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1748

 467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
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1749 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 1798

 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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1799 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1848

 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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1849 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1898

 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
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 534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
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1949 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1998

 551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
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 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
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 617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
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 634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
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 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
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2349 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2398

 684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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2399 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2448

 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
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2449 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2498

 717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
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 734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
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2549 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2598

 751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
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 767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
            Quality:  781.00              Length:    781
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V58442   ..
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Align seg 1/1 to: V58442 from: 1 to: 3392

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     17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
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    336 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 385

     34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
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    386 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 435

     51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
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     67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
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     84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
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    536 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 585

    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
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    586 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 635

    117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
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    134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
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    686 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 735

    151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
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    736 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 785

    167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
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    184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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    836 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 885

    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
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    217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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   1186 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1235

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   1436 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1485

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    434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
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    451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
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   1636 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1685

    467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
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   1686 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 1735

    484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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   1736 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1785

    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1786 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1835

    517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1836 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1885

    534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1886 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1935

    551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1936 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 1985

    567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1986 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 2035

    584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   2036 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2085
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     601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2086 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 2135

     617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2136 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2185

     634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2186 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2235

     651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2236 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2285

     667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2286 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2335

     684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2336 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2385

     701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2386 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2435

     717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2436 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2485

     734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
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    2486 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2535

     751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2536 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2585

     767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
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    2586 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628

seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;


alignment_scores:
           Quality:  781.00              Length:    781
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V58443   ..

 Align seg 1/1  to: V58443  from: 1  to: 3323

       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 17
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     217 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 266

      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     267 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 316

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     317 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 366

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     367 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 416

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     417 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 466

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     467 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 516

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     517 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 566

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     567 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 616

     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     617 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 666

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     667 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 716

     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     717 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 766

     184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     767 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 816

     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     817 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 866

     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     867 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 916

     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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 917 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 966

 251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 967 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1016

 267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1017 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1066

 284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1067 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1116

 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1117 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1166

 317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1167 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1216

 334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1217 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1266

 351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1267 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1316

 367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1317 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1366

 384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1367 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1416

 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1417 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCT 1466

 417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1467 CTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAG 1516

 434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1517 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1566

 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1567 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1616

 467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1617 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 1666

 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1667 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1716

 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1717 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1766

 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1767 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1816

 534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1817 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1866
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 551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1867 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 1916

 567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1917 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 1966

 584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1967 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2016

 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2017 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 2066

 617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2067 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2116

 634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2117 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2166

 651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2167 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2216

 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2217 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2266

 684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2267 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2316

 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2317 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2366

 717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2367 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2416

 734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2417 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2466

 751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2467 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2516

 767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
     ||||||||||||||||||||||||||||||||||||||||||||
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seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
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PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


alignment_scores:
            Quality:  781.00              Length:    781
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V58444    ..

 Align seg 1/1  to: V58444  from: 1  to: 3266

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     160 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 209

      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     210 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 259

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     260 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 309

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     310 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 359

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     360 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 409

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     410 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 459

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     460 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 509

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     510 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 559

     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     560 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 609

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     610 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 659

     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     660 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 709

     184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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     710 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 759

     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     760 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 809

     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     810 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 859

     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     860 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 909

     251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     910 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 959

     267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     960 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1009

     284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1010 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1059

     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1060 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1109

     317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
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     334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
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     351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
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    1210 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1259

     367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
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    1260 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1309

     384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
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     401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
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     417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
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 1660 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1709

  517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
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 1710 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1759

  534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
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  567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
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 1910 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1959

  601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
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 2110 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2159

  667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
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 2160 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2209

  684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
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  701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
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 2260 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2309

  717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
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  734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
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seq_name: N_Geneseq_36:V58445

seq_documentation_block:

ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;


alignment_scores:
           Quality:  781.00            Length:    781
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58445  from: 1  to: 3113

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       7 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 56

      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
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      57 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 106

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
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     107 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 156

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 206

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
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     207 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 256

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
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     257 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 306

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 356

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
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     357 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 406
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 134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
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 407 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 456

 151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
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 457 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 506

 167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
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 507 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 556

 184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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 557 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 606

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 607 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 656

 217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
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 657 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 706

 234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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 707 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 756

 251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
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 267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
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 807 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 856

 284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 857 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 906

 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 907 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 956

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     ||||||||||||||||||||||||||||||||||||||||||||||||||
 957 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1006

 334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1007 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1056

 351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
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1057 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1106

 367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
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 384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
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 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
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1357 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1406

 467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
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 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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 634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
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1907 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 1956

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 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
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2007 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2056

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seq_documentation_block:
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;


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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     267 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 316

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
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      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     367 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 416

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     417 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 466

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     467 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 516

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     517 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 566

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     567 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 616

     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     617 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 666

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     667 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 716

     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     717 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 766

     184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     767 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 816

     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     817 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 866

     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     867 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 916

     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     917 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 966

     251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     967 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1016

     267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1017 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1066

     284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
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     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1117 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1166

     317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
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     351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1267 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1316

     367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
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    1317 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1366
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 384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
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1367 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1416

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1417 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCT 1466

 417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
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 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
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1567 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1616

 467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
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1617 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 1666

 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
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 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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1717 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1766

 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1767 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1816

 534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
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1817 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1866

 551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1867 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 1916

 567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1917 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 1966

 584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1967 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2016

 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2017 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 2066

 617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
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2067 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2116

 634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
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2117 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2166

 651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
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2167 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2216

 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2217 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2266

 684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
```

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     ||||||||||||||||||||||||||||||||||||||||||||||||||
2267 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2316

 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2317 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2366

 717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2367 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2416

 734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
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2417 GATCAGATGAAGCAGATGCAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2466

 751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2467 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2516

 767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
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2517 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559
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seq_name: N_Geneseq_36:V54990

seq_documentation_block:
ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  781.00             Length:    781
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V54990  ..
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Align seg 1/1 to: V54990 from: 1 to: 3555

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      1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 17
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    448 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 497

     17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    498 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 547

     34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    548 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 597

     51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    598 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 647

     67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    648 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 697

     84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    698 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 747

    101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    748 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 797

    117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    798 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 847

    134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    848 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 897

    151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    898 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 947

    167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    948 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 997

    184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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    998 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1047

    201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1048 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 1097

    217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1098 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1147

    234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
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   1148 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1197

    251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1198 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1247

    267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1248 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1297

    284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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   1298 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1347

    301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1348 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1397

    317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1398 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1447

    334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
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   1448 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1497

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        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
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   1548 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1597

    384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
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   1598 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1647

    401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
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   1648 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCT 1697

    417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
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   1748 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1797

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    467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
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    501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
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   1948 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1997

    517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1998 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 2047

    534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
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    551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
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    567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   2148 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 2197

    584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
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   2198 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2247
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 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
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2248 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 2297

 617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
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2348 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2397

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     ||||||||||||||||||||||||||||||||||||||||||||||||||
2398 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2447

 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2448 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2497

 684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2498 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2547

 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2548 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2597

 717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2598 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2647

 734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2648 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2697

 751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2698 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2747

 767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
     |||||||||||||||||||||||||||||||||||||||||
2748 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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seq_name: N_Geneseq_36:V54991

seq_documentation_block:

ID V54991 standard; DNA; 3218 BP.
AC V54991;
DT 26-NOV-1998 (first entry)
DE DNA sequence of the specification.
KW Minimal promoter; tetracycline responsive expression vector; TREV;
KW transcriptional transactivation domain; TTD;
KW tetracycline repressor protein; TRP; tetracycline operator;
KW production; stable cell line; protein production;
KW tumour suppressor protein; treatment; cancer; ss.
OS Unidentified.
FH Key Location/Qualifiers
FT CDS 7. .2457
FT /*tag= a
PN WO9837185-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03092.
PR 20-FEB-1997; US-038755.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71355.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 153-157; 190pp; English.

CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3218 BP; 1080 A; 595 C; 561 G; 982 T;

alignment_scores:

Quality: 781.00 Length: 781
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-026-459A-37 x V54991 ..

Align seg 1/1 to: V54991 from: 1 to: 3218

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   1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 17
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 112 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 161

  17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 162 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 211

  34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 212 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 261

  51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 262 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 311

  67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 312 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 361

  84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 362 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 411

 101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 412 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 461

 117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 462 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 511

 134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 512 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 561

 151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 562 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 611

 167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 612 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 661

 184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 662 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 711
```

```
 201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 712 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 761

 217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 762 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 811

 234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 812 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 861

 251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 862 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 911

 267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 912 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 961

 284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 962 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1011

 301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1012 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1061

 317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1062 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1111

 334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1112 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1161

 351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1162 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1211

 367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1212 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1261

 384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1262 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1311

 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1312 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCT 1361

 417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1362 CTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAG 1411

 434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1412 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1461

 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1462 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1511

 467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1512 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 1561

 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1562 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 1611

 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1612 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 1661

 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1662 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 1711

 534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1712 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 1761

 551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1762 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 1811

 567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1812 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 1861

 584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1862 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 1911

 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1912 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 1961

 617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1962 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2011

 634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2012 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2061

 651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2062 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2111

 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2112 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2161

 684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2162 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2211

 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2212 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2261

 717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2262 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2311

 734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2312 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2361

 751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2362 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2411

 767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
     |||||||||||||||||||||||||||||||||||||||||||
2412 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2454
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seq_name: N_Geneseq_36:V40004

seq_documentation_block:
ID V40004 standard; DNA; 2994 BP.
AC V40004;
DT 15-FEB-1999 (first entry)

```
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;


alignment_scores:
            Quality:  781.00              Length:    781
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-37 x V40004   ..

 Align seg 1/1  to: V40004  from: 1  to: 2994

       1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLy 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAA 629

      17 sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     630 ATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGA 679

      34 leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     680 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 729

      51 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     730 TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT 779

      67 eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     780 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 829

      84 roProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     830 CTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAAT 879

     101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAl 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGC 929

     117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     930 AAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC 979

     134 isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     980 ATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATA 1029

     151 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1030 CCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGT 1079

     167 lGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspL 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1080 TGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATC 1129

     184 euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1130 TAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCT 1179

     201 IleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1180 ATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGA 1229

     217 uGluValAsnValIleProProHisThrProValArgThrValMetAsnT 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1230 AGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACA 1279

     234 hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1280 CTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCA 1329

     251 GluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1330 GAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG 1379

     267 rIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheA 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1380 TATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTG 1429

     284 laLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1430 CTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAA 1479

     301 LeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGl 317
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1480 CTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGA 1529

     317 uGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnI 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1530 AGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACA 1579

     334 lePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1580 TTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACA 1629

     351 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPh 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1630 TATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTT 1679

     367 eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 384
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1680 CCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAG 1729

     384 alIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIle 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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1730 TGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA 1779

 401 LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe 417
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1780 AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCT 1829

 417 uSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluG 434
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1830 CTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAG 1879

 434 lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1880 GACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAG 1929

 451 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLy 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1930 AATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAA 1979

 467 sLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrG 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1980 GAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACAC 2029

 484 lnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu 500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2030 AAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTT 2079

 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnTh 517
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATAC 2129

 517 rLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleT 534
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2130 ACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCT 2179

 534 rpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2180 GGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGAC 2229

 551 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysVa 567
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2230 AGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGT 2279

 567 lLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspL 584
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2280 GAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC 2329

 584 euProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGlu 600
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2330 TTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG 2379

 601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLe 617
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2380 GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACT 2429

 617 uLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 634
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2430 GAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCAC 2479

 634 roIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 650
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2480 CAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTA 2529

 651 ArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLy 667
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2530 CGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAA 2579

 667 sIleSerGluGlyLeuProThrProThrLysMetThrProArgSerArgI 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2580 AATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAA 2629

 684 leLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2630 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2679

 701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl 717
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGA 2729

 717 uGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluG 734
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2730 AGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAG 2779

 734 lySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPhe 750
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2780 GATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTT 2829

 751 GlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGl 767
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2830 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCA 2879

 767 nLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 781
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2880 GAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922
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OM of: US-09-026-459A-39 to: N_Geneseq_36:* out_format : pfs

Date: Feb 13, 2000 2:32 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
-DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=oligo.rng -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
-THREADS=1

Search information block:
Query: US-09-026-459A-39
Query length: 851
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	! Documentation ..
N_Geneseq_36:V58446	+	851.00	13367.95	0.0	3323	! Modified retinoblastoma tumou
N_Geneseq_36:Q04713	+	821.00	12896.39	0.0	2994	! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545	+	821.00	12896.39	0.0	2994	! Retinoblastoma gene. Method c
N_Geneseq_36:V58447	+	821.00	12895.39	0.0	3461	! Modified retinoblastoma tumou
N_Geneseq_36:V58440	+	821.00	12895.20	0.0	3555	! Modified retinoblastoma tumou
N_Geneseq_36:V58441	+	821.00	12895.40	0.0	3455	! Modified retinoblastoma tumou
N_Geneseq_36:V58442	+	821.00	12895.53	0.0	3392	! Modified retinoblastoma tumou
N_Geneseq_36:V58443	+	821.00	12895.67	0.0	3323	! Modified retinoblastoma tumou
N_Geneseq_36:V58444	+	821.00	12895.79	0.0	3266	! Modified retinoblastoma tumou
N_Geneseq_36:V54990	+	821.00	12895.20	0.0	3555	! DNA sequence of the specifica
N_Geneseq_36:V40004	+	821.00	12896.39	0.0	2994	! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737	+	821.00	12896.38	0.0	2995	! cDNA encoding a retinoblastom
N_Geneseq_36:Q72690	+	820.00	12880.11	0.0	3233	! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58452	+	816.00	12816.49	0.0	3554	! Modified retinoblastoma tumou
N_Geneseq_36:V54991	+	816.00	12817.17	0.0	3218	! DNA sequence of the specifica
N_Geneseq_36:V58445	+	781.00	12266.41	0.0	3113	! Modified retinoblastoma tumou
N_Geneseq_36:X04501	+	770.00	12090.55	0.0	4597	! Human retinoblastoma gene cDN
N_Geneseq_36:V58448	+	747.00	11730.66	0.0	3347	! Modified retinoblastoma tumou
N_Geneseq_36:Q70536	+	734.00	11523.81	0.0	4597	! Human retinoblastoma gene. Di
N_Geneseq_36:N81369	+	720.00	11303.42	0.0	4597	! Human retinoblastoma gene Dia
N_Geneseq_36:Q90059	+	720.00	11306.37	0.0	2995	! Retinoblastoma tumour suppres
N_Geneseq_36:V58449	+	687.00	10786.49	0.0	3161	! Modified retinoblastoma tumou
N_Geneseq_36:V58450	+	687.00	10786.03	0.0	3377	! Modified retinoblastoma tumou
N_Geneseq_36:V58451	+	628.00	9857.20	0.0	3383	! Modified retinoblastoma tumour
N_Geneseq_36:Q86398	+	593.00	9307.04	0.0	2995	! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489	+	474.00	7430.05	0.0	5056	! cDNA of human retinoblastoma g
N_Geneseq_36:N81261	+	286.00	4471.10	1.9e-241	4579	! Probe for retinoblastoma gene.
N_Geneseq_36:X04502	+	65.00	982.41	4.0e-47	18303	! Human retinoblastoma gene. Is
N_Geneseq_36:N90490	+	55.00	825.03	2.4e-38	18177	! DNA of human retinoblastoma g
N_Geneseq_36:N91077	+	10.00	134.10	7.20	1433	! Sequence encoding alpha-1-anti
N_Geneseq_36:Q55750	-	10.00	133.76	7.52	1505	! Genomic clone G11F, includes a
N_Geneseq_36:Q67401	+	10.00	120.47	41.37	10366	! Huntingtin DNA\IT15 gene. New
N_Geneseq_36:T02461	+	10.00	133.01	8.29	1680	! Wilms' tumour WT1 cDNA. Monocl
N_Geneseq_36:T02462	+	10.00	139.73	3.50	633	! Wilms' tumour antigen WT1-6F cD
N_Geneseq_36:Q99257	+	10.00	129.39	13.18	2841	! Yeast coagulation gene FLO8. Y
N_Geneseq_36:T42476	-	10.00	139.60	3.56	645	! HuntL4 coding sequence. HuntL a
N_Geneseq_36:T45133	+	10.00	141.97	2.62	457	! Wilms' tumour gene exon 1. Leuk
N_Geneseq_36:T75529	+	10.00	139.73	3.50	633	! cDNA encoding Wilms' tumour prc
N_Geneseq_36:T97924	+	10.00	120.47	41.37	10366	! Composite sequence of a novel
N_Geneseq_36:T88434	-	10.00	131.17	10.50	2195	! Human 5-lipoxygenase gene p
N_Geneseq_36:V05828	+	10.00	120.47	41.37	10366	! Human huntingtin coding se
N_Geneseq_36:V17757	+	10.00	129.09	13.69	2965	! Fractionated X irradiation-
N_Geneseq_36:X15842	+	10.00	141.97	2.62	457	! Nucleotide sequence of the s
N_Geneseq_36:X18930	+	10.00	141.15	2.92	515	! Human huntingtin gene. Trans
N_Geneseq_36:X02974	+	10.00	128.57	14.64	3198	! Human IL-1ra BAC contiguous

seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

alignment_scores:
Quality: 851.00 Length: 851
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-39 x V58446 ..

Align seg 1/1 to: V58446 from: 1 to: 3323

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      1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAl 17
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      7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGC 56

     17 aAlaGluProProAlaProProProProProProGluValAspLeuA 34
        ||||||||||||||||||||||||||||||||||||||||||||||||
     57 CGCGGAACCCCCGGCACCGCCGCCGCCGCCCCCTCCTGAGGTCGACCTAG 106

     34 spGluMetSerPheThrPheThrGluLeuGlnLysAsnIleGluIleSer 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    107 ATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGT 156

     51 ValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysVa 67
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    157 GTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGT 206

     67 lAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaL 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    207 TGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCAC 256

     84 euPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnPro 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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 257 TCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 306

 101 SerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSe 117
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 307 AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC 356

 117 rTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspA 134
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 357 TTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATG 406

 134 spLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 407 ATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 456

 151 LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIl 167
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 457 AAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTAT 506

 167 eProIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerA 184
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 507 ACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTG 556

 184 laArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeu 200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 557 CACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTC 606

 201 CysLysGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLy 217
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 607 TGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAA 656

 217 sAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyL 234
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 657 AAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGAC 706

 234 euProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys 250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 707 TTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAA 756

 251 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGl 267
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 757 AATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCA 806

 267 nThrAspSerIleAspSerPheGluThrGlnArgThrProArgLysSerA 284
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 807 GACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTA 856

 284 snLeuAspGluGluValAsnValIleProProHisThrProValArgThr 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 857 ACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACT 906

 301 ValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAs 317
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 907 GTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGA 956

 317 pGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnP 334
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 957 TCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATC 1006

 334 roLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1007 CAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAA 1056

 351 GluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGl 367
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1057 GAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACA 1106

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1107 GCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGC 1156

 384 euLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeu 400
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1157 TTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1206

 401 AsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValVa 417
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1207 AATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGT 1256

 417 lMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrA 434
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1257 AATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAG 1306

 434 spLeuSerProProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAsp 450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1307 ATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGAT 1356

 451 PheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrAr 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1357 TTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAG 1406

 467 gGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSerL 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1407 AGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCC 1456

 484 euAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLys 500
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1457 TTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAG 1506

 501 AspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLe 517
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1507 GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCT 1556

 517 uProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValA 534
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1557 TCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAA 1606

 534 rgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn 550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1607 GATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAAT 1656

 551 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSe 567
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1657 GCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATC 1706

 567 rThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuA 584
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1707 TACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCC 1756

 584 rgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGlu 600
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1757 GGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAA 1806

 601 HisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLe 617
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1807 CATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 1856

 617 uMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyI 634
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1857 CATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCA 1906

 634 leCysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAla 650
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1907 TATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCA 1956

 651 TyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIl 667
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1957 TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGAT 2006

 667 eLysGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheM 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2007 CAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCA 2056

 684 etGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProPro 700
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2057 TGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCT 2106
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     701 ThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSe 717
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    2107 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAG 2156

     717 rSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysS 734
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2157 TTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGA 2206

     734 erProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 750
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    2207 GTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2256

     751 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLy 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2257 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAA 2306

     767 sPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysA 784
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    2307 GTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAA 2356

     784 rgSerAlaGluGlySerAsnProProLysProLeuLysLysLeuArgPhe 800
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    2357 GAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2406

     801 AspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGl 817
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    2407 GATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGA 2456

     817 uSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgM 834
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     834 etGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGlu 850
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     851 Lys 851
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seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID Q04713 standard; cDNA; 2994 BP.
AC Q04713;
DT 11-OCT-1990 (first entry)
DE Cancer supressing gene (CSG).
KW Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW RB; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 139. .2922
FT /*tag= a
PN WO9005180-A.
PD 17-MAY-1990.
PF 30-OCT-1989; 004808.
PR 31-OCT-1988; US-265829.
PA (REGC) Univ of Caifornia.
PI Lee WH, Huang HJS;
DR WPI; 90-178822/23.
DR P-PSDB; R05305.
PT Controlling cancer -
PT by replacing ineffective cancer suppressing gene with cloned,
PT active gene.
PS Claim 35; Page 86; 105pp; English.
CC Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC By installing a working CSG, safe and specific treatment and
CC prophylaxis can be given to cancer patients.
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

alignment_scores:
Quality: 821.00 Length: 821
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-39 x Q04713 ..

Align seg 1/1 to: Q04713 from: 1 to: 2994

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     460 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 509

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     510 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 559

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     560 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 709

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
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     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
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     181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
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     214 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 230
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     231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
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     281 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 297
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 314 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 330
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 331 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 347
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 347 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 364
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 364 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 380
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 397 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 414
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 414 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 430
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 447 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 464
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 464 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 480
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1760 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1809

 481 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 497
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 497 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 514
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1910 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

 531 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 547
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 547 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 564
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2010 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 2059

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 631 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 647
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 764 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
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seq_documentation_block:
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
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OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x Q41545   ..

 Align seg 1/1  to: Q41545  from: 1  to: 2994

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      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
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      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
     860 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

     181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
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     197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
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     231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
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     364 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 380
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     431 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 447
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    1660 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1709

     447 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 464
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:

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ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;
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      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
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 464 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 480
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seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.

CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x V58440   ..

 Align seg 1/1  to: V58440  from: 1  to: 3555

      31 ValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIl 47
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     328 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 377

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     378 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 427

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     428 GTACCAAAGTTGATAATGGTATGTCAAGACTGTTGAAGAAGTATGATGTA 477

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     478 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 527

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     528 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 577

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     578 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 627

     131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     628 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 677

     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     678 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 727

     164 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     728 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 777

     181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
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     778 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 827

     197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
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     214 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     878 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 927

     231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     928 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 977

     247 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 264
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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 978 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 1027

 264 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 280
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1028 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1077

 281 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 297
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1078 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1127

 297 oValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnS 314
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1128 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 1177

 314 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 330
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1178 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1227

 331 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 347
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1228 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1277

 347 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 364
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1278 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1327

 364 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 380
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1328 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1377

 381 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 397
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1378 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1427

 397 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 414
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1428 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1477

 414 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 430
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1478 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1527

 431 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 447
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1528 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1577

 447 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 464
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1578 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1627

 464 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 480
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1628 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1677

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1678 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1727

 497 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 514
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1728 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1777

 514 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 530
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 547 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 564
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1878 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1927

 564 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 580
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1928 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1977

 581 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 597
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1978 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2027

 597 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 614
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2028 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 2077

 614 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 630
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2078 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2127

 631 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 647
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2128 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2177

 647 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 664
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2178 TGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAAC 2227

 664 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 680
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2228 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2277

 681 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 697
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2278 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2327

 697 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 714
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2328 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACA 2377

 714 ysProProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 730
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2378 AGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2427

 731 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 747
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2428 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2477

 747 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 764
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2478 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2527

 764 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
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2528 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2577

 781 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 797
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2578 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2627

 797 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 814
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 814 euProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 830
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2678 TCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2727

 831 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 847
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seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


alignment_scores:
           Quality:  821.00            Length:    821
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x V58441   ..

 Align seg 1/1  to: V58441  from: 1  to: 3455

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      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     279 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 328

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     329 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 378

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     379 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 428

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     429 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 478

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     479 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 528

     131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     529 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 578

     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     579 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 628

     164 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     629 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 678

     181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     679 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 728

     197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
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     729 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 778

     214 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     779 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 828

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     829 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 878

     247 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 264
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     264 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 280
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     929 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 978

     281 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 297
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     979 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1028

     297 oValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnS 314
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     314 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 330
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    1079 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1128

     331 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 347
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    1129 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1178

     347 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 364
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     364 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 380
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    1229 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1278

     381 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 397
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     397 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 414
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1329 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1378

     414 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 430
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1379 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1428

     431 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 447
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1429 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1478

     447 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 464
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1479 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1528

 464 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 480
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1529 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1578

 481 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 497
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1579 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1628

 497 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 514
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1629 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1678

 514 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 530
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1679 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1728

 531 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 547
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1729 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 1778

 547 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 564
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1779 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1828

 564 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 580
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1829 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1878

 581 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 597
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1879 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1928

 597 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 614
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1929 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 1978

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 747 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 764
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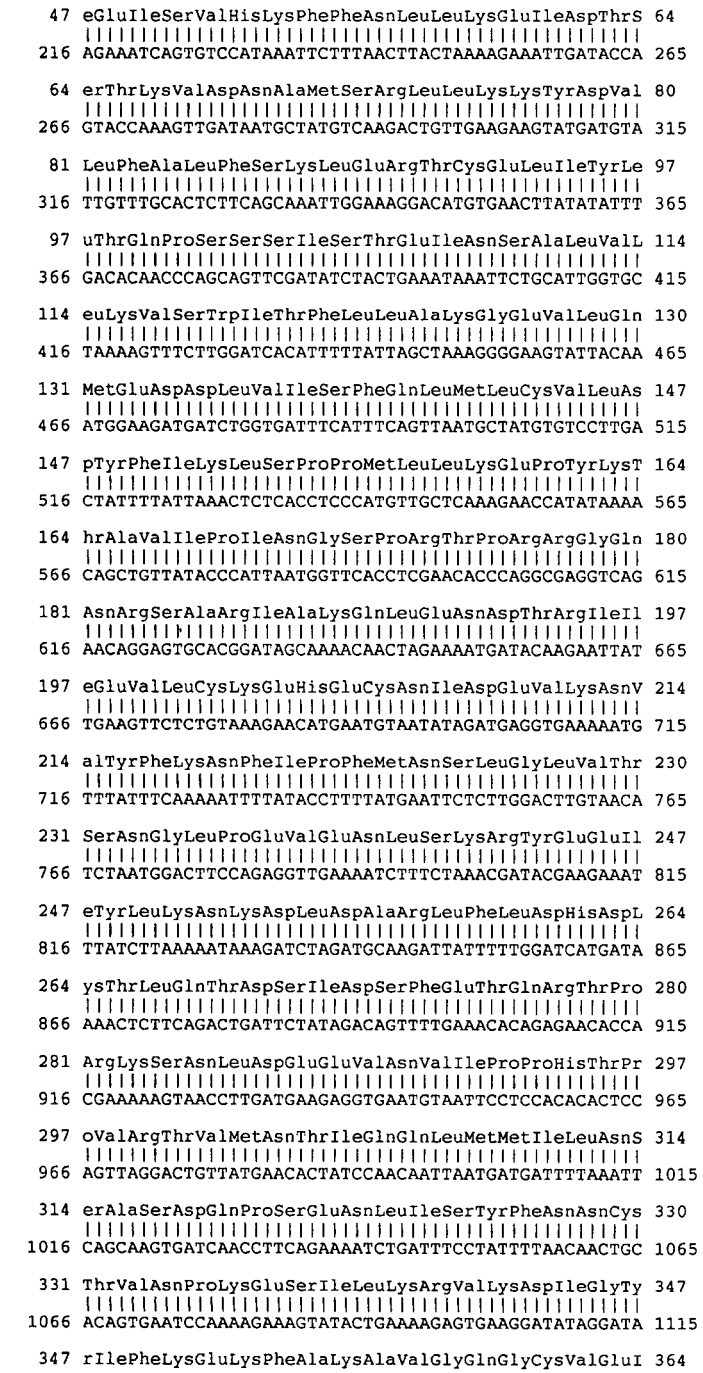
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ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


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231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
766 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 815
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1166 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1215
381 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 397
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ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;
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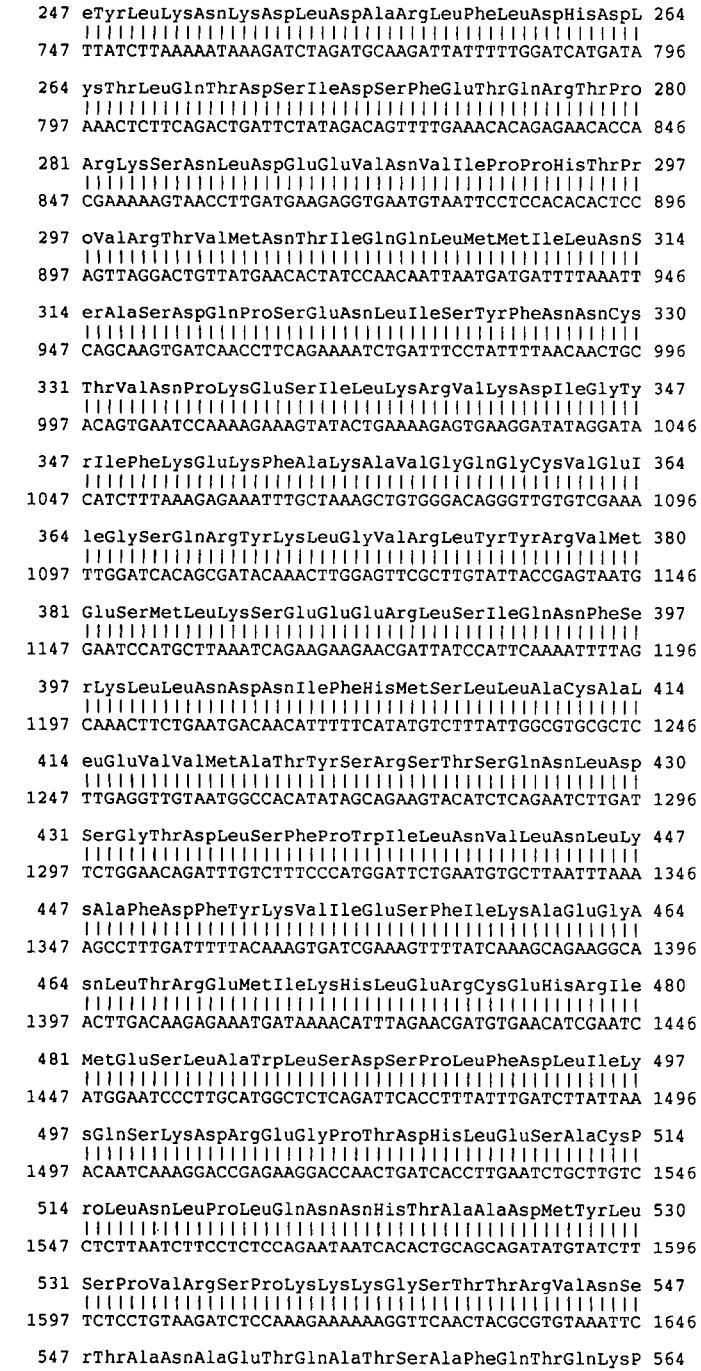
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547 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 564
1647 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1696
564 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 580
1697 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1746
581 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 597
1747 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1796
597 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 614
1797 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 1846
614 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 630
1847 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1896
631 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 647
1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1946
647 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 664
1947 TGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAAC 1996
664 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 680
1997 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2046
681 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 697
2047 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2096
697 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 714
2097 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACA 2146
714 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 730
2147 AGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2196
731 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 747
2197 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2246
747 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 764
2247 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2296
764 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
2297 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2346
781 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 797
2347 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2396
797 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 814
2397 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATC 2446
814 euProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 830
2447 TCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2496
831 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 847
2497 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2546
847 nLysGluGluLys 851

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    2547 CAAGGAAGAGAAA 2559

seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x V58444   ..

 Align seg 1/1  to: V58444  from: 1  to: 3266

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      40 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 89

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      90 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 139

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     140 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 189

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     190 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 239

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     240 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 289

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     290 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 339

     131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     340 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 389

     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     390 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 439

     164 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     440 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 489

     181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     490 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 539

     197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     540 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 589

     214 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 230
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     590 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 639

     231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     640 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 689

     247 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 264
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     690 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 739

     264 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 280
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     740 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 789

     281 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 297
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     790 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 839

     297 oValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnS 314
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     840 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 889

     314 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 330
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     890 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 939

     331 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 347
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     940 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 989

     347 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 364
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     990 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1039

     364 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 380
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1040 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1089

     381 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 397
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1090 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1139

     397 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 414
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    1140 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1189

     414 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 430
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1190 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1239

     431 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 447
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1240 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1289
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 447 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 464
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1290 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1339

 464 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 480
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1340 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1389

 481 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 497
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1390 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1439

 497 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 514
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1440 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1489

 514 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 530
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1490 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1539

 531 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 547
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1540 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 1589

 547 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 564
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1590 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1639

 564 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 580
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1640 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1689

 581 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 597
     |||||||||||||||||||||||||||||||||||||||||||||||||||
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 597 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 614
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 614 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 630
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 631 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 647
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1840 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1889

 647 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 664
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1890 TGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAAC 1939

 664 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 680
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1940 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 1989

 681 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 697
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1990 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2039

 697 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 714
     |||||||||||||||||||||||||||||||||||||||||||||||||||
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 714 ysProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 730
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 731 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 747
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2140 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2189

 747 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 764
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2190 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2239

 764 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2240 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2289

 781 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 797
     |||||||||||||||||||||||||||||||||||||||||||||||||||
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 797 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 814
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seq_name: N_Geneseq_36:V54990

seq_documentation_block:

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ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2798
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;     1171 A;     684 C;     653 G;     1047 T;
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alignment_scores:

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            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x V54990   ..

 Align seg 1/1  to: V54990  from: 1  to: 3555

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     328 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 377

      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     378 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 427

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     428 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 477

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     478 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 527

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     528 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 577

     114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     578 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 627

     131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     628 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 677

     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     678 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 727

     164 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     728 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 777

     181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 197
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     778 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 827

     197 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 214
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     828 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 877

     214 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 230
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     878 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 927

     231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     928 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 977

     247 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 264
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     264 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 280
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    1028 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1077

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     314 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 330
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     331 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 347
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     347 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 364
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    1278 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1327

     364 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 380
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     381 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 397
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 2778 CAAGGAAGAGAAA 2790

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seq_documentation_block:
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139.  2925
FT                   /*tag=  a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;

alignment_scores:
           Quality:  821.00              Length:    821
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-39 x V40004    ..

 Align seg 1/1  to: V40004  from: 1  to: 2994

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   47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
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  510 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 559

   64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  560 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

   81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
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   97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
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  114 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 130
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  131 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 147
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 147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
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 231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
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 281 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 297
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1910 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

 531 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 547
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AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence  2995 BP;  975 A;  618 C;  593 G;  809 T;

alignment_scores:
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 Percent Similarity: 100.000   Percent Identity: 100.000

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      47 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 64
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     510 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 559

      64 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 80
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     560 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 609

      81 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 97
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     610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

      97 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 114
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     147 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 164
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
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    1010 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

     231 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 247
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     247 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 264
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1110 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 1159
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 597 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 614
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 664 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 680
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 697 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 714
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 847 nLysGluGluLys 851
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2910 CAAGGAAGAGAAA 2922

seq_name: N_Geneseq_36:Q72690
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seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag= a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
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              Ratio:  1.000                 Gaps:      0
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alignment_block:
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       7 GACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGA 56

      48 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 65
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

      65 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 81
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     107 CCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTG 156

      82 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 98
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

      98 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 115
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     257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

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     148 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 165
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     357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

     165 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 181
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     407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

     182 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 198
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     457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

     198 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 215
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     232 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 248
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     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 656

     248 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 265
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     657 TCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAA 706

     265 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 281
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     298 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 315
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     807 TAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAG 856

     315 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 331
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     857 CAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 906

     332 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 348
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACAT 956

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     365 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 381
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1007 GATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAA 1056

     382 SerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLy 398
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1057 TCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAA 1106

     398 sLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuG 415
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1107 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTG 1156

     415 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 431
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1157 AGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1206

     432 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 448
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 482 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGl 498
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 498 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 515
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 515 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 531
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 532 ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerTh 548
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 548 rAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProL 565
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 732 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMe 748
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
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AC V58452;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69376.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 226-230; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3554 BP; 1170 A; 683 C; 653 G; 1048 T;

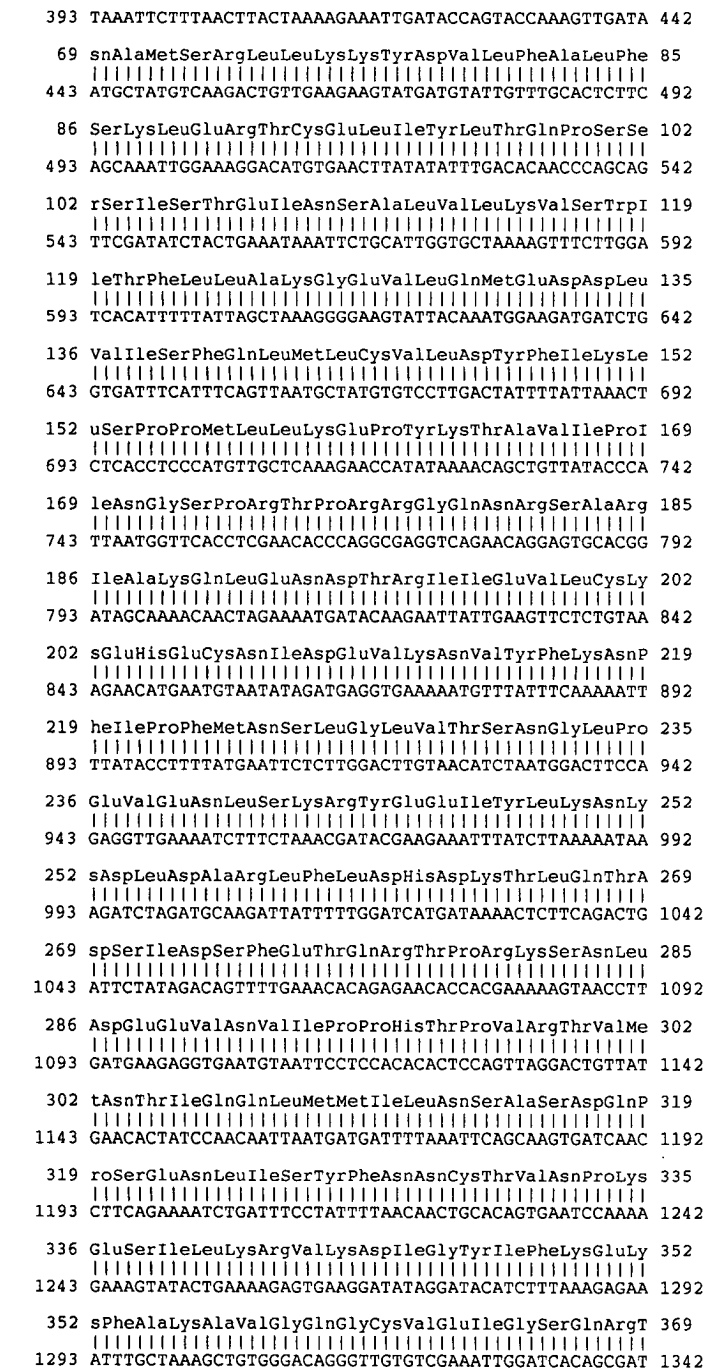
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Align seg 1/1 to: V58452 from: 1 to: 3554

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 343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 392

  52 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 69
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393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442
69 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 85
443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492
86 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 102
493 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 542
102 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 119
543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592
119 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 135
593 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642
136 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 152
643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 692
152 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 169
693 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 742
169 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 185
743 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 792
186 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 202
793 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 842
202 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 219
843 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 892
219 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 235
893 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 942
236 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 252
943 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 992
252 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 269
993 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 1042
269 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 285
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286 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 302
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319 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 335
1193 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242
336 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 352
1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1292
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386 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 402
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519 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 535
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586 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 602
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2143 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAA 2192
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seq_documentation_block:
ID   V54991 standard; DNA; 3218 BP.
AC   V54991;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2457
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PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71355.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 153-157; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3218 BP;    1080 A;    595 C;    561 G;    982 T;


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     ||||||||||||||||||||||||||||||||||||||||||||||||||
 907 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 956

 352 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 369
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 957 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1006

 369 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 385
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1007 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1056

 386 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 402
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1057 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1106

 402 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 419
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1107 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1156

 419 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 435
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1157 CCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1206

 436 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 452
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1207 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1256

 452 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 469
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1257 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1306

 469 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 485
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1307 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 1356

 486 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 502
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1357 TGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCG 1406

 502 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 519
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1407 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1456

 519 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 535
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1457 TCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1506

 536 ProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGl 552
     ||||||||||||||||||||||||||||||||||||||||||||||||||

1507 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1556

 552 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 569
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1557 GACACAAGCAACCTCAGCGTTCCAGACCCAGAAGCCATTGAAATCTACCT 1606

 569 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 585
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1607 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1656

 586 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 602
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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 602 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 619
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1707 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 1756

 619 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 635
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1757 GAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 1806

 636 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 652
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1807 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAA 1856

 652 sAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysG 669
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1857 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 1906

 669 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 685
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1907 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 1956

 686 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 702
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1957 AGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTT 2006

 702 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 719
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2007 GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCAC 2056

 719 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 735
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2057 CCTTACGGATTCCTGGAGGGAAGATCTATATTTCACCCCTGAAGAGTCCA 2106

 736 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSe 752
      ||||||||||||||||||||||||||||||||||||||||||||||||||
2107 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATC 2156

 752 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 769
      ||||||||||||||||||||||||||||||||||||||||||||||||||
2157 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2206

 769 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 785
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2207 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2256

 786 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 802
      ||||||||||||||||||||||||||||||||||||||||||||||||||
2257 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2306

 802 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 819
      ||||||||||||||||||||||||||||||||||||||||||||||||||
2307 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2356

 819 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 835
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2357 AATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2406

 836 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 851
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2407 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2454
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OM of: US-09-026-459A-41 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 13, 2000  2:34 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=x1p
 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=oligo.rng -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-41
Query length: 897
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence              Strd Orig    ZScore    EScore Len   ! Documentation  ..
N_Geneseq_36:V58447    +  897.00 14086.32  0.0       3461  ! Modified retinoblastoma tumou
N_Geneseq_36:Q04713    +  821.00 12891.32  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545    +  821.00 12891.32  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:V58440    +  821.00 12890.14  0.0       3555  ! Modified retinoblastoma tumou
N_Geneseq_36:V58441    +  821.00 12890.34  0.0       3455  ! Modified retinoblastoma tumou
N_Geneseq_36:V58442    +  821.00 12890.47  0.0       3392  ! Modified retinoblastoma tumou
N_Geneseq_36:V58443    +  821.00 12890.61  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:V58444    +  821.00 12890.73  0.0       3266  ! Modified retinoblastoma tumou
N_Geneseq_36:V58446    +  821.00 12890.61  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:V54990    +  821.00 12890.14  0.0       3555  ! DNA sequence of the specifica
N_Geneseq_36:V40004    +  821.00 12891.32  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737    +  821.00 12891.32  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:Q72690    +  820.00 12875.06  0.0       3233  ! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58452    +  816.00 12811.46  0.0       3554  ! Modified retinoblastoma tumou
N_Geneseq_36:V54991    +  816.00 12812.14  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:V58445    +  781.00 12261.59  0.0       3113  ! Modified retinoblastoma tumou
N_Geneseq_36:X04501    +  770.00 12085.80  0.0       4597  ! Human retinoblastoma gene cDN
N_Geneseq_36:V58448    +  747.00 11726.04  0.0       3347  ! Modified retinoblastoma tumou
N_Geneseq_36:Q70536    +  734.00 11519.28  0.0       4597  ! Human retinoblastoma gene. Di
N_Geneseq_36:N81369    +  720.00 11298.97  0.0       4597  ! Human retinoblastoma gene Dia
N_Geneseq_36:Q90059    +  720.00 11301.91  0.0       2995  ! Retinoblastoma tumour suppres
N_Geneseq_36:V58449    +  687.00 10782.22  0.0       3161  ! Modified retinoblastoma tumou
N_Geneseq_36:V58450    +  687.00 10781.77  0.0       3377  ! Modified retinoblastoma tumou
N_Geneseq_36:V58451    +  628.00 9853.29   0.0       3383  ! Modified retinoblastoma tumour
N_Geneseq_36:Q86398    +  593.00 9303.34   0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489    +  474.00 7427.07   0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261    +  286.00 4469.24   2.4e-241  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502    +   65.00  981.90   4.3e-47   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490    +   55.00  824.58   2.5e-38   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:N91077    +   10.00  133.87   7.42      1433  ! Sequence encoding alpha-1-anti
N_Geneseq_36:Q55750    -   10.00  133.53   7.75      1505  ! Genomic clone G11F, includes a
N_Geneseq_36:Q67401    +   10.00  120.28   42.41     10366  ! Huntingtin DNA\IT15 gene. New
N_Geneseq_36:T02461    +   10.00  132.78   8.54      1680  ! Wilms' tumour WT1 cDNA. Monocl
N_Geneseq_36:T02462    +   10.00  139.48   3.61      633  ! Wilms' tumour antigen WT1-6F cD
N_Geneseq_36:Q99257    +   10.00  129.17   13.56     2841  ! Yeast coagulation gene FLO8. Y
N_Geneseq_36:T42476    -   10.00  139.35   3.67      645  ! HuntL4 coding sequence. HuntL a
N_Geneseq_36:T45133    +   10.00  141.71   2.71      457  ! Wilms' tumour gene exon 1. Leuk
N_Geneseq_36:T75529    +   10.00  139.48   3.61      633  ! cDNA encoding Wilms' tumour pro
N_Geneseq_36:T97924    +   10.00  120.28   42.41     10366  ! Composite sequence of a novel
N_Geneseq_36:T88434    -   10.00  130.94   10.81     2195  ! Human 5-lipoxygenase gene p
N_Geneseq_36:V05828    +   10.00  120.28   42.41     10366  ! Human huntingtin coding se
N_Geneseq_36:V17757    +   10.00  128.87   14.08     2965  ! Fractionated X irradiation-
N_Geneseq_36:V27112    -   10.00  111.90   124.15    35099  ! Adenovirus 17. Recombinant
N_Geneseq_36:X15842    +   10.00  141.71   2.71      457  ! Nucleotide sequence of the s
N_Geneseq_36:X18930    +   10.00  140.89   3.01      515  ! Human huntingtin gene. Trans

seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


alignment_scores:
            Quality:  897.00              Length:    897
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x V58447   ..

 Align seg 1/1  to: V58447  from: 1  to: 3461

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       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGC 56

      17 aAlaGluProProAlaProProProProProProGluGluAspProG 34
         ||||||||||||||||||||||||||||||||||||||||||||||||
      57 CGCGGAACCCCCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAG 106

      34 luGlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGlu 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 AGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAA 156

      51 GluThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIlePr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACC 206

      67 oAspHisValArgGluArgAlaTrpLeuValAspLeuAspGluMetSerP 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 AGATCATGTCAGAGAGAGAGCTTGGTTGGTCGACCTAGATGAGATGTCGT 256

      84 heThrPheThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhe 100
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257 TCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTC 306

101 PheAsnLeuLeuLysGluIleAspThrSerThrLysValAspAsnAlaMe 117
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307 TTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTAT 356

117 tSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysL 134
    ||||||||||||||||||||||||||||||||||||||||||||||||||
357 GTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAAT 406

134 euGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIle 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
407 TGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATA 456

151 SerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPh 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||
457 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 506

167 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 184
    ||||||||||||||||||||||||||||||||||||||||||||||||||
507 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 556

184 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
557 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 606

201 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 217
    ||||||||||||||||||||||||||||||||||||||||||||||||||
607 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 656

217 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 234
    ||||||||||||||||||||||||||||||||||||||||||||||||||
657 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 706

234 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
707 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 756

251 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 267
    ||||||||||||||||||||||||||||||||||||||||||||||||||
757 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 806

267 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 284
    ||||||||||||||||||||||||||||||||||||||||||||||||||
807 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 856

284 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 300
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857 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 906

301 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 317
    ||||||||||||||||||||||||||||||||||||||||||||||||||
907 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 956

317 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 334
    ||||||||||||||||||||||||||||||||||||||||||||||||||
957 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 1006

334 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1007 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1056

351 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 367
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1057 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1106

367 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 384
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1107 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1156

384 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
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401 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 417
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1207 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1256

417 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 434
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1257 TGGAGTTCGCTTGTATTACGAGTAATGGAATCCATGCTTAAATCAGAAG 1306

434 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 450
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1307 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1356

451 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 467
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1357 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1406

467 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 484
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1407 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1456

484 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 500
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1457 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1506

501 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 517
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1507 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1556

517 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 534
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1557 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCT 1606

534 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 550
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1607 CAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1656

551 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 567
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1657 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1706

567 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 584
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1707 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1756

584 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 600
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601 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 617
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1807 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1856

617 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 634
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634 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 650
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1907 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1956

651 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 667
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1957 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2006

667 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 684
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2007 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA 2056

684 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 700
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    767 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 784
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   2307 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2356

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seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of California.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.

CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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     93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
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    110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
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    127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
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    143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
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    160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
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    177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
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    760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 809

    193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
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1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1909

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1910 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

 577 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 593
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1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 2009

 593 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 610
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AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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     127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     610 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 659

     143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     660 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 709

     160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     710 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 759

     177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 809

     193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     810 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 859

     210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     860 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 909

     227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     243 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     960 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 1009

     260 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 276
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1010 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059

     277 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 293
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1060 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 1109

     293 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 310
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     310 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 326
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    1160 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1209

     327 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 343
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    1210 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1259

     343 oValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnS 360
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    1260 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 1309

     360 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 376
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    1310 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1359

     377 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 393
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1360 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1409

     393 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 410
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1410 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1459

     410 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 426
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     427 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 443
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     443 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 460
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     460 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 476
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    1610 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659
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 477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
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 493 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 510
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 510 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 526
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 543 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 560
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1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1909

 560 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 576
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1910 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

 577 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 593
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1960 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 2009

 593 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 610
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2010 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 2059

 610 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 626
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 627 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 643
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2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

 643 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 660
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2160 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 2209

 660 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 676
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2210 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2259

 677 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 693
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 693 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 710
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 710 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 726
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 727 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 743
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 743 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 760
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 760 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 776
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 777 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 793
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2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2609

 793 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 810
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2610 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2659

 810 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 826
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 827 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 843
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 843 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 860
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2810 TCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2859

 877 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 893
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2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2909

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seq_name: N_Geneseq_36:V58440

seq_documentation_block:

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ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;
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alignment_scores:

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            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

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 US-09-026-459A-41 x V58440   ..
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Align seg 1/1 to: V58440 from: 1 to: 3555

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 77 ValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnLysAsnIl 93
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328 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 377

 93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
    ||||||||||||||||||||||||||||||||||||||||||||||||||
378 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 427

110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
    ||||||||||||||||||||||||||||||||||||||||||||||||||
428 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 477

127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
    ||||||||||||||||||||||||||||||||||||||||||||||||||
478 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 527

143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
    ||||||||||||||||||||||||||||||||||||||||||||||||||
528 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 577

160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
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578 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 627

177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
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628 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 677

193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
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678 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 727

210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
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728 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 777

227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
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778 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 827

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828 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 877

260 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 276
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878 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 927

277 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 293
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928 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 977

293 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 310
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978 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 1027

310 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 326
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1028 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 1077

327 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 343
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1128 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 1177

360 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 376
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1178 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1227

377 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 393
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1228 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1277

393 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 410
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1278 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1327

410 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 426
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1328 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1377

427 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 443
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1378 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1427

443 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 460
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1428 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1477

460 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 476
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1478 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1527

477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
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1528 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1577

493 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 510
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1578 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1627

510 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 526
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1628 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1677

527 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 543
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1678 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1727

543 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 560
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1728 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1777

560 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 576
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1778 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1827

577 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 593
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1828 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 1877

593 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 610
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1878 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1927

610 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 626
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1928 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1977

627 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 643
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1978 GCCTATCTCCGGCTAAATACACTTGTGAACGCCTTCTGTCTGAGCACCC 2027

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660 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 676
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2078 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 2127
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     677 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 693
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    2228 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2277

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     743 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 760
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    2328 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACA 2377

     760 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 776
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    2378 AGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2427

     777 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 793
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2428 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2477

     793 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 810
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2478 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2527

     810 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 826
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2528 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2577

     827 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 843
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2578 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2627

     843 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 860
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2628 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATC 2677

     860 euProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 876
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2678 TCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2727

     877 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 893
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2728 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2777

     893 nLysGluGluLys 897
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    2778 CAAGGAAGAGAAA 2790

seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;   1153 A;   631 C;   627 G;   1044 T;


alignment_scores:
           Quality:  821.00            Length:    821
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x V58441   ..

 Align seg 1/1  to: V58441  from: 1  to: 3455

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     229 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 278

      93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     279 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 328

     110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     329 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 378

     127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     379 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 428

     143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     429 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 478

     160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     479 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 528

     177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     529 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 578

     193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     579 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 628

     210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     629 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 678

     227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
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     679 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 728

     243 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     729 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 778

     260 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 276
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 779 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 828

 277 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 293
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 829 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 878

 293 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 310
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 879 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 928

 310 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 326
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 929 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 978

 327 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 343
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 979 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 1028

 343 oValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnS 360
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1029 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 1078

 360 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 376
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1079 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1128

 377 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 393
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1129 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1178

 393 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 410
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1179 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1228

 410 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 426
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1229 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1278

 427 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 443
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1279 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1328

 443 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 460
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1329 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1378

 460 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 476
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1379 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1428

 477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1429 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1478

 493 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 510
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1479 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1528

 510 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 526
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1529 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1578

 527 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 543
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 543 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 560
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1629 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1678

 560 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 576
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1679 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1728

 577 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 593
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1729 TCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTC 1778

 593 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 610
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1779 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1828

 610 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 626
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1829 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1878

 627 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 643
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 643 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 660
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 660 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 676
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 677 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 693
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 693 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 710
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 710 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 726
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2129 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2178

 727 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 743
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 743 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 760
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 760 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 776
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 810 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 826
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2429 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2478

 827 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 843
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
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 843 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 860
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2529 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATC 2578

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seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
            Quality:  821.00             Length:    821
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x V58442   ..

 Align seg 1/1  to: V58442  from: 1  to: 3392

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      93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     266 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 315

     127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     316 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 365

     143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
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     366 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 415

     160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
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     416 TAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAA 465

     177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
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     466 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 515

     193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
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     227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
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     616 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 665

     243 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 260
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     260 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 276
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     716 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 765

     277 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 293
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     766 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 815

     293 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 310
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     310 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 326
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     327 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 343
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    1016 CAGCAAGTGATCAACCTTGAGAAAATCTGATTTCCTATTTTAACAACTGC 1065

     377 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 393
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1066 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1115

     393 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 410
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    1116 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1165

     410 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 426
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    1166 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1215

     427 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 443
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1216 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1265

     443 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 460
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1266 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1315

     460 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 476
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1316 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1365

 477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1366 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1415

 493 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 510
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1416 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1465

 510 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 526
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1466 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1515

 527 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 543
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1516 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1565

 543 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 560
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1566 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1615

 560 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 576
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 577 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 593
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 593 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 610
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 610 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 626
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 643 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 660
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1866 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 1915

 660 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 676
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1916 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1965

 677 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 693
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1966 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2015

 693 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 710
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2016 TGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAAC 2065

 710 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 726
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2066 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2115

 727 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 743
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2116 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2165

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 760 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 776
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2216 AGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2265

 777 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 793
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2266 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2315

 793 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 810
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2316 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2365

 810 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 826
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 827 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 843
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2416 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2465

 843 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 860
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2466 ACTACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATC 2515

 860 euProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr 876
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2516 TCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACT 2565

 877 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 893
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2566 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2615

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seq_name: N_Geneseq_36:V58443

seq_documentation_block:

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ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;
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alignment_scores:

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           Quality:  821.00              Length:    821
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

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US-09-026-459A-41 x V58443   ..

Align seg 1/1  to: V58443  from: 1  to: 3323

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     97 GTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTACAGAAAAACAT 146

     93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    147 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 196

    110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    197 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 246

    127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    247 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 296

    143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    297 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 346

    160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
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    177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    397 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGA 446

    193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
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    447 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 496

    210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    497 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 546

    227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    547 AACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTAT 596

    243 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 260
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    597 TGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATG 646

    260 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 276
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    293 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 310
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        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    393 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 410
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   1047 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1096

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   1097 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1146

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        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    460 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 476
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1247 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1296

    477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
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    493 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 510
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1347 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1396

    510 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 526
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    593 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 610
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    610 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 626
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 1897 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 1946

  693 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 710
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 1947 TGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAAC 1996

  710 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 726
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seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x V58444   ..

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      93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      90 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 139

     110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
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     160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
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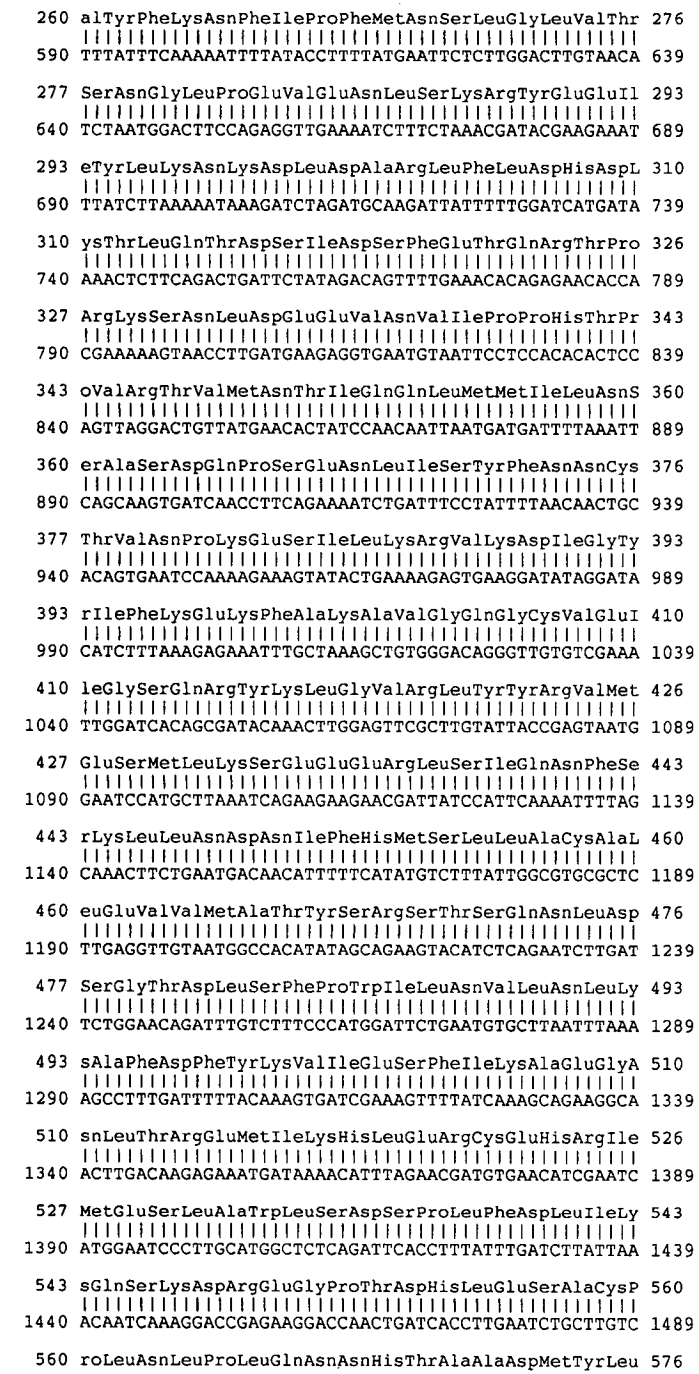
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     227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
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     243 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 260
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seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;


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AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
```

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CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  821.00              Length:    821
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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      93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     378 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 427

     110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     428 GTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 477

     127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     478 TTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTT 527

     143 uThrGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValL 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     528 GACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGC 577

     160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
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     193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
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     678 CTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA 727

     210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     728 CAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAG 777

     227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
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     443 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 460
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    1428 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1477

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     477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
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     610 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 626
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    1928 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1977
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   643 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 660
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   710 rgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsn 726
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   727 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 743
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   743 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 760
       |||||||||||||||||||||||||||||||||||||||||||||||||||
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   777 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 793
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   827 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 843
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   893 nLysGluGluLys 897
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  2778 CAAGGAAGAGAAA 2790

seq_name: N_Geneseq_36:V40004

seq_documentation_block:
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag= a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis.
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465). A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain. Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease. Tissue-specific expression of E2F-RB fusions is
CC   provided. The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;    974 A;    618 C;    593 G;    809 T;


alignment_scores:
           Quality:  821.00              Length:    821
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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 US-09-026-459A-41 x V40004   ..

 Align seg 1/1  to: V40004  from: 1  to: 2994

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     110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
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 160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
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 177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
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 193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
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 210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
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1610 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1659

 477 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLy 493
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1710 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1759

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 527 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 543
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1810 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1859

 543 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 560
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1860 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1909

 560 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 576
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1910 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1959

 577 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 593
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 593 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 610
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 627 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 643
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2110 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 2159

 643 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 660
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 660 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 676
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 743 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 760
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   827 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 843
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seq_documentation_block:

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ID   X00737 standard; cDNA; 2995 BP.
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DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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FT                   /product= RB_protein
FT                   /transl_except= (pos: 226. .228, aa: Glu)
PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
PR   13-SEP-1994; US-306513.
PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;
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alignment_scores:

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            Quality:  821.00              Length:    821
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alignment_block:

US-09-026-459A-41 x X00737 ..

Align seg 1/1 to: X00737 from: 1 to: 2995

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     93 eGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrS 110
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    510 AGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCA 559

    110 erThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 126
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    127 LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLe 143
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    160 euLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 176
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    177 MetGluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAs 193
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    193 pTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysT 210
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    210 hrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGln 226
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    227 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIl 243
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    243 eGluValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnV 260
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    260 alTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr 276
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   1010 TTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA 1059
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 277 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 293
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 293 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 310
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1110 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 1159

 310 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 326
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 327 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 343
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 577 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 593
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seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
            Quality:  820.00              Length:    820
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x Q72690   ..

 Align seg 1/1  to: Q72690  from: 1  to: 3233

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      94 uIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSerT 111
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 AATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTA 106

     111 hrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeu 127
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     128 PheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuTh 144
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     157 TTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGAC 206

     144 rGlnProSerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuL 161
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 ACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAA 256

     161 ysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGlnMet 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     257 AAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATG 306

     178 GluAspAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTy 194
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     307 GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA 356

     194 rPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLysThrA 211
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     357 TTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAG 406

     211 laValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsn 227
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     407 CTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAAC 456

     228 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGl 244
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     457 AGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGA 506

     244 uValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValT 261
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     507 AGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTT 556

     261 yrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 277
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     557 ATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCT 606

     278 AsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTy 294
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     607 AATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTA 656

     294 rLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysT 311
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     311 hrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArg 327
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     328 LysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVa 344
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     344 lArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerA 361
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     361 laSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThr 377
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     378 ValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIl 394
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     907 GTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACAT 956

     394 ePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleG 411
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     411 lySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGlu 427
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     461 luValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSer 477
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 478 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAl 494
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 494 aPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnL 511
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 544 nSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProL 561
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 561 euAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSer 577
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 594 rAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProL 611
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 611 euLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 627
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 678 TyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleVa 694
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 694 lThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArgV 711
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 711 alLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSer 727
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 761 heProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPro 777
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 794 tThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrS 811
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2157 GACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTT 2206

 811 erGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal 827
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2257 CTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACT 2306

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 861 roGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArg 877
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2457 GGAAGAGAAA 2466
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


alignment_scores:
            Quality:  816.00              Length:    816
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-41 x V58452   ..
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Align seg 1/1 to: V58452 from: 1 to: 3554

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343 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 392

 98 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 115
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393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442

115 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 131
    ||||||||||||||||||||||||||||||||||||||||||||||||||
443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492

132 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 148
    ||||||||||||||||||||||||||||||||||||||||||||||||||
493 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 542

148 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 165
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543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592

165 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 181
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593 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

182 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 198
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643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 692

198 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 215
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693 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 742

215 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 231
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743 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 792

232 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 248
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793 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 842

248 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 265
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843 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 892

265 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 281
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893 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 942

282 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 298
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943 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 992

298 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 315
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993 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 1042

315 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 331
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1043 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 1092

332 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 348
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1093 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 1142

348 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 365
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1143 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1192

365 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 381
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1193 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1242

382 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 398
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1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1292

398 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 415
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415 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 431
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1343 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1392

432 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 448
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1393 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1442

448 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 465
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1443 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1492

465 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 481
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482 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 498
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515 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 531
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532 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 548
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548 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 565
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565 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 581
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598 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 615
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1893 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1942

615 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 631
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1943 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1992

632 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 648
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1993 AATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATAT 2042

648 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 665
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    2243 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 2292

     732 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 748
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    2293 AGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTT 2342

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     765 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 781
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2393 CCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2442

     782 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSe 798
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2443 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATC 2492

     798 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 815
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2493 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2542

     815 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 831
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2543 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2592

     832 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 848
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2593 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2642

     848 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 865
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     865 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 881
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    2693 AATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2742

     882 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 897
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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seq_name: N_Geneseq_36:V54991

seq_documentation_block:

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ID   V54991 standard; DNA; 3218 BP.
AC   V54991;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2457
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71355.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 153-157; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3218 BP;    1080 A;    595 C;    561 G;    982 T;
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alignment_scores:

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             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

US-09-026-459A-41 x V54991 ..

Align seg 1/1 to: V54991 from: 1 to: 3218

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      98 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 115
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
      57 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 106

     115 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 131
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     107 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 156

     132 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     157 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 206

     148 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 165
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     207 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 256

     165 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 181
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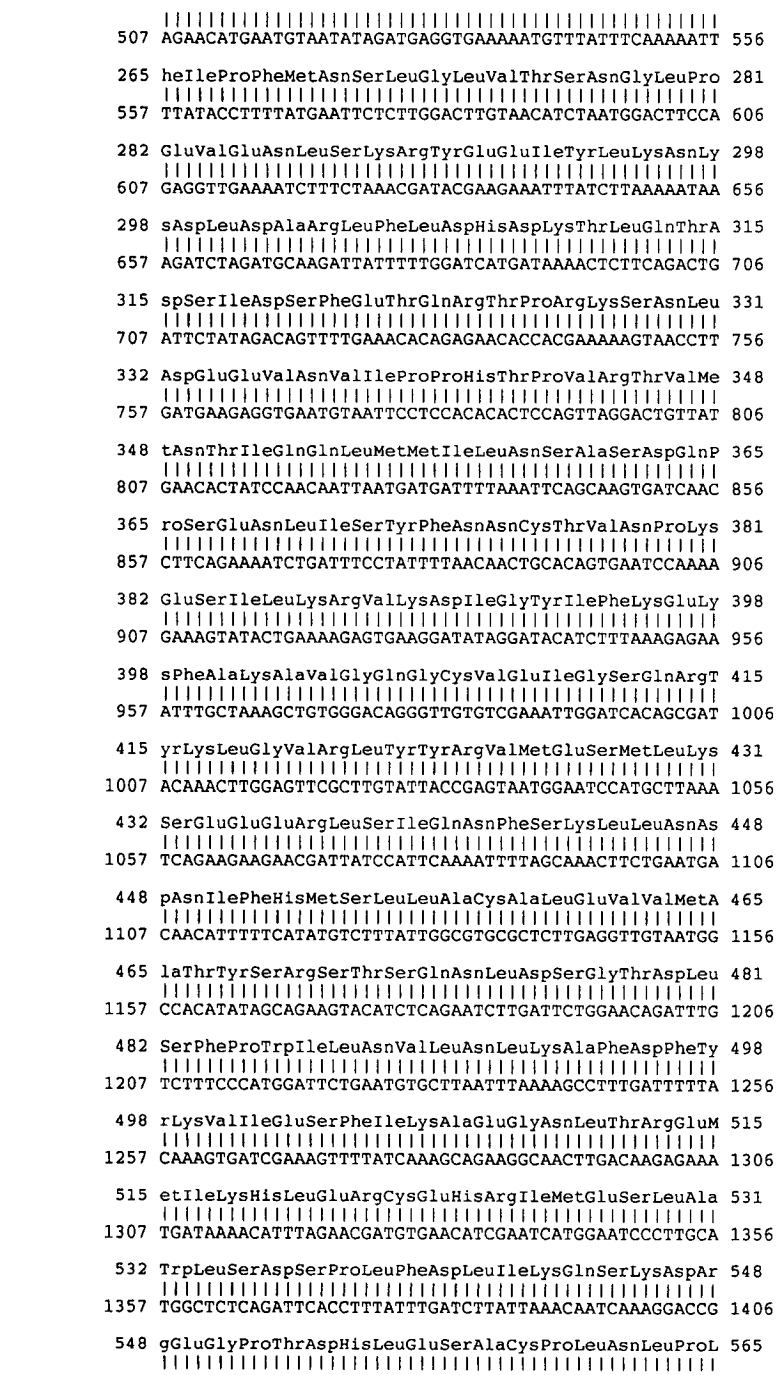
     182 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 198
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     307 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 356

     198 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     357 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 406

     215 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 231
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     407 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 456

     232 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 248
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     457 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 506

     248 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 265
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507 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 556
265 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 281
557 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 606
282 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 298
607 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 656
298 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 315
657 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 706
315 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 331
707 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 756
332 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 348
757 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 806
348 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 365
807 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 856
365 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 381
857 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 906
382 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 398
907 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 956
398 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 415
957 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1006
415 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 431
1007 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1056
432 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 448
1057 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1106
448 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 465
1107 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1156
465 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 481
1157 CCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1206
482 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 498
1207 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1256
498 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 515
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515 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 531
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532 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 548
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1557 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1606
615 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 631
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632 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 648
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1707 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 1756
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715 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 731
1907 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 1956
732 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 748
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748 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 765
2007 GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCAC 2056
765 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 781
2057 CCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2106
782 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSe 798
2107 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATC 2156
798 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 815
2157 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2206
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832 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 848
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 865 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 881
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2357 AATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2406

 882 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 897
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Date: Feb 13, 2000  2:36 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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Search information block:
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score_list:
Sequence           Strd Orig    ZScore    EScore Len   ! Documentation  ..
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N_Geneseq_36:Q04713  +   747.00 11728.83  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545  +   747.00 11728.83  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:Q72690  +   747.00 11728.31  0.0       3233  ! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58447  +   747.00 11727.84  0.0       3461  ! Modified retinoblastoma tumou
N_Geneseq_36:V58452  +   747.00 11727.66  0.0       3554  ! Modified retinoblastoma tumou
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N_Geneseq_36:V58446  +   747.00 11728.12  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:V54990  +   747.00 11727.66  0.0       3555  ! DNA sequence of the specifica
N_Geneseq_36:V54991  +   747.00 11728.34  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:V40004  +   747.00 11728.83  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737  +   747.00 11728.83  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:X04501  +   696.00 10923.23  0.0       4597  ! Human retinoblastoma gene cDN
N_Geneseq_36:V58449  +   687.00 10784.12  0.0       3161  ! Modified retinoblastoma tumou
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N_Geneseq_36:Q70536  +   660.00 10356.63  0.0       4597  ! Human retinoblastoma gene. Di
N_Geneseq_36:N81369  +   646.00 10136.28  0.0       4597  ! Human retinoblastoma gene Dia
N_Geneseq_36:Q90059  +.  646.00 10139.19  0.0       2995  ! Retinoblastoma tumour suppres
N_Geneseq_36:V58451  +   628.00 9855.06   0.0       3383  ! Modified retinoblastoma tumour
N_Geneseq_36:Q86398  +   593.00 9305.03   0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489  +   474.00 7428.53   0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261  +   286.00 4470.29   2.1e-241  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502  +    65.00  982.56   4.0e-47   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490  +    55.00  825.22   2.3e-38   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:N91077  +    10.00  134.24   7.08      1433  ! Sequence encoding alpha-1-anti
N_Geneseq_36:Q55750  -    10.00  133.90   7.39      1505  ! Genomic clone G11F, includes a
N_Geneseq_36:Q67401  +    10.00  120.78   39.75     10366  ! Huntingtin DNA\IT15 gene. New
N_Geneseq_36:T02461  +    10.00  133.16   8.13      1680  ! Wilms' tumour WT1 cDNA. Monocl
N_Geneseq_36:T02462  +    10.00  139.79   3.47      633  ! Wilms' tumour antigen WT1-6F cD
N_Geneseq_36:Q99257  +    10.00  129.58   12.86     2841  ! Yeast coagulation gene FLO8. Y
N_Geneseq_36:T42476  -    10.00  139.67   3.53      645  ! HuntL4 coding sequence. HuntL a
N_Geneseq_36:T45133  +    10.00  142.01   2.61      457  ! Wilms' tumour gene exon 1. Leuk
N_Geneseq_36:T75529  +    10.00  139.79   3.47      633  ! cDNA encoding Wilms' tumour prc
N_Geneseq_36:T97924  +    10.00  120.78   39.75     10366  ! Composite sequence of a novel
N_Geneseq_36:T88434  -    10.00  131.34   10.27     2195  ! Human 5-lipoxygenase gene p
N_Geneseq_36:V05828  +    10.00  120.78   39.75     10366  ! Human huntingtin coding se
N_Geneseq_36:V17757  +    10.00  129.29   13.34     2965  ! Fractionated X irradiation-
N_Geneseq_36:V27112  -    10.00  112.49   115.15    35099  ! Adenovirus 17. Recombinant
N_Geneseq_36:X15842  +    10.00  142.01   2.61      457  ! Nucleotide sequence of the s
N_Geneseq_36:X18930  +    10.00  141.20   2.90      515  ! Human huntingtin gene. Trans

seq_name: N_Geneseq_36:V58448

seq_documentation_block:
ID   V58448 standard; DNA; 3347 BP.
AC   V58448;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2586
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69372.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 196-200; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3347 BP;    1096 A;    650 C;    617 G;    984 T;


alignment_scores:
           Quality:  859.00            Length:    859
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x V58448   ..

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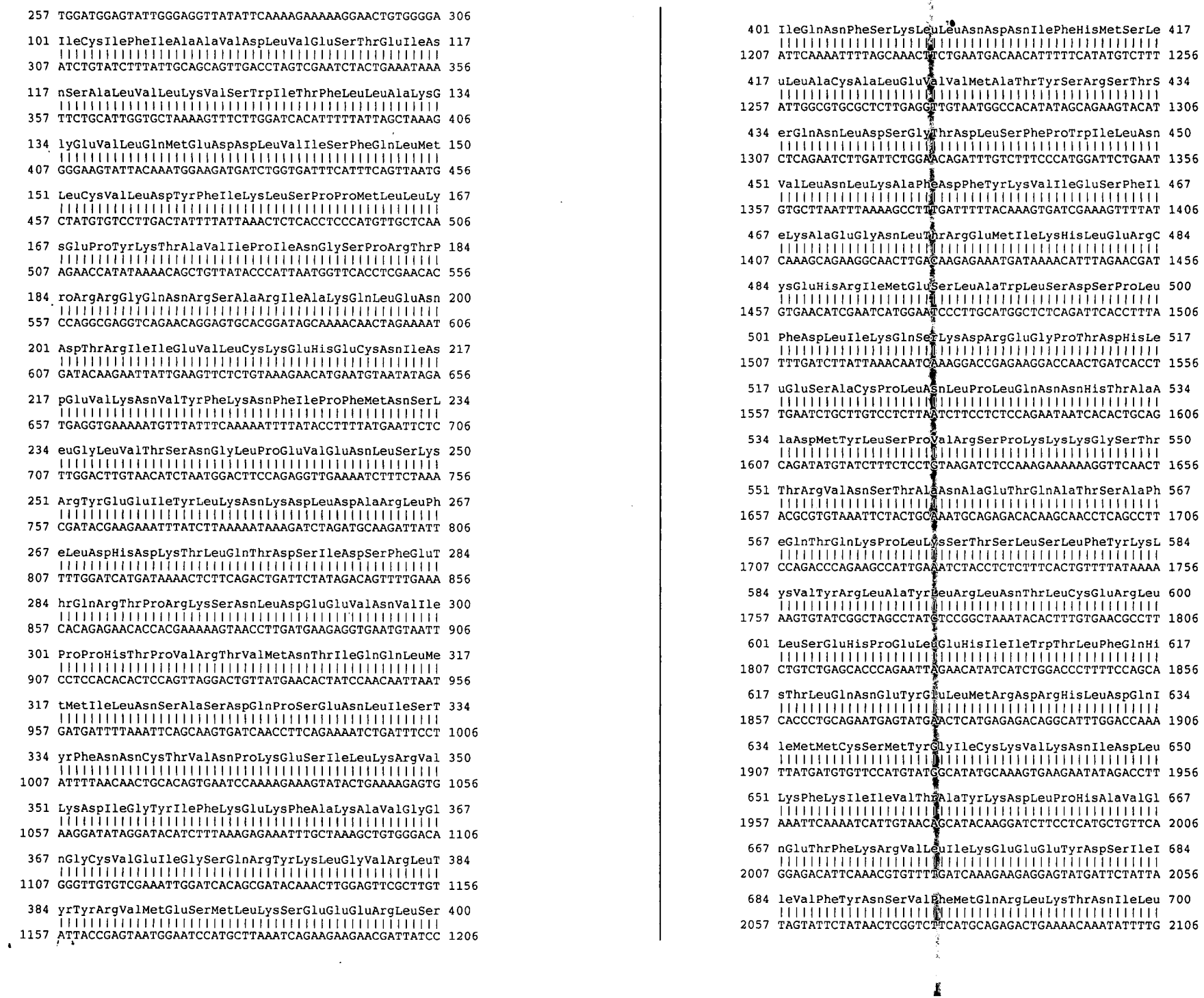
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      34 luGlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGlu 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 AGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAA 156

      51 GluThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIlePr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACC 206

      67 oAspHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerServ 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 AGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTG 256

      84 alAspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGly 100
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257 TGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306
101 IleCysIlePheIleAlaAlaValAspLeuValGluSerThrGluIleAs 117
307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGTCGAATCTACTGAAATAAA 356
117 nSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysG 134
357 TTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAG 406
134 lyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMet 150
407 GGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATG 456
151 LeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLy 167
457 CTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAA 506
167 sGluProTyrLysThrAlaValIleProIleAsnGlySerProArgThrP 184
507 AGAACCATATAAAACAGCTGTTATACCCATTAATGGTTCACCTCGAACAC 556
184 roArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsn 200
557 CCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAAT 606
201 AspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAs 217
607 GATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGA 656
217 pGluValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerL 234
657 TGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTC 706
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707 TTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAA 756
251 ArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPh 267
757 CGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATT 806
267 eLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluT 284
807 TTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAA 856
284 hrGlnArgThrProArgLysSerAsnLeuAspGluGluValAsnValIle 300
857 CACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATT 906
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907 CCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAAT 956
317 tMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerT 334
957 GATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCT 1006
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seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;


alignment_scores:
           Quality:  747.00            Length:    747
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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     682 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
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     732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 781

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
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     782 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 831

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
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     832 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 881

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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     882 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 931

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
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     932 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

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     246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
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     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
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     346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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     379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
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 413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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1582 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1631

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 446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
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 463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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1732 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1781

 479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
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 496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
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 513 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 529
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 529 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 546
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1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1981

 546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
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 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231

 629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
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 646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
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2382 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGA 2431

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seq_documentation_block:
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
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CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
           Quality:  747.00            Length:    747
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x Q41545   ..

 Align seg 1/1  to: Q41545  from: 1  to: 2994

     113 SerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPh 129
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     682 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 731

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     732 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 781

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     782 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 831

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     832 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 881

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     882 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 931

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     932 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 981

     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     982 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 1031

     229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1032 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 1081

     246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1082 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 1131

     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1132 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 1181

     279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1182 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 1231

     296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1282 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1331

     329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
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    1332 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1381

     346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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    1382 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1431

     363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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     379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1482 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1531

     396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1532 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1581

     413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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     429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1632 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1681

     446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
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    1682 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1731

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     496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
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     513 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 529
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    1882 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1931

     529 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 546
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    1932 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1981

     546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
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    1982 AAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 2031

     563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
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    2032 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 2081

     579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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    2082 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACAC 2131

     596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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    2132 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2181

     613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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    2182 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2231
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  629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
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  646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
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  663 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 679
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  679 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 696
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  696 ysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPro 712
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  713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
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 2482 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2531

  729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
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 2532 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2581

  746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2582 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2631

  763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
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 2632 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2681

  779 eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluG 796
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  796 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 812
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 2732 GAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2781

  813 SerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGl 829
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 2782 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2831

  829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
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 2832 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGA 2881

  846 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 859
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 2882 AAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2922

seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
           Quality:  747.00              Length:    747
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x Q72690   ..

 Align seg 1/1  to: Q72690  from: 1  to: 3233

  113 SerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPh 129
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  226 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 275

  129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  276 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 325

  146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  326 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 375

  163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  376 CCCATGTTGCTCAAAGAACGATATAAAACAGCTGTTATACCCATTAATGG 425

  179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  426 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 475

  196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  476 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 525

  213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  526 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 575

  229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  576 TTTTATGAATTCTCTTGGAGTTGTAACATCTAATGGACTTCCAGAGGTTG 625

  246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  626 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 675

  263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  676 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 725

  279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  726 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 775

  296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
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 776 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 825

 313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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 826 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 875

 329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 876 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 925

 346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 926 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 975

 363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 976 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1025

 379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
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1026 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1075

 396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1076 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1125

 413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1126 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1175

 429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1176 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1225

 446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
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1226 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1275

 463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1276 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1325

 479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
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1326 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCT 1375

 496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1376 CAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1425

 513 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 529
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1426 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1475

 529 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 546
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1476 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1525

 546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
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1526 AAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1575

 563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1576 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1625

 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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1676 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1725

 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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1726 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1775

 629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
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1776 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA 1825

 646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
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 663 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 679
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1876 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1925

 679 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 696
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1926 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGA 1975

 696 ysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPro 712
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1976 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2025

 713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
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 729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
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2076 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2125

 746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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2126 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2175

 763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2176 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2225

 779 eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluG 796
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2226 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAG 2275

 796 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 812
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2276 GAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2325

 813 SerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGl 829
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2326 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2375

 829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2376 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGA 2425

 846 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 859
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:

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ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
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FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


alignment_scores:
            Quality:  747.00              Length:    747
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x V58447   ..

 Align seg 1/1  to: V58447  from: 1  to: 3461

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     457 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 506

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     507 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 556

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     557 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 606

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     607 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 656

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
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     707 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 756

     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
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     229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
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     807 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 856

     246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     857 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 906

     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
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     907 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 956

     279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
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     296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
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    1007 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1056

     313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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     363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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     379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
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    1257 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1306

     396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
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     413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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     429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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    1457 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1506

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     479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
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    1557 ACATTTAGAACGATGTGAAGATGGAATCATGGAATCCCTTGCATGGCTCT 1606

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     513 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 529
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     579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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     613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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     696 ysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPro 712
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     713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
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     729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


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 Percent Similarity: 100.000   Percent Identity: 100.000

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     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
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     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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 279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
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 313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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1150 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1199

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1200 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1249

 346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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 363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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1650 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCT 1699

 496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
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1900 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1949

 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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 596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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2000 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2049

 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2050 ACCCTTTTCCAGCACACCGTGCAGAATGAGTATGAACTCATGAGAGACAG 2099

 629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2100 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA 2149

 646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2150 AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 2199

 663 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 679
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2200 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2249

 679 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 696
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2250 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGA 2299

 696 ysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPro 712
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2300 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2349

 713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2350 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2399

 729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
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2400 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2449

 746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2450 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2499

 763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
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2500 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2549

 779 eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluG 796
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2550 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAG 2599

 796 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 812
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2600 GAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2649

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2650 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2699

 829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
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2700 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGA 2749

 846 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 859
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seq_name: N_Geneseq_36:V58440
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seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  747.00              Length:    747
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x V58440   ..

 Align seg 1/1  to: V58440  from: 1  to: 3555

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     550 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 599

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     600 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 649

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     650 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 699

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     700 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 749

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     750 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 799

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     800 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 849

     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     850 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 899

     229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     900 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 949

     246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     950 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 999

     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1000 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 1049

     279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1050 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 1099

     296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1100 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1149

     313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1150 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1199

     329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
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    1200 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1249

     346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1250 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1299

     363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1300 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1349

     379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1350 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1399

     396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1400 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1449

     413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1450 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1499

     429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1500 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1549

     446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1550 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1599

     463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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    1600 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1649

     479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1650 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCT 1699

     496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
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    1750 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1799

     529 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 546
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    1800 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1849
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  563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
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 1900 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1949

  579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1950 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACAC 1999

  596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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 2000 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 2049

  613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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 2050 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2099

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 2100 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA 2149

  646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
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 2150 AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 2199

  663 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 679
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2300 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2349

  713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
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 2350 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2399

  729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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  746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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 2450 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2499

  763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
      ||||||||||||||||||||||||||||||||||||||||||||||||||
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  779 eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluG 796
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  796 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 812
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 2600 GAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2649

  813 SerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGl 829
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2650 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2699

  829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 2700 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGA 2749

  846 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 859
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seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


alignment_scores:
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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58441  from: 1  to: 3455

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     451 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 500

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     501 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 550

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     551 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 600

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     601 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 650

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     651 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 700

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
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     701 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 750

     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
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 751 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 800

 229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
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 801 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 850

 246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 851 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 900

 263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 901 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 950

 279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 951 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 1000

 296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
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1001 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 1050

 313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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1051 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1100

 329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
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1101 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1150

 346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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1151 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1200

 363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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1201 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1250

 379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
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1251 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1300

 396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
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1301 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1350

 413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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1351 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1400

 429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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1401 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1450

 446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1451 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1500

 463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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1501 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1550

 479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
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1551 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCT 1600

 496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
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1601 CAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1650

 513 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 529
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1651 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1700
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 529 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 546
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 546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
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1751 AAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1800

 563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
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1801 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1850

 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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1851 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACAC 1900

 596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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1951 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 2000

 629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
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 663 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 679
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 713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
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 729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
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2301 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2350

 746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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 763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
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 796 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 812
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2551 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2600
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     829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
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     846 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 859
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;


alignment_scores:
            Quality:  747.00             Length:    747
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58442  from: 1  to: 3392

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     388 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 437

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     438 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 487

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     488 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 537

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     538 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 587

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     588 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 637

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
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     638 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 687

     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
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     688 GAATGTAATATAGATGAGCTGAAAAATGTTTATTTCAAAAATTTTATACC 737

     229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
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     738 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 787

     246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
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     788 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 837

     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
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     838 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 887

     279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
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     888 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 937

     296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
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     938 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 987

     313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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     988 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 1037

     329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
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    1038 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1087

     346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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    1088 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1137

     363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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    1138 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1187

     379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1188 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1237

     396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
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    1238 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1287

     413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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    1288 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1337

     429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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 596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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 629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
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 679 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 696
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 829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
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2538 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGA 2587

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2588 AAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628
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seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID V58443 standard; DNA; 3323 BP.
AC V58443;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

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Quality: 747.00 Length: 747
Ratio: 1.000 Gaps: 0
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alignment_block:
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 129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
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 369 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 418

 146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
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 419 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 468

 163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
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 469 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 518
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179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
519 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 568
196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
569 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 618
213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
619 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 668
229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
669 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 718
246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
719 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 768
263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
769 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 818
279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
819 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 868
296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
869 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 918
313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
919 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 968
329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
969 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1018
346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
1119 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1168
396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
1169 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1218
413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
1219 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1268
429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
1269 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1318
446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
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463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
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713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
2119 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2168
729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
2169 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2218
746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
2219 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2268
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seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


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     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
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     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
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     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
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     562 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 611

     229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
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     246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
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     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
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     296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
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     346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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     429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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 563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
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 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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1812 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA 1861

 646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
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 679 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 696
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 746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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seq_name: N_Geneseq_36:V58445

seq_documentation_block:
ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998 (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;

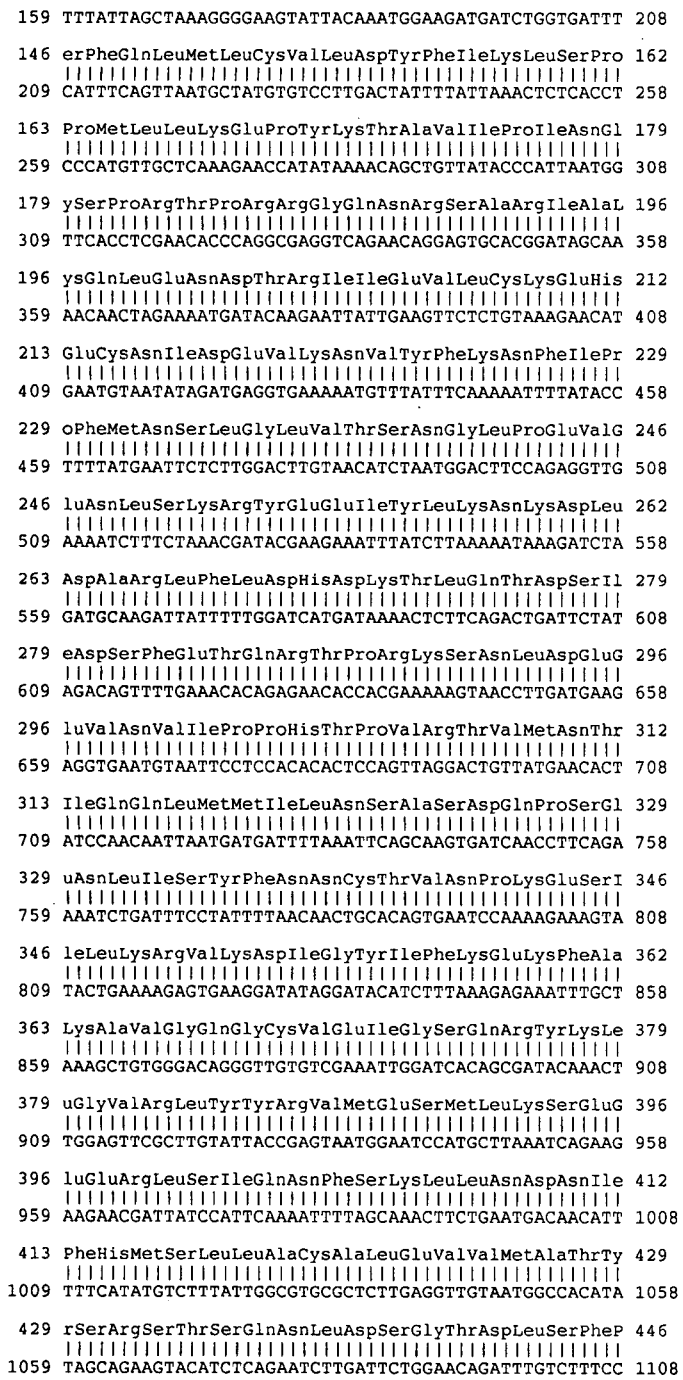

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146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
209 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 258
163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
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179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
359 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 408
213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
409 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 458
229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
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246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
509 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 558
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659 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 708
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859 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 908
379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
909 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 958
396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
959 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1008
413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
1009 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1058
429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
1059 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1108
446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
1109 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1158
463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
1159 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1208
479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
1209 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCT 1258
496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
1259 CAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1308
513 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 529
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529 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 546
1359 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1408
546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
1409 AAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1458
563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
1459 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1508
579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
1509 ACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACAC 1558
596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
1559 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1608
613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
1609 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1658
629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
1659 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA 1708
646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
1709 AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 1758
663 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 679
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679 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 696
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696 ysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPro 712
1859 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 1908
713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
1909 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 1958
729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
1959 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2008

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     746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
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    2009 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2058

     763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2059 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2108

     779 eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluG 796
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     796 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 812
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2159 GAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2208

     813 SerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGl 829
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2209 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2258

     829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
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    2259 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGA 2308

     846 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 859
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    2309 AAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2349
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seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

alignment_scores:
Quality: 747.00 Length: 747
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-43 x V58446 ..

Align seg 1/1 to: V58446 from: 1 to: 3323

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     319 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 368

     129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     369 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 418

     146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     419 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 468

     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     469 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 518

     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     519 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 568

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     569 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 618

     213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     619 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 668

     229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     669 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 718

     246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     719 AAAATCTTTCTAAACGATAGGAAGAAATTTATCTTAAAAATAAAGATCTA 768

     263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     769 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 818

     279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     819 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 868

     296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     869 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 918

     313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     919 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 968

     329 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 346
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     969 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 1018

     346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1019 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 1068

     363 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 379
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    1069 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 1118

     379 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 396
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1119 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1168

     396 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 412
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    1169 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1218

     413 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 429
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1219 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1268

 429 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 446
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1269 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1318

 446 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 462
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1319 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1368

 463 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 479
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1369 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1418

 479 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 496
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1419 ACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCT 1468

 496 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 512
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1469 CAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1518

 513 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 529
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1519 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1568

 529 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 546
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1569 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1618

 546 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 562
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1619 AAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAA 1668

 563 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 579
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1669 GCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1718

 579 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 596
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 596 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 612
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1769 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1818

 613 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 629
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1819 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1868

 629 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 646
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1869 GCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA 1918

 646 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 662
     |||||||||||||||||||||||||||||||||||||||||||||||||||
1919 AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 1968

 663 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 679
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1969 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 2018

 679 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 696
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2019 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGA 2068

 696 ysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPro 712
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2069 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 2118

 713 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 729
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2119 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2168

 729 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 746
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2169 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2218

 746 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 762
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2219 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2268

 763 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 779
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2269 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2318

 779 eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluG 796
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 796 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 812
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2369 GAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2418

 813 SerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGl 829
     |||||||||||||||||||||||||||||||||||||||||||||||||||
2419 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2468

 829 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 846
     |||||||||||||||||||||||||||||||||||||||||||||||||||
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 846 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 859
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seq_name: N_Geneseq_36:V54990

seq_documentation_block:

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ID   V54990 standard; DNA; 3555 BP.
AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71354.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers.
PS   Disclosure; Pages 145-150; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
```

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SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;

alignment_scores:
           Quality:  747.00              Length:    747
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-43 x V54990   ..

 Align seg 1/1  to: V54990  from: 1  to: 3555

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    550 TCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATT 599

    129 eLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleS 146
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    600 TTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTT 649

    146 erPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 162
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    650 CATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCT 699

    163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    700 CCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCATTAATGG 749

    179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    750 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 799

    196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    800 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 849

    213 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 229
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    850 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 899

    229 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 246
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    900 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 949

    246 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 262
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    950 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 999

    263 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 279
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   1000 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 1049

    279 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 296
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   1050 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 1099

    296 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 312
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    313 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 329
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    346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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seq_documentation_block:
ID   V54991 standard; DNA; 3218 BP.
AC   V54991;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2457
FT                   /*tag= a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71355.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 153-157; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3218 BP;    1080 A;    595 C;    561 G;    982 T;


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             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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     163 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGl 179
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     179 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 196
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     414 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 463

     196 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 212
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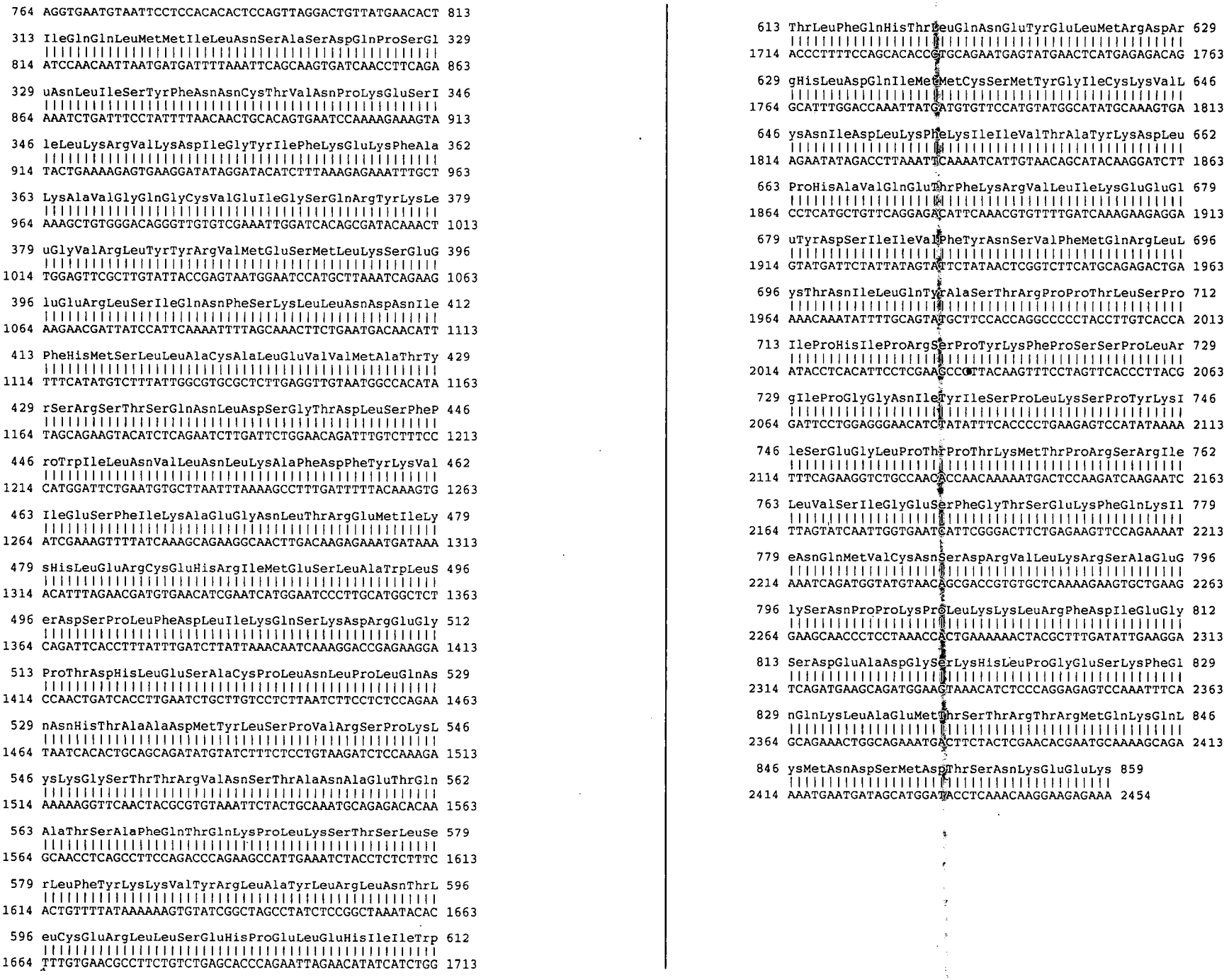
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346 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 362
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Date: Feb 13, 2000  2:38 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

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N_Geneseq_36:Q41545  +  687.00 10761.53  0.0       2994  ! Retinoblastoma gene. Method c
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N_Geneseq_36:X00737  +  687.00 10761.53  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:X04501  +  636.00  9957.68  0.0       4597  ! Human retinoblastoma gene cDNA
N_Geneseq_36:V58451  +  628.00  9834.12  0.0       3383  ! Modified retinoblastoma tumour
N_Geneseq_36:Q70536  +  600.00  9392.31  0.0       4597  ! Human retinoblastoma gene. Dia
N_Geneseq_36:N81369  +  586.00  9172.44  0.0       4597  ! Human retinoblastoma gene Diag
N_Geneseq_36:Q86398  +  586.00  9175.35  0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:Q90059  +  586.00  9175.35  0.0       2995  ! Retinoblastoma tumour suppress
N_Geneseq_36:N90489  +  474.00  7412.87  0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261  +  286.00  4461.05  7.0e-241  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502  +   65.00   980.91  4.9e-47   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490  +   55.00   823.91  2.7e-38   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:N91077  +   10.00   134.42  6.91      1433  ! Sequence encoding alpha-1-anti
N_Geneseq_36:Q55750  -   10.00   134.09  7.21      1505  ! Genomic clone G11F, includes a
N_Geneseq_36:Q67401  +   10.00   121.00  38.64     10366  ! Huntingtin DNA\IT15 gene. New
N_Geneseq_36:T02461  +   10.00   133.34  7.94      1680  ! Wilms' tumour WT1 cDNA. Monocl
N_Geneseq_36:T02462  +   10.00   139.96  3.40      633  ! Wilms' tumour antigen WT1-6F cD
N_Geneseq_36:Q99257  +   10.00   129.78  12.54     2841  ! Yeast coagulation gene FLO8. Y
N_Geneseq_36:T42476  -   10.00   139.83  3.45      645  ! HuntL4 coding sequence. HuntL a
N_Geneseq_36:T45133  +   10.00   142.17  2.56      457  ! Wilms' tumour gene exon 1. Leuk
N_Geneseq_36:T75529  +   10.00   139.96  3.40      633  ! cDNA encoding Wilms' tumour pro
N_Geneseq_36:T97924  +   10.00   121.00  38.64     10366  ! Composite sequence of a novel
N_Geneseq_36:T88434  -   10.00   131.53  10.02     2195  ! Human 5-lipoxygenase gene p
N_Geneseq_36:V05828  +   10.00   121.00  38.64     10366  ! Human huntingtin coding se
N_Geneseq_36:V17757  +   10.00   129.49  13.01     2965  ! Fractionated X irradiation-
N_Geneseq_36:V27112  -   10.00   112.73  111.61    35099  ! Adenovirus 17. Recombinant
N_Geneseq_36:X15842  +   10.00   142.17  2.56      457  ! Nucleotide sequence of the s
N_Geneseq_36:X18930  +   10.00   141.36  2.84      515  ! Human huntingtin gene. Trans

seq_name: N_Geneseq_36:V58449

seq_documentation_block:
ID   V58449 standard; DNA; 3161 BP.
AC   V58449;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2400
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69373.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 203-207; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3161 BP;    1037 A;    619 C;    586 G;    919 T;


alignment_scores:
            Quality:  797.00              Length:    797
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x V58449   ..

 Align seg 1/1  to: V58449  from: 1  to: 3161

       1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAl 17
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       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGC 56

      17 aAlaGluProProAlaProProProProProProProGluGluAspProG 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 CGCGGAACCCCCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAG 106

      34 luGlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGlu 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 AGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAA 156

      51 GluThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIlePr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACC 206

      67 oAspHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerServ 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 AGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTG 256

      84 alAspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGly 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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 257 TGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

 101 IleCysIlePheIleAlaAlaValAspLeuAlaValIleProIleAsnGl 117
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGCTGTTATACCCATTAATGG 356

 117 ySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaL 134
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 357 TTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAA 406

 134 ysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluHis 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 407 AACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACAT 456

 151 GluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIlePr 167
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 457 GAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACC 506

 167 oPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValG 184
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 507 TTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 556

 184 luAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeu 200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 557 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTA 606

 201 AspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIl 217
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 607 GATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTAT 656

 217 eAspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluG 234
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 657 AGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAG 706

 234 luValAsnValIleProProHisThrProValArgThrValMetAsnThr 250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 707 AGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACT 756

 251 IleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGl 267
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 757 ATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGA 806

 267 uAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerI 284
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 807 AAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTA 856

 284 leLeuLysArgValLysAspIleGlyTyrIlePheLysGluLysPheAla 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 857 TACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCT 906

 301 LysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLe 317
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 907 AAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACT 956

 317 uGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluG 334
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 957 TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAG 1006

 334 luGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIle 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1007 AAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATT 1056

 351 PheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTy 367
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1057 TTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATA 1106

 367 rSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheP 384
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1107 TAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCC 1156

 384 roTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysVal 400
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1157 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTG 1206

 401 IleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLy 417
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1207 ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAA 1256

 417 sHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuS 434
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 434 erAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGluGly 450
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1307 CAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGA 1356

 451 ProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAs 467
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1357 CCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAA 1406

 467 nAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysL 484
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1407 TAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGA 1456

 484 ysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGln 500
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 501 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSe 517
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 517 rLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrL 534
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 534 euCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrp 550
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1607 TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGG 1656

 551 ThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspAr 567
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1657 ACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAG 1706

 567 gHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValL 584
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 584 ysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 600
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1757 AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTT 1806

 601 ProHisAlaValGlnGluThrPheLysArgValLeuIleLysGluGluGl 617
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1807 CCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGA 1856

 617 uTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuL 634
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1857 GTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGA 1906

 634 ysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerPro 650
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1907 AAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCA 1956

 651 IleProHisIleProArgSerProTyrLysPheProSerSerProLeuAr 667
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1957 ATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACG 2006

 667 gIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysI 684
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2007 GATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA 2056

 684 leSerGluGlyLeuProThrProThrLysMetThrProArgSerArgIle 700
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2057 TTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATC 2106
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     701 LeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIl 717
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2107 TTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAAT 2156

     717 eAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluG 734
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2157 AAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAG 2206

     734 lySerAsnProProLysProLeuLysLysLeuArgPheAspIleGluGly 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2207 GAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGA 2256

     751 SerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGl 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2257 TCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCA 2306

     767 nGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnL 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2307 GCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGA 2356

     784 ysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 797
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seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID Q04713 standard; cDNA; 2994 BP.
AC Q04713;
DT 11-OCT-1990 (first entry)
DE Cancer supressing gene (CSG).
KW Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW RB; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 139. .2922
FT /*tag= a
PN WO9005180-A.
PD 17-MAY-1990.
PF 30-OCT-1989; 004808.
PR 31-OCT-1988; US-265829.
PA (REGC) Univ of Caifornia.
PI Lee WH, Huang HJS;
DR WPI; 90-178822/23.
DR P-PSDB; R05305.
PT Controlling cancer -
PT by replacing ineffective cancer suppressing gene with cloned,
PT active gene.
PS Claim 35; Page 86; 105pp; English.
CC Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC By installing a working CSG, safe and specific treatment and
CC prophylaxis can be given to cancer patients.
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T;

alignment_scores:
Quality: 687.00 Length: 687
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: Q04713 from: 1 to: 2994

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     862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 961

     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     962 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 1011

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1012 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 1061

     177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1062 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 1111

     194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
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    1112 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1161

     211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

     227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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    1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 1261

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    1262 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1311

     261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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    1312 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1361

     277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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     294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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    1412 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1461

     311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1462 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1511

     327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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     344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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    1562 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1611

     361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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    1612 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1661

     377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1662 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1711

     394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1712 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

     411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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     444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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1862 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1911

 461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1912 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1961

 477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1962 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 2011

 494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2012 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

 511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

 527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 2161

 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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2162 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 2211

 561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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2212 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2261

 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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2362 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2411

 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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 644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
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 677 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 694
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 694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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2612 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2661

 711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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 727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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seq_name: N_Geneseq_36:Q41545

seq_documentation_block:
ID Q41545 standard; DNA; 2994 BP.
AC Q41545;
DT 24-AUG-1993 (first entry)
DE Retinoblastoma gene.
KW RB gene product; p56RB portion; cell cycle progression control;
KW combination; therapeutic methods; arrest; tumourigenesis;
KW regulation; physiological processes; blood cell prodn.;
KW gamete prodn.; ss.
OS Homo sapiens SR-40 cell line.
FH Key Location/Qualifiers
FT cds 139. .2925
FT /*tag= a
FT /note= "Rb protein"
PN WO9308267-A.
PD 29-APR-1993.
PF 16-OCT-1992; U08918.
PR 17-OCT-1991; US-778510.
PA (REGC) UNIV CALIFORNIA.
PI Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR WPI; 93-152462/18.
DR P-PSDB; R36534.
PT Method of controlling cell cycle progression - uses purified
PT retinoblastoma protein or fragment, for use in combination with
PT therapeutic methods to arrest tumorigenesis
PS Disclosure; Fig 9; 68pp; English.
CC The sequence is that of the retinoblastoma gene which encodes the
CC retinoblastoma (RB) protein which may be used as part of a method of
CC controlling cell cycle progression which may be used in combination
CC with therapeutic methods to arrest tumourigenesis in organisms. The
CC cell cycle can be reversibly arrested in a convenient and safe
CC manner. The protein is used in a compsn. is relatively inexpensive
CC and readily obtainable, and shows little or no toxic effects on
CC healthy cells. It is also compatible with other methods and devices
CC for regulating certain physiological processes of the body, such as
CC blood cell prodn. and gamete prodn. Fragments of the protein are
CC soluble in low concns. of glycerol thus enhancing their value in
CC pharmaceutical applicns.
SQ Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T;

alignment_scores:
Quality: 687.00 Length: 687
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-45 x Q41545 ..

Align seg 1/1 to: Q41545 from: 1 to: 2994

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 862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

 127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
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 912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 961

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 962 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 1011

 161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
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1012 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 1061

 177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
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1062 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 1111

 194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
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 211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
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1162 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1211

 227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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1212 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 1261

 244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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 261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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1312 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1361

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1362 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1411

 294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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 311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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 327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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 411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1861

 444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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1862 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1911

 461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1912 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1961

 477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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1962 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 2011

 494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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 561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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2212 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2261

 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
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 Align seg 1/1  to: Q72690  from: 1  to: 3233

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     606 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 655

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     756 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 805

     244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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     806 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 855

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     906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 955

     294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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     956 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1005

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    1006 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1055

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     377 rGlyThrAspLeuSerProTrpIleLeuAsnValLeuAsnLeuLysA 394
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    1306 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1355

     427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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    1356 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1405

     444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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    1406 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1455

     461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1456 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1505

 477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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1506 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 1555

 494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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 511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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 527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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1656 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 1705

 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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1706 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1755

 561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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 644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
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 677 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 694
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 694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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 711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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2206 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2255

 727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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 794 ysGluGluLys 797
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2456 AGGAAGAGAAA 2466

seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


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           Quality:  687.00            Length:    687
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58447  from: 1  to: 3461

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     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     687 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 736

     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     737 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 786

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
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     177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
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 211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
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 937 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 986

 227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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 987 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 1036

 244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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1037 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1086

 261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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1087 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1136

 277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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1137 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1186

 294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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1187 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1236

 311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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1237 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1286

 327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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1287 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1336

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1337 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1386

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1387 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1436

 377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
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1437 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1486

 394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
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1487 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1536

 411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1537 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1586

 427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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1637 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1686

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1687 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1736

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 494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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1887 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 1936

 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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1937 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1986

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1987 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2036

 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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2037 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 2086

 594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
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 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2137 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2186

 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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2187 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 2236

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2437 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2486

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2537 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2586

 761 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 777
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2587 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2636

 777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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 794 ysGluGluLys 797
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    2687 AGGAAGAGAAA 2697

seq_name: N_Geneseq_36:V58448

seq_documentation_block:
ID   V58448 standard; DNA; 3347 BP.
AC   V58448;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2586
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69372.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 196-200; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3347 BP;    1096 A;    650 C;    617 G;    984 T;


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     211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
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     227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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     873 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 922

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     261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     973 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1022

     277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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     294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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    1073 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1122

     311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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     327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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     361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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     377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
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    1323 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1372

     394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1373 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1422

     411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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    1423 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1472

     427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1473 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1522

     444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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    1523 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1572

     461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1573 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1622

     477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1623 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 1672

     494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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     511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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    527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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   1773 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 1822

    544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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    561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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   1873 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1922

    577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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   1923 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 1972

    594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
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   2023 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2072

    627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   2073 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 2122

    644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   2123 GGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2172

    661 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 677
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   2173 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2222

    677 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 694
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   2223 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAA 2272

    694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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   2273 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2322

    711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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   2323 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2372

    727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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   2373 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2422

    744 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 760
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   2423 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2472

    761 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 777
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    777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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seq_name: N_Geneseq_36:V58450

seq_documentation_block:
ID   V58450 standard; DNA; 3377 BP.
AC   V58450;

DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2616
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69374.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 210-215; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3377 BP;    1113 A;    654 C;    626 G;    984 T;


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            Quality:  687.00              Length:    687
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     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     603 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 652

     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     653 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 702

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     703 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 752

     177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     753 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 802

     194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     803 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 852

     211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     853 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 902

     227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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     903 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 952

     244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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 953 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1002

 261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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1003 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1052

 277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1053 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1102

 294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1103 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1152

 311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1153 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1202

 327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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 344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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1253 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1302

 361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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1303 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1352

 377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
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1353 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1402

 394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1403 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1452

 411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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 427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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1503 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1552

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 461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1603 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1652

 477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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1903 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1952

 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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1953 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 2002

 594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2003 TAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2052

 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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2103 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 2152

 644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
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2153 GGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2202

 661 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 677
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 677 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 694
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2353 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2402

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2453 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2502

 761 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 777
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 777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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 794 ysGluGluLys 797
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seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
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FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


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     930 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 979

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     980 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1029

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     244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1280 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1329

      311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1330 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1379

      327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1380 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1429

      344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1430 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1479

      361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1480 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1529

      377 rGlyThrAspLeuSerProTrpIleLeuAsnValLeuAsnLeuLysA 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1530 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1579

      394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1580 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1629

      411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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    1630 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1679

      427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
          |||||||||||||||||||||||||||||||||||||||||||||||||||
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      444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
          |||||||||||||||||||||||||||||||||||||||||||||||||||
    1730 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1779

      461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
          |||||||||||||||||||||||||||||||||||||||||||||||||||
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      477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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      494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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    1880 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1929

      511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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    1930 TTGAAATCTACCTCTCTTTGACTGTTTTATAAAAAAGTGTATCGGCTAGC 1979

      527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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      561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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    2230 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2279

     627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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    2330 GGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2379

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    2380 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2429

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     694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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    2480 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2529

     711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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     727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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     744 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 760
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     761 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 777
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     794 ysGluGluLys 797
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    2780 AGGAAGAGAAA 2790

seq_name: N_Geneseq_36:V58440

seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  687.00              Length:    687
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58440  from: 1  to: 3555

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     730 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 779

     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     780 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 829

     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     830 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 879

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     880 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 929

     177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     930 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 979

     194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     980 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1029

     211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1030 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 1079

     227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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    1080 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 1129

     244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1130 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1179

     261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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    1180 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1229

     277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1230 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1279

     294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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    1280 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1329
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 311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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1330 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1379

 327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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1380 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1429

 344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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1430 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1479

 361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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1480 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1529

 377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
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1530 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1579

 394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1580 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1629

 411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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1630 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1679

 427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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 444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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1730 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1779

 461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1780 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1829

 477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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 494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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1880 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1929

 511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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1930 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1979

 527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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1980 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 2029

 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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2030 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 2079

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 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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2130 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 2179

 594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
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2180 TAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2229

 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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2280 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 2329

 644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
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2330 GGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2379

 661 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 677
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2380 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2429

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2430 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAA 2479

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 727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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2580 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2629

 744 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 760
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 761 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 777
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seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
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CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


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 Percent Similarity: 100.000   Percent Identity: 100.000

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     631 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 680

     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
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     681 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 730

     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
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     731 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 780

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
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     177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
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     831 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 880

     194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     881 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 930

     211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
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     931 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 980

     227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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     981 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 1030

     244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1031 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1080

     261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1081 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1130

     277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1131 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1180

     294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1181 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1230

     311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1231 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1280

     327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1281 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1330

     344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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    1331 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1380

     361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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    1381 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430

     377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
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    1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1480

     394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
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    1481 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1530

     411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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     427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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    1581 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1630

     444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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     461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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     477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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    1731 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 1780

     494 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 510
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     511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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     527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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    1881 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 1930

     544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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    1931 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1980

     561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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    1981 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2030

     577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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     627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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    2181 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 2230
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     694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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    2381 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2430

     711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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    2431 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2480

     727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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     744 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 760
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    2531 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2580

     761 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 777
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    2581 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2630

     777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;

alignment_scores:
            Quality:  687.00              Length:    687
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x V58442 *  ..

 Align seg 1/1  to: V58442  from: 1  to: 3392

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     568 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 617

     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
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     618 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 667

     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     668 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 717

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     718 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 767

     177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
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     768 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 817

     194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
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     818 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 867

     211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
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     868 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 917

     227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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     918 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 967

     244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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     968 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1017

     261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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    1018 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1067

     277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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    1068 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1117

     294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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    1118 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1167

     311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1168 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1217

     327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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    1218 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1267

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    1268 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1317

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     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1368 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1417

 394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1418 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1467

 411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1468 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1517

 427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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1518 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1567

 444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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1568 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1617

 461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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1868 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1917

 561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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1918 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1967

 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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1968 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 2017

 594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
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2018 TAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2067

 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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2068 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 2117

 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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 694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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 727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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2418 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2467

 744 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 760
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 761 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 777
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2518 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2567

 777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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2618 AGGAAGAGAAA 2628
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seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;


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              Ratio:  1.000                 Gaps:      0
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alignment_block:
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    127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
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    144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
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    599 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 648

    161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
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    649 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 698

    177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
        ||||||||||||||||||||||||||||||||||||||||||||||||||
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    194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    749 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 798

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    799 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 848

    227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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    849 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 898

    244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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    899 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 948

    261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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    949 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 998

    277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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    999 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1048

    294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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    311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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   1099 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1148

    327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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    477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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   1749 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 1798

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   1899 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 1948

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     777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


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            Quality:  687.00              Length:    687
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
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     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     542 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 591

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
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     227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
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     792 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 841

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     261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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     327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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    1242 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1291

     394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
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    1292 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1341

     411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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1942 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 1991

 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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 644 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 660
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seq_documentation_block:
ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;


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 389 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 438

 161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
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 439 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 488

 177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
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 489 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 538

 194 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 210
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 539 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 588

 211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 589 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 638

 227 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 244
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 639 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 688

 244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 689 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 738

 261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 739 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 788

 277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 789 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 838

 294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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 839 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 888

 311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 889 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 938

 327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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 939 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 988

 344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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 361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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 377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
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 411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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 444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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 461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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1339 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1388

 477 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 494
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 511 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 527
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 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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1589 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1638

 561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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1639 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1688

 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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 594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
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 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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1989 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAA 2038

 694 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 710
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2039 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2088

 711 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 727
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2089 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2138

 727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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2139 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2188

 744 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 760
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2189 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2238
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seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;


alignment_scores:
           Quality:  687.00            Length:    687
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-45 x V58446   ..

 Align seg 1/1  to: V58446  from: 1  to: 3323

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     499 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 548

     127 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 144
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     549 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 598

     144 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 160
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     599 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 648

     161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     649 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 698

     177 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 194
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     699 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 748

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     749 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 798

     211 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 227
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     799 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 848

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     849 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 898

     244 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 260
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     899 TTAGGACTGTTATGAACAGTATCCAACAATTAATGATGATTTTAAATTCA 948

     261 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 277
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     277 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 294
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     999 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1048

     294 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 310
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    1049 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1098

     311 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 327
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    1099 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1148

     327 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 344
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     344 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 360
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    1199 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1248

     361 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 377
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    1249 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1298

     377 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 394
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    1299 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1348

     394 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 410
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    1349 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1398

     411 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 427
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     427 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 444
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     444 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 460
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    1499 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1548

     461 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 477
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    1549 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1598

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1649 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1698

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 527 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 544
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1749 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 1798

 544 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 560
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1799 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1848

 561 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 577
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 577 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 594
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 594 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 610
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1949 TAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1998

 611 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 627
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 627 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 644
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 727 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 744
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2449 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2498

 777 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 794
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 794 ysGluGluLys 797
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Date: Feb 13, 2000  2:39 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
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 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
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Query length: 869
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence            Strd Orig    ZScore    EScore Len   ! Documentation  ..
N_Geneseq_36:V58450   +  869.00 13671.22  0.0       3377  ! Modified retinoblastoma tumou
N_Geneseq_36:Q04713   +  687.00 10802.67  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545   +  687.00 10802.67  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:Q72690   +  687.00 10802.15  0.0       3233  ! Retinoblastoma 94kD therapeut
N_Geneseq_36:V58447   +  687.00 10801.68  0.0       3461  ! Modified retinoblastoma tumou
N_Geneseq_36:V58448   +  687.00 10801.91  0.0       3347  ! Modified retinoblastoma tumou
N_Geneseq_36:V58449   +  687.00 10802.30  0.0       3161  ! Modified retinoblastoma tumou
N_Geneseq_36:V58452   +  687.00 10801.50  0.0       3554  ! Modified retinoblastoma tumou
N_Geneseq_36:V58440   +  687.00 10801.50  0.0       3555  ! Modified retinoblastoma tumou
N_Geneseq_36:V58441   +  687.00 10801.69  0.0       3455  ! Modified retinoblastoma tumou
N_Geneseq_36:V58442   +  687.00 10801.82  0.0       3392  ! Modified retinoblastoma tumou
N_Geneseq_36:V58443   +  687.00 10801.96  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:V58444   +  687.00 10802.08  0.0       3266  ! Modified retinoblastoma tumou
N_Geneseq_36:V58445   +  687.00 10802.41  0.0       3113  ! Modified retinoblastoma tumou
N_Geneseq_36:V58446   +  687.00 10801.96  0.0       3323  ! Modified retinoblastoma tumou
N_Geneseq_36:V54990   +  687.00 10801.50  0.0       3555  ! DNA sequence of the specifica
N_Geneseq_36:V54991   +  687.00 10802.18  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:V40004   +  687.00 10802.67  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737   +  687.00 10802.67  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:X04501   +  636.00  9995.69  0.0       4597  ! Human retinoblastoma gene cDNA
N_Geneseq_36:V58451   +  628.00  9871.66  0.0       3383  ! Modified retinoblastoma tumour
N_Geneseq_36:Q70536   +  600.00  9428.12  0.0       4597  ! Human retinoblastoma gene. Dia
N_Geneseq_36:N81369   +  586.00  9207.40  0.0       4597  ! Human retinoblastoma gene Diag
N_Geneseq_36:Q86398   +  586.00  9210.33  0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:Q90059   +  586.00  9210.33  0.0       2995  ! Retinoblastoma tumour suppress
N_Geneseq_36:N90489   +  474.00  7440.98  0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261   +  286.00  4477.70  8.3e-242  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502   +   65.00   983.99  3.3e-47   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490   +   55.00   826.37  2.0e-38   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:N91077   +   10.00   134.30  7.02      1433  ! Sequence encoding alpha-1-anti
N_Geneseq_36:Q55750   -   10.00   133.97  7.33      1505  ! Genomic clone G11F, includes a
N_Geneseq_36:Q67401   +   10.00   120.76  39.87     10366  ! Huntingtin DNA\IT15 gene. New
N_Geneseq_36:T02461   +   10.00   133.21  8.07      1680  ! Wilms' tumour WT1 cDNA. Monocl
N_Geneseq_36:T02462   +   10.00   139.89  3.43      633  ! Wilms' tumour antigen WT1-6F cD
N_Geneseq_36:Q99257   +   10.00   129.62  12.80     2841  ! Yeast coagulation gene FLO8. Y
N_Geneseq_36:T42476   -   10.00   139.76  3.48      645  ! HuntL4 coding sequence. HuntL a
N_Geneseq_36:T45133   +   10.00   142.12  2.58      457  ! Wilms' tumour gene exon 1. Leuk
N_Geneseq_36:T75529   +   10.00   139.89  3.43      633  ! cDNA encoding Wilms' tumour pro
N_Geneseq_36:T97924   +   10.00   120.76  39.87     10366  ! Composite sequence of a novel
N_Geneseq_36:T88434   -   10.00   131.38  10.21     2195  ! Human 5-lipoxygenase gene p
N_Geneseq_36:V05828   +   10.00   120.76  39.87     10366  ! Human huntingtin coding se
N_Geneseq_36:V17757   +   10.00   129.32  13.29     2965  ! Fractionated X irradiation-
N_Geneseq_36:V27112   -   10.00   112.41  116.30    35099  ! Adenovirus 17. Recombinant
N_Geneseq_36:X15842   +   10.00   142.12  2.58      457  ! Nucleotide sequence of the s
N_Geneseq_36:X18930   +   10.00   141.30  2.86      515  ! Human huntingtin gene. Trans

seq_name: N_Geneseq_36:V58450

seq_documentation_block:
ID   V58450 standard; DNA; 3377 BP.
AC   V58450;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2616
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69374.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 210-215; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3377 BP;    1113 A;    654 C;    626 G;    984 T;


alignment_scores:
            Quality:  869.00              Length:    869
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x V58450   ..

 Align seg 1/1  to: V58450  from: 1  to: 3377

       1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAl 17
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       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGC 56

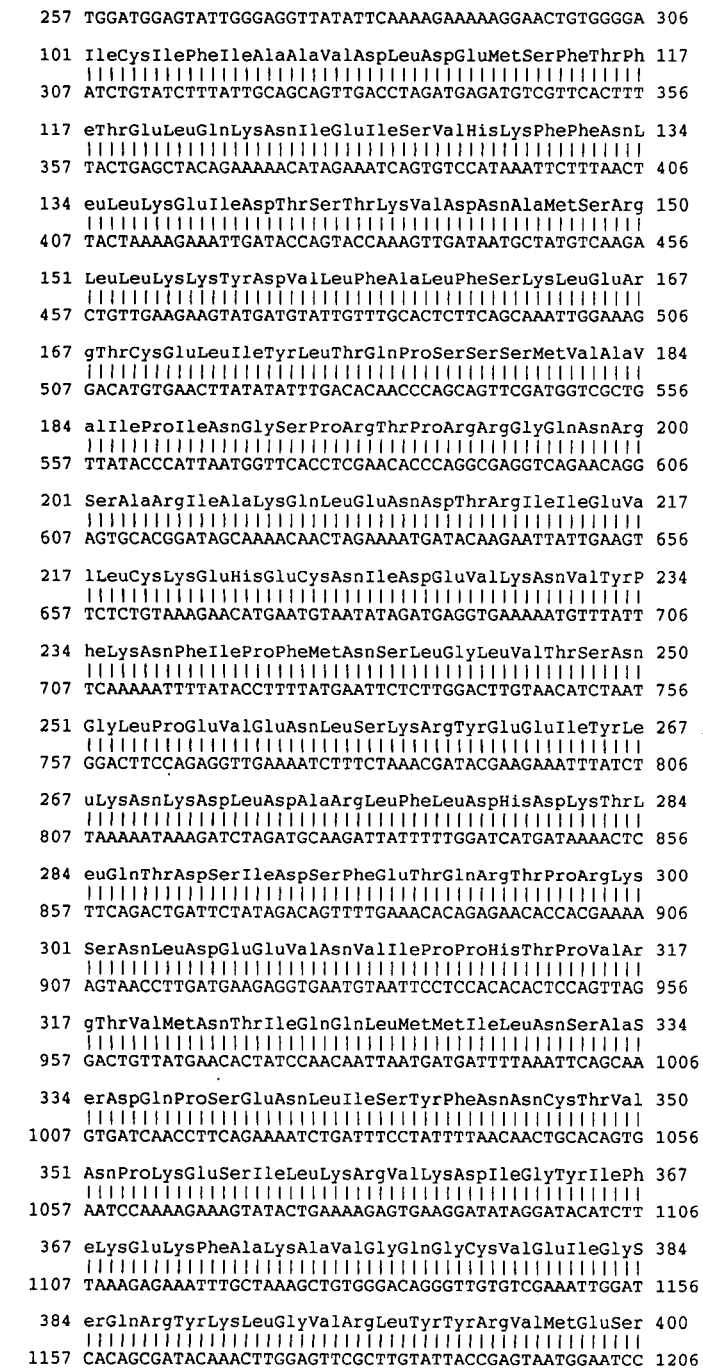
      17 aAlaGluProProAlaProProProProProProProGluGluAspProG 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      57 CGCGGAACCCCCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAG 106

      34 luGlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGlu 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 AGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAA 156

      51 GluThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIlePr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACC 206

      67 oAspHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerServ 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 AGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTG 256

      84 alAspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGly 100
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257 TGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306
101 IleCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrPh 117
307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTT 356
117 eThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnL 134
357 TACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACT 406
134 euLeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArg 150
407 TACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGA 456
151 LeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluAr 167
457 CTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAG 506
167 gThrCysGluLeuIleTyrLeuThrGlnProSerSerSerMetValAlaV 184
507 GACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATGGTCGCTG 556
184 alIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsnArg 200
557 TTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGG 606
201 SerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluVa 217
607 AGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGT 656
217 lLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnValTyrP 234
657 TCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATT 706
234 heLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsn 250
707 TCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAAT 756
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757 GGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCT 806
267 uLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrL 284
807 TAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTC 856
284 euGlnThrAspSerIleAspSerPheGluThrGlnArgThrProArgLys 300
857 TTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAA 906
301 SerAsnLeuAspGluGluValAsnValIleProProHisThrProValAr 317
907 AGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAG 956
317 gThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaS 334
957 GACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAA 1006
334 erAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrVal 350
1007 GTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTG 1056
351 AsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePh 367
1057 AATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTT 1106
367 eLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIleGlyS 384
1107 TAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGAT 1156
384 erGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSer 400
1157 CACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCC 1206
401 MetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLe 417
1207 ATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACT 1256
417 uLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluV 434
1257 TCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGG 1306
434 alValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGly 450
1307 TTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGA 1356
451 ThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPh 467
1357 ACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTT 1406
467 eAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsnLeuT 484
1407 TGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGA 1456
484 hrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGlu 500
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501 SerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSe 517
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517 rLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuA 534
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584 ysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyr 600
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601 LeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLe 617
1807 CTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATT 1856
617 uGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrG 634
1857 AGAACATATCATCTGGACCGTTTTCCAGCACACCCTGCAGAATGAGTATG 1906
634 luLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyr 650
1907 AACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTAT 1956
651 GlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleValTh 667
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667 rAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValL 684
2007 AGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTT 2056
684 euIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSerVal 700
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     701 PheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgPr 717
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     717 oProThrLeuSerProIleProHisIleProArgSerProTyrLysPheP 734
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    2157 CCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTC 2206

     734 roSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeu 750
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    2207 CTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTG 2256

     751 LysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetTh 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2257 AAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGAC 2306

     767 rProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerG 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     851 ArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGl 867
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     867 uGluLys 869
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    2607 AGAGAAA 2613

seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;

alignment_scores:
            Quality:  687.00              Length:    687
              Ratio:  1.000                 Gaps:      0
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alignment_block:
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 Align seg 1/1  to: Q04713  from: 1  to: 2994

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     299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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     333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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     349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
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     366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
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     383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
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     399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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    1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1561

     416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
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 449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1662 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1711

 466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1712 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

 483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
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1762 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1811

 499 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 516
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1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1861

 516 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 532
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1862 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1911

 533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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1912 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1961

 549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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1962 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 2011

 566 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 582
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2012 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 2061

 583 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 599
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2062 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 2111

 599 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 616
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2112 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 2161

 616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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2162 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 2211

 633 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 649
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2212 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 2261

 649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
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 666 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 682
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 683 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 699
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 699 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 716
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2412 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 2461

 716 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 732
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2462 GGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2511

 733 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 749
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2512 TTTCCTAGTTCACCCTTAGGGATTCCTGGAGGGAACATCTATATTTCACC 2561

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2562 CCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAA 2611

 766 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 782
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 783 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 799
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2712 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2761

 816 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 832
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2762 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2811

 833 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 849
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2812 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2861

 849 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 866
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2862 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 2911

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seq_name: N_Geneseq_36:Q41545

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seq_documentation_block:
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
```

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CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


alignment_scores:
            Quality:  687.00              Length:    687
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x Q41545   ..

 Align seg 1/1  to: Q41545  from: 1  to: 2994

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     862 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 911

     199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
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     912 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 961

     216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     962 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 1011

     233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
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    1012 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 1061

     249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
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     266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
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     299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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     316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
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    1262 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1311

     333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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     349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
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     383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
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     399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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    1512 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1561

     416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
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    1562 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1611

     433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
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    1612 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1661

     449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
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    1662 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1711

     466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
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    1712 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1761

     483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
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    1812 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1861

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     533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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     549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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     616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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    2162 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 2211

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     649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
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     733 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 749
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     849 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 866
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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag= a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


alignment_scores:
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              Ratio:  1.000                 Gaps:      0
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 Percent Similarity: 100.000   Percent Identity: 100.000

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     199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
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     506 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 555

     233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
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     556 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 605

     249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
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     266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
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     656 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 705

     283 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 299
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     706 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 755

     299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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     756 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 805

     316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
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     806 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 855

     333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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     349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
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     906 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 955

     366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
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     956 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1005

     383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
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    1006 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1055

     399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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    1056 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1105

     416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
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    1106 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1155

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     449 rGlyThrAspLeuSerProTrpIleLeuAsnValLeuAsnLeuLysA 466
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 549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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 866 ysGluGluLys 869
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2456 AGGAAGAGAAA 2466
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


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           Quality:  687.00              Length:    687
             Ratio:  1.000                 Gaps:      0
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alignment_block:
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 199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
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 687 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 736

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 316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
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 333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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1087 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1136

 349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
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1137 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1186

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 483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
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seq_name: N_Geneseq_36:V58448

seq_documentation_block:
ID   V58448 standard; DNA; 3347 BP.
AC   V58448;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2586
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69372.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 196-200; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3347 BP;    1096 A;    650 C;    617 G;    984 T;


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     299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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     349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
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    1023 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1072

     366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
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     383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
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    1123 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1172

     399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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    1173 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1222

     416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
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     433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
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    1273 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1322

     449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
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     466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
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    1373 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1422

     483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
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 533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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 549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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 616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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 633 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 649
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1873 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1922

 649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
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1923 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 1972

 666 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 682
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 683 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 699
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 699 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 716
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2123 GGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 2172

 733 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 749
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 749 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 766
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 766 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 782
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2273 TGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACT 2322

 783 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 799
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2323 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2372

 799 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 816
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2373 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2422

 816 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 832
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2423 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2472

 833 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 849
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 849 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 866
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seq_name: N_Geneseq_36:V58449

seq_documentation_block:

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ID   V58449 standard; DNA; 3161 BP.
AC   V58449;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2400
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69373.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 203-207; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3161 BP;    1037 A;    619 C;    586 G;    919 T;
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alignment_scores:
            Quality:  687.00              Length:    687
              Ratio:  1.000                 Gaps:      0
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 Align seg 1/1  to: V58449  from: 1  to: 3161

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     337 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 386

     199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     387 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 436

     216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     437 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 486

     233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
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487 TATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACATC 536
249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
537 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 586
266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
587 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 636
283 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 299
637 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 686
299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
687 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 736
316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
737 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 786
333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
787 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 836
349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
837 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 886
366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
887 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 936
383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
937 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 986
399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
987 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1036
416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
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433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
1087 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1136
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466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
1187 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1236
483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
1237 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1286
499 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 516
1287 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1336
516 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 532
1337 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1386
533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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1537 TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGC 1586
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1587 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 1636
616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
1637 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1686
633 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 649
1687 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1736
649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
1737 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 1786
666 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 682
1787 TAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1836
683 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 699
1837 GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTC 1886
699 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 716
1887 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 1936
716 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 732
1937 GGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAG 1986
733 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 749
1987 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 2036
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799 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 816
2187 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2236
816 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 832
2237 TACGCTTTGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTC 2286
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seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


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     780 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 829

     216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
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     249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     930 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 979

     266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
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     980 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 1029

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    1680 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1729

     516 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 532
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     533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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    1780 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1829

     549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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    1830 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 1879

     566 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 582
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1880 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1929

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1980 CTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAG 2029

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 749 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 766
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seq_name: N_Geneseq_36:V58440

seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


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           Quality:  687.00              Length:    687
             Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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     199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
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     780 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 829

     216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
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     830 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 879

     233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
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     249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
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     930 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 979

     266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
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     283 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 299
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1080 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 1129

 316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
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 399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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1380 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1429

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 599 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 616
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 616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID   V58441 standard; DNA; 3455 BP.
AC   V58441;
DT   02-DEC-1998  (first entry)
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DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2694
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69365.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 142-147; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3455 BP;    1153 A;    631 C;    627 G;    1044 T;


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     433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1381 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1430

     449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1431 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1480

     466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1481 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1530

     483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
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    1531 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1580

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     516 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 532
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     533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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    1681 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1730

     549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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     566 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 582
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    1781 CTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA 1830

     583 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 599
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         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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     633 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 649
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     649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
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     683 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 699
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     699 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 716
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     716 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 732
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     749 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 766
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     766 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 782
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     816 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 832
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     833 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 849
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     849 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 866
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    2631 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 2680

     866 ysGluGluLys 869
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    2681 AGGAAGAGAAA 2691

seq_name: N_Geneseq_36:V58442

seq_documentation_block:
ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a

PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence 3392 BP;  1137 A;  614 C;  607 G;  1034 T;

alignment_scores:
            Quality:  687.00              Length:    687
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x V58442   ..

 Align seg 1/1  to: V58442  from: 1  to: 3392

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     568 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 617

     199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     618 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 667

     216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     668 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 717

     233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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     768 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 817

     266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
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     818 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 867

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     868 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 917

     299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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     918 AAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG 967

     316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
     968 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 1017

     333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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    1018 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 1067

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1068 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1117

 366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
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1118 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1167

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1168 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1217

 399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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1218 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1267

 416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
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1268 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1317

 433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
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1318 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1367

 449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
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1368 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1417

 466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
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1418 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1467

 483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1468 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1517

 499 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 516
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1518 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1567

 516 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 532
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1568 AATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCT 1617

 533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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 549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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1668 TCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTA 1717

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 599 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 616
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 616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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 633 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 649
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1918 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1967

 649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
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1968 GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTG 2017

 666 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 682
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2018 TAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 2067

 683 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 699
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 699 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 716
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2118 GGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA 2167

 716 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 732
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 749 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 766
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 766 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 782
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2368 TCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGT 2417

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2618 AGGAAGAGAAA 2628

seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
```

DR WPI; 98-480788/41.
DR P-PSDB; W69367.
PT Retinoblastoma suppressor protein with N-terminal modification - inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 158-162; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor protein (RTSP) of the invention. The proteins can be used for inhibiting cellular proliferation, when coadministered with a p53 protein. The RTSPs can be used for treating diseases characterised by abnormal cellular proliferation, particularly cancers. The RTSPs have a broader spectrum of activity than wild type RTSPs.
SQ Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T;

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Quality: 687.00 Length: 687
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: V58443 from: 1 to: 3323

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 199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
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 549 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 598

 216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
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 599 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 648

 233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
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 249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
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 699 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 748

 266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
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 749 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 798

 283 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 299
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 799 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 848

 299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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 316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
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 899 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 948

 333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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 349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
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 999 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 1048

 366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
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1049 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 1098

 383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
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1099 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1148

 399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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1149 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 1198

 416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
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 433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
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 449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
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seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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  216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
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1142 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1191

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seq_documentation_block:
ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;
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     689 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 738

     333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     739 GCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCAC 788

     349 rValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrI 366
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     789 AGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACA 838

     366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     839 TCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATT 888

     383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     889 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 938

     399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     939 ATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCA 988

     416 ysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 432
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     989 AACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTT 1038

     433 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSe 449
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1039 GAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTC 1088

     449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1089 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1138

     466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1139 CCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAAC 1188

     483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     499 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 516
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     533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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     549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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     566 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 582
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     616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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     649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
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     666 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 682
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     683 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 699
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     716 rgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 732
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     733 PheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSerPr 749
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    1939 TTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC 1988
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     749 oLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysM 766
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     766 etThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyThr 782
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     783 SerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVa 799
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     799 lLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysL 816
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    2139 GCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAAC 2188

     816 euArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeu 832
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     833 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrAr 849
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    2239 CCAGGAGAGTCCAAATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCG 2288

     849 gThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnL 866
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    2289 AACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACA 2338

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    2339 AGGAAGAGAAA 2349

seq_name: N_Geneseq_36:V58446

seq_documentation_block:
ID   V58446 standard; DNA; 3323 BP.
AC   V58446;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69370.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 180-184; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1099 A;    647 C;    588 G;    989 T;


alignment_scores:
            Quality:  687.00              Length:    687
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-47 x V58446   ..
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Align seg 1/1  to: V58446  from: 1  to: 3323

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    499 GCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAA 548

    199 nArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleG 216
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    549 CAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 598

    216 luValLeuCysLysGluHisGluCysAsnIleAspGluValLysAsnVal 232
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    599 AAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTT 648

    233 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSe 249
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    649 TATTTCAAAAATTTTATAGCTTTTATGAATTCTCTTGGACTTGTAACATC 698

    249 rAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleT 266
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    699 TAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTT 748

    266 yrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLys 282
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    749 ATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAA 798

    283 ThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrProAr 299
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    799 ACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACG 848

    299 gLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProV 316
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    316 alArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSer 332
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    899 TTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA 948

    333 AlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCysTh 349
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    366 lePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluIle 382
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    383 GlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGl 399
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   1099 GGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGA 1148

    399 uSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerL 416
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    449 rGlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysA 466
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   1299 TGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAG 1348

    466 laPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyAsn 482
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 483 LeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMe 499
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1399 TTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCAT 1448

 499 tGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysG 516
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1449 GGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC 1498

 516 lnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysPro 532
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 533 LeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSe 549
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1549 CTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTTTC 1598

 549 rProValArgSerProLysLysLysGlySerThrThrArgValAsnSerT 566
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 566 hrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysPro 582
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 583 LeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAl 599
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 599 aTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProG 616
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 616 luLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlu 632
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1799 AATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAG 1848

 633 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMe 649
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1849 TATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCAT 1898

 649 tTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIleV 666
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 666 alThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArg 682
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1949 TAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGT 1998

 683 ValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSe 699
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 699 rValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrA 716
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OM of: US-09-026-459A-49 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 13, 2000  2:41 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=oligo.rng -GAPOP=4.500
 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
 -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-026-459A-49
Query length: 871
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence              Strd Orig    ZScore    EScore Len  ! Documentation  ..
N_Geneseq_36:V58451   +   871.00 13679.65  0.0       3383  ! Modified retinoblastoma tumou
N_Geneseq_36:Q04713   +   628.00  9855.83  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545   +   628.00  9855.83  0.0       2994  ! Retinoblastoma gene. Method of
N_Geneseq_36:Q72690   +   628.00  9855.30  0.0       3233  ! Retinoblastoma 94kD therapeuti
N_Geneseq_36:V58447   +   628.00  9854.83  0.0       3461  ! Modified retinoblastoma tumour
N_Geneseq_36:V58448   +   628.00  9855.06  0.0       3347  ! Modified retinoblastoma tumour
N_Geneseq_36:V58449   +   628.00  9855.45  0.0       3161  ! Modified retinoblastoma tumour
N_Geneseq_36:V58450   +   628.00  9855.00  0.0       3377  ! Modified retinoblastoma tumour
N_Geneseq_36:V58452   +   628.00  9854.65  0.0       3554  ! Modified retinoblastoma tumour
N_Geneseq_36:V58440   +   628.00  9854.65  0.0       3555  ! Modified retinoblastoma tumour
N_Geneseq_36:V58441   +   628.00  9854.84  0.0       3455  ! Modified retinoblastoma tumour
N_Geneseq_36:V58442   +   628.00  9854.97  0.0       3392  ! Modified retinoblastoma tumour
N_Geneseq_36:V58443   +   628.00  9855.11  0.0       3323  ! Modified retinoblastoma tumour
N_Geneseq_36:V58444   +   628.00  9855.23  0.0       3266  ! Modified retinoblastoma tumour
N_Geneseq_36:V58445   +   628.00  9855.56  0.0       3113  ! Modified retinoblastoma tumour
N_Geneseq_36:V58446   +   628.00  9855.11  0.0       3323  ! Modified retinoblastoma tumour
N_Geneseq_36:V54990   +   628.00  9854.65  0.0       3555  ! DNA sequence of the specificat
N_Geneseq_36:V54991   +   628.00  9855.33  0.0       3218  ! DNA sequence of the specificat
N_Geneseq_36:V40004   +   628.00  9855.83  0.0       2994  ! Retinoblastoma protein RB. New
N_Geneseq_36:X00737   +   628.00  9855.82  0.0       2995  ! cDNA encoding a retinoblastoma
N_Geneseq_36:Q70536   +   591.00  9270.53  0.0       4597  ! Human retinoblastoma gene. Dia
N_Geneseq_36:Q90059   +   583.00  9147.55  0.0       2995  ! Retinoblastoma tumour suppress
N_Geneseq_36:X04501   +   577.00  9050.18  0.0       4597  ! Human retinoblastoma gene cDNA
N_Geneseq_36:N81369   +   527.00  8263.21  0.0       4597  ! Human retinoblastoma gene Diag
N_Geneseq_36:Q86398   +   527.00  8266.15  0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489   +   474.00  7428.37  0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261   +   286.00  4470.05  2.2e-241  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502   +    65.00   982.15  4.2e-47   18303  ! Human retinoblastoma gene. Is
N_Geneseq_36:N90490   +    55.00   824.81  2.4e-38   18177  ! DNA of human retinoblastoma g
N_Geneseq_36:N91077   +    10.00   133.95  7.34      1433  ! Sequence encoding alpha-1-anti
N_Geneseq_36:Q55750   -    10.00   133.62  7.67      1505  ! Genomic clone G11F, includes a
N_Geneseq_36:Q67401   +    10.00   120.39  41.83     10366  ! Huntingtin DNA\IT15 gene. New
N_Geneseq_36:T02461   +    10.00   132.86  8.44      1680  ! Wilms' tumour WT1 cDNA. Monocl
N_Geneseq_36:T02462   +    10.00   139.55  3.58      633  ! Wilms' tumour antigen WT1-6F cD
N_Geneseq_36:Q99257   +    10.00   129.26  13.40     2841  ! Yeast coagulation gene FLO8. Y
N_Geneseq_36:T42476   -    10.00   139.43  3.64      645  ! HuntL4 coding sequence. HuntL a
N_Geneseq_36:T45133   +    10.00   141.79  2..69     457  ! Wilms' tumour gene exon 1. Leuk
N_Geneseq_36:T75529   +    10.00   139.55  3.58      633  ! cDNA encoding Wilms' tumour prd
N_Geneseq_36:T97924   +    10.00   120.39  41.83     10366  ! Composite sequence of a novel
N_Geneseq_36:T88434   -    10.00   131.03  10.68     2195  ! Human 5-lipoxygenase gene p
N_Geneseq_36:V05828   +    10.00   120.39  41.83     10366  ! Human huntingtin coding se
N_Geneseq_36:V17757   +    10.00   128.97  13.92     2965  ! Fractionated X irradiation-
N_Geneseq_36:V27112   -    10.00   112.02  122.26    35099  ! Adenovirus 17. Recombinant
N_Geneseq_36:X15842   +    10.00   141.79  2.69      457  ! Nucleotide sequence of the s
N_Geneseq_36:X18930   +    10.00   140.97  2.99      515  ! Human huntingtin gene. Trans

seq_name: N_Geneseq_36:V58451

seq_documentation_block:
ID   V58451 standard; DNA; 3383 BP.
AC   V58451;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2622
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69375.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 218-222; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3383 BP;    1104 A;    657 C;    623 G;    999 T;


alignment_scores:
            Quality:  871.00              Length:    871
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x V58451   ..

 Align seg 1/1  to: V58451  from: 1  to: 3383

       1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAl 17
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       7 ATGCCGCCCAAAACCCCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGC 56

      17 aAlaGluProProAlaProProProProProProGluGluAspProG 34
         ||||||||||||||||||||||||||||||||||||||||||||||||
      57 CGCGGAACCCCCGGCACCGCCGCCGCCGCCCCCTCCTGAGGAGGACCCAG 106

      34 luGlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGlu 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     107 AGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAA 156

      51 GluThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIlePr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACC 206

      67 oAspHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerServ 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 AGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTG 256

      84 alAspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGly 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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257 TGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAACTGTGGGGA 306

101 IleCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrPh 117
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTT 356

117 eThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnL 134
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
357 TACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACT 406

134 euLeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArg 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
407 TACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGA 456

151 LeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluAr 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
457 CTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAG 506

167 gThrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrG 184
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
507 GACATGTGAACTTATATATTTGACACAACCCAGCAGTTCGATATCTACTG 556

184 luIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
557 AAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA 606

201 AlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGl 217
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
607 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCA 656

217 nLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetL 234
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
657 GTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGT 706

234 euLeuLysGluProTyrLysThrGlySerAsnSerLeuGlyLeuValThr 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
707 TGCTCAAAGAACCATATAAAACAGGGTCGAATTCTCTTGGACTTGTAACA 756

251 SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIl 267
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
757 TCTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAAGAAAT 806

267 eTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspL 284
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
807 TTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGATA 856

284 ysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
857 AAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCA 906

301 ArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPr 317
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
907 CGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCC 956

317 oValArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnS 334
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
957 AGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATT 1006

334 erAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheAsnAsnCys 350
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1007 CAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC 1056

351 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTy 367
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1057 ACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATA 1106

367 rIlePheLysGluLysPheAlaLysAlaValGlyGlnGlyCysValGluI 384
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1107 CATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAA 1156

384 leGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMet 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1157 TTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATG 1206

401 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSe 417
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1207 GAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAG 1256

417 rLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaL 434
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1257 CAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTC 1306

434 euGluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAsp 450
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1307 TTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1356

451 SerGlyThrAspLeuSerProProTrpIleLeuAsnValLeuAsnLeuLy 467
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1357 TCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTAAA 1406

467 sAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGlyA 484
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1407 AGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCA 1456

484 snLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIle 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1457 ACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATC 1506

501 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLy 517
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1507 ATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAA 1556

517 sGlnSerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysP 534
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1557 ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTC 1606

534 roLeuAsnLeuProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu 550
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1607 CTCTTAATCTTCCTCTCCAGAATAATCACACTGCAGCAGATATGTATCTT 1656

551 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSe 567
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1657 TCTCCTGTAAGATCTCCAAAGAAAAAAAGGTTCAACTACGCGTGTAAATTC 1706

567 rThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysP 584
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1707 TACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGC 1756

584 roLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1757 CATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1806

601 AlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisPr 617
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1807 GCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCC 1856

617 oGluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnG 634
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1857 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATG 1906

634 luTyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
1907 AGTATGAACTCATGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCC 1956

651 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPheLysIleIl 667
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1957 ATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCAT 2006

667 eValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysA 684
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2007 TGTAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAAC 2056

684 rgValLeuIleLysGluGluGlnTyrAspSerIleIleValPheTyrAsn 700
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2057 GTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAC 2106
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     701 SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerTh 717
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    2107 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAC 2156

     717 rArgProProThrLeuSerProIleProHisIleProArgSerProTyrL 734
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2157 CAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACA 2206

     734 ysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 750
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    2207 AGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCA 2256

     751 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLy 767
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2257 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAA 2306

     767 sMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGlyT 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2307 AATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGA 2356

     784 hrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 800
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2357 CTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2406

     801 ValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLy 817
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2407 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAA 2456

     817 sLeuArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisL 834
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     851 ArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAs 867
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    2557 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAA 2606

     867 nLysGluGluLys 871
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    2607 CAAGGAAGAGAAA 2619

seq_name: N_Geneseq_36:Q04713

seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag=  a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;

alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x Q04713   ..

 Align seg 1/1  to: Q04713  from: 1  to: 2994

     244 AsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLe 260
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    1039 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 1088

     260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1089 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 1138

     277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1139 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 1188

     294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1189 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1238

     310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1239 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAAC 1288

     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1289 AATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1338

     344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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    1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 1388

     360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
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    1389 AAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTG 1438

     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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    1439 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 1488

     394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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     410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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     427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
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    1589 TGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

     444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 460
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     460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1689 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 1738

     477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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     494 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSe 510
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 510 rProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrA 527
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 527 spHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 543
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1889 ATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

 544 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGl 560
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1939 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGG 1988

 560 ySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrS 577
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 577 erAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPhe 593
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 594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
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2389 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2438

 710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
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 727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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 794 MetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAs 810
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      827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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      844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
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      860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_documentation_block:
ID   Q41545 standard; DNA; 2994 BP.
AC   Q41545;
DT   24-AUG-1993  (first entry)
DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
FH   Key             Location/Qualifiers
FT   cds             139. .2925
FT                   /*tag= a
FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;   974 A;   618 C;   594 G;   808 T;


alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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1089 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 1138

 277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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1139 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 1188

 294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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1189 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1238

 310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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1239 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAAC 1288

 327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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 344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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1339 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 1388

 360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
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1439 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 1488

 394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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 410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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1539 ATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1588

 427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
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1589 TGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1638

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1639 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 1688

 460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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 494 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSe 510
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1889 ATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1938

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 560 ySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrS 577
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1989 TTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCT 2038

 577 erAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPhe 593
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 610 uArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuP 627
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2139 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTT 2188

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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID   Q72690 standard; DNA; 3233 BP.
AC   Q72690;
DT   01-JUN-1995  (first entry)
DE   Retinoblastoma 94kD therapeutic protein encoding DNA.
KW   Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             19. .2469
FT                   /*tag=  a
PN   WO9421115-A.
PD   29-SEP-1994.
PF   24-MAR-1994; U03211.
PR   25-MAR-1993; US-038760.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PI   Benedict WF,  Xu H,  Xu S;
DR   WPI; 94-316534/39.
DR   P-PSDB; R63564.
PT   Broad spectrum tumour suppressor gene - by using retinoblastoma
PT   gene product p94RB to suppress abnormal cell proliferation in the
PT   treatment of cancer
PS   Claim 4; Fig 1; 115pp; English.
CC   Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC   gene) which encodes the 94kD therapeutic retinoblastoma protein
CC   R63564. Expression of this protein in an abnormally proliferating
CC   cell causes that cell to enter a senescent-like state, terminating
CC   the proliferation. R63564 also has the advantage of engendering a low
CC   incidence of tumour suppressor gene resistance in a population of
CC   treated cells.
SQ   Sequence   3233 BP;    1086 A;    597 C;    567 G;    983 T;


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             Ratio:  1.000               Gaps:      0
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     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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     394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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     410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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     427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
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     444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 460
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     477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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     494 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSe 510
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    1333 GAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTC 1382

     510 rProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrA 527
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     527 spHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 543
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     544 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGl 560
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    1483 ACTGCAGCAGATATGTATGTTTCTCCTGTAAGATCTCCAAAGAAAAAAGG 1532

     560 ySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrS 577
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     627 heGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 643
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 1933 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 1982

  710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
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  760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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 2133 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2182

  777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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  827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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  844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
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  860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:
ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;


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          Quality:  628.00              Length:    628
            Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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  814 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 863

  260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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  864 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 913

  277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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  914 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 963

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  964 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1013

  310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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 1014 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAAC 1063

  327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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  344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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 1114 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 1163

  360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
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 1164 AAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTG 1213

  377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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 1214 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 1263

  394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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 1264 CGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1313

  410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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 460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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1464 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 1513

 477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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 527 spHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 543
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 594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
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 710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
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2214 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 2263

 727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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 744 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGl 760
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 777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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2514 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATG 2563

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seq_name: N_Geneseq_36:V58448

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seq_documentation_block:
ID   V58448 standard; DNA; 3347 BP.
AC   V58448;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2586
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69372.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 196-200; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3347 BP;    1096 A;    650 C;    617 G;    984 T;


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  260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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 1300 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 1349

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 1650 TTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCT 1699

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  594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
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  610 uArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuP 627
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  627 heGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 643
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  660 eAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisA 677
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 1950 AGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATG 1999

  677 laValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAsp 693
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  727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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  760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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 2250 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2299

  777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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  827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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     860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_name: N_Geneseq_36:V58449

seq_documentation_block:
ID   V58449 standard; DNA; 3161 BP.
AC   V58449;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2400
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69373.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 203-207; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3161 BP;    1037 A;    619 C;    586 G;    919 T;


alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x V58449   ..

 Align seg 1/1  to: V58449  from: 1  to: 3161

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     514 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 563

     260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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     277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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     294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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     310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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     864 AAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTG 913

     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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     914 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 963

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     964 CGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1013

     410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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     427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
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     444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 460
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    1114 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 1163

     460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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    1164 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 1213

     477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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   1914 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 1963

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    827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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    860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_name: N_Geneseq_36:V58450

seq_documentation_block:
ID V58450 standard; DNA; 3377 BP.
AC V58450;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2616
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69374.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 210-215; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3377 BP; 1113 A; 654 C; 626 G; 984 T;

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Ratio: 1.000 Gaps: 0
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Align seg 1/1 to: V58450 from: 1 to: 3377

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    260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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1830 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTT 1879

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 644 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIl 660
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1930 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATAT 1979

 660 eAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisA 677
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1980 AGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATG 2029

 677 laValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAsp 693
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2030 CTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGAT 2079

 694 SerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAs 710
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2080 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2129

 710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2130 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 2179

 727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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2180 ACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2229

 744 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGl 760
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2230 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGA 2279

 760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2280 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2329

 777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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2330 CAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAG 2379

 794 MetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAs 810
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2380 ATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2429

 810 nProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspG 827
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2430 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATG 2479

 827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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2480 AAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2529

 844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
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2530 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAA 2579

 860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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2580 TGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2613
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID V58452 standard; DNA; 3554 BP.
AC V58452;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2793
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69376.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 226-230; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3554 BP; 1170 A; 683 C; 653 G; 1048 T;

alignment_scores:
Quality: 628.00 Length: 628
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:
 US-09-026-459A-49 x V58452   ..

 Align seg 1/1  to: V58452  from: 1  to: 3554

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    907 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 956

    260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    957 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 1006

    277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   1007 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 1056

    294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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   1057 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1106

    310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   1107 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAAC 1156

    327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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   1157 AATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1206

    344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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   1207 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 1256

    360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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    377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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   1307 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 1356

    394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   1357 CGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1406

    410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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   1407 ATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1456

    427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
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    444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 460
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   1507 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 1556

    460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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   1557 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 1606

    477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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   1607 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 1656

    494 GluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSe 510
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    510 rProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrA 527
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   1707 ACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTG 1756

    527 spHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 543
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   1757 ATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1806

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   1807 ACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGG 1856

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   1857 TTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCT 1906

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    594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
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    610 uArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuP 627
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   2007 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTT 2056

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    644 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIl 660
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    660 eAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisA 677
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   2157 AGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATG 2206

    677 laValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAsp 693
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   2207 CTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGAT 2256

    694 SerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAs 710
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
   2257 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2306

    710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
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   2307 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 2356

    727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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    744 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGl 760
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    760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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   2457 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2506

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     827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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     844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
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    2707 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAA 2756

     860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_name: N_Geneseq_36:V58440

seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: V58440  from: 1  to: 3555

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     907 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 956

     260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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     957 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 1006

     277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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     344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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     360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
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     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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     394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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     410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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     527 spHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 543
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    1857 TTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCT 1906

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     594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1957 TATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGA 2006

     610 uArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuP 627
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  2057 TCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG 2106

   644 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIl 660
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2107 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATAT 2156

   660 eAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisA 677
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  2157 AGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATG 2206

   677 laValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAsp 693
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2207 CTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGAT 2256

   694 SerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAs 710
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   710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
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  2307 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 2356

   727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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  2357 ACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2406

   744 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGl 760
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  2407 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGA 2456

   760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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  2457 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2506

   777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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   794 MetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAs 810
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  2557 ATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2606

   810 nProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspG 827
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   827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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   844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
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  2707 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAA 2756

   860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID V58441 standard; DNA; 3455 BP.
AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers

FT CDS 7. .2694
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 T;

alignment_scores:
Quality: 628.00 Length: 628
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-49 x V58441 ..

Align seg 1/1 to: V58441 from: 1 to: 3455

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   808 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 857

   260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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   858 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 907

   277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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   908 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 957

   294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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   958 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 1007

   310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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  1008 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAAC 1057

   327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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  1058 AATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 1107

   344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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  1108 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 1157

   360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
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   377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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  1208 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 1257

   394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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1358 TGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1407

 444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 460
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1408 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 1457

 460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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 477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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1908 ACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTT 1957

 627 heGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 643
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 710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
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 727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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2508 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATG 2557

 827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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 844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:

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ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;
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              Ratio:  1.000                 Gaps:      0
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alignment_block:
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     260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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     394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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    2095 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2144

     710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
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     727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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     744 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGl 760
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     760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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    2295 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2344

     777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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    2345 CAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAG 2394

     794 MetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAs 810
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    2395 ATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2444
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     810 nProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspG 827
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2445 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATG 2494

     827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2495 AAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2544

     844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2545 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAA 2594

     860 nAspSerMetAspThrSerAsnLysGluGluLys 871
         ||||||||||||||||||||||||||||||||||
    2595 TGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2628

seq_name: N_Geneseq_36:V58443

seq_documentation_block:
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2562
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;


alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x V58443   ..

 Align seg 1/1  to: V58443  from: 1  to: 3323

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
     676 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 725

     260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     726 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 775

     277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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     776 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 825

     294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     826 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 875

     310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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     876 TGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAAC 925

     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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     926 AATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG 975

     344 IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLy 360
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     976 ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAGTATACTGAA 1025

     360 sArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaV 377
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    1026 AAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTG 1075

     377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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    1076 TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTT 1125

     394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1126 CGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1175

     410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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    1176 ATTATCCATTCAAAATTTAAGCAAACTTCTGAATGACAACATTTTTCATA 1225

     427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1226 TGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1275

     444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerProTrpIl 460
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    1276 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 1325

     460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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    1326 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 1375

     477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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    1376 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 1425

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    1426 GAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTC 1475

     510 rProLeuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrA 527
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    1476 ACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTG 1525

     527 spHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 543
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    1526 ATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATCAC 1575

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     577 erAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPhe 593
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     594 TyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGl 610
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       ||||||||||||||||||||||||||||||||||||||||||||||||||
  1976 CTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGAT 2025

   694 SerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAs 710
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2026 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2075

   710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2076 TATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTC 2125

   727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
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  2126 ACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2175

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       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2176 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGA 2225

   760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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  2226 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2275

   777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
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   810 nProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspG 827
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2376 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATG 2425

   827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2426 AAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2475

   844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
       ||||||||||||||||||||||||||||||||||||||||||||||||||
  2476 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAA 2525

   860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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  2526 TGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2559

seq_name: N_Geneseq_36:V58444

seq_documentation_block:
ID   V58444 standard; DNA; 3266 BP.
AC   V58444;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2505
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69368.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 166-170; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3266 BP;    1092 A;    602 C;    574 G;    998 T;


alignment_scores:
            Quality:  628.00              Length:    628
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x V58444    ..

 Align seg 1/1  to: V58444  from: 1  to: 3266

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    619 AATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCT 668

    260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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    669 TTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 718

    277 rgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSer 293
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    719 GATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGT 768

    294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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    769 TTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAA 818

    310 nValIleProProHisThrProValArgThrValMetAsnThrIleGlnG 327
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    327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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    377 alGlyGlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyVal 393
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 394 ArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluGluAr 410
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1069 CGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG 1118

 410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
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1119 ATTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATA 1168

 427 etSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 443
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1169 TGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA 1218

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1219 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGAT 1268

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1269 TCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAA 1318

 477 erPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeu 493
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1319 GTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTA 1368

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 560 ySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrS 577
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1919 CTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGGAGTATGAT 1968

 694 SerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAs 710
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1969 TCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAA 2018

 710 nIleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProH 727
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2019 TATTTTGCAGTATGCTTCGACCAGGCCCCCTACCTTGTCACCAATACCTC 2068

 727 isIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 743
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2069 ACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCT 2118

 744 GlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGl 760
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2119 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGA 2168

 760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2169 AGGTCTGCCAACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTAT 2218

 777 erIleGlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGln 793
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2219 CAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAG 2268

 794 MetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAs 810
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2269 ATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAGCAA 2318

 810 nProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspG 827
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2319 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATG 2368

 827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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2369 AAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2418

 844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAs 860
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2419 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAA 2468

 860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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seq_name: N_Geneseq_36:V58445

seq_documentation_block:

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ID   V58445 standard; DNA; 3113 BP.
AC   V58445;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2352
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69369.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 173-177; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
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CC   activity than wild type RTSPs.
SQ   Sequence   3113 BP;    1039 A;    577 C;    547 G;    950 T;


alignment_scores:
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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-49 x V58445   ..

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     260 uSerLysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaA 277
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     294 PheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluValAs 310
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     327 lnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 343
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     410 gLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisM 427
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     444 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIl 460
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     460 eLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluS 477
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    1966 GGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGA 2015

     760 uGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValS 777
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 794 MetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAs 810
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 810 nProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspG 827
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2166 CCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATCAGATG 2215

 827 luAlaAspGlySerLysHisLeuProGlyGluSerLysPheGlnGlnLys 843
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2216 AAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCAAATTTCAGCAGAAA 2265

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2266 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAA 2315

 860 nAspSerMetAspThrSerAsnLysGluGluLys 871
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2316 TGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2349
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Date: Feb 13, 2000  2:43 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
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 -Q=/cgn2_1/USPTO_spool/US09026459/runat_12022000_171248_15959/app_query.fasta.1
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Search information block:
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Query length: 928
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 501.080000

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Sequence            Strd Orig    ZScore    EScore Len  ! Documentation  ..
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N_Geneseq_36:Q04713  +  816.00 12847.20  0.0       2994  ! Cancer supressing gene (CSG).
N_Geneseq_36:Q41545  +  816.00 12847.20  0.0       2994  ! Retinoblastoma gene. Method c
N_Geneseq_36:Q72690  +  816.00 12846.67  0.0       3233  ! Retinoblastoma 94kD therapeut
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N_Geneseq_36:V54990  +  816.00 12846.01  0.0       3555  ! DNA sequence of the specifica
N_Geneseq_36:V54991  +  816.00 12846.70  0.0       3218  ! DNA sequence of the specifica
N_Geneseq_36:V40004  +  816.00 12847.20  0.0       2994  ! Retinoblastoma protein RB. Ne
N_Geneseq_36:X00737  +  816.00 12847.19  0.0       2995  ! cDNA encoding a retinoblastom
N_Geneseq_36:V58445  +  781.00 12294.64  0.0       3113  ! Modified retinoblastoma tumou
N_Geneseq_36:X04501  +  765.00 12039.48  0.0       4597  ! Human retinoblastoma gene cDN
N_Geneseq_36:V58448  +  747.00 11757.63  0.0       3347  ! Modified retinoblastoma tumou
N_Geneseq_36:Q70536  +  729.00 11471.41  0.0       4597  ! Human retinoblastoma gene. Di
N_Geneseq_36:N81369  +  715.00 11250.50  0.0       4597  ! Human retinoblastoma gene Dia
N_Geneseq_36:Q90059  +  715.00 11253.45  0.0       2995  ! Retinoblastoma tumour suppres
N_Geneseq_36:V58449  +  687.00 10811.25  0.0       3161  ! Modified retinoblastoma tumou
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N_Geneseq_36:Q86398  +  593.00 9328.33   0.0       2995  ! Human Rb110 cDNA. Admin. of a
N_Geneseq_36:N90489  +  474.00 7446.95   0.0       5056  ! cDNA of human retinoblastoma g
N_Geneseq_36:N81261  +  286.00 4481.06   5.4e-242  4579  ! Probe for retinoblastoma gene.
N_Geneseq_36:X04502  +   65.00  984.21   3.2e-47   18303  ! Human retinoblastoma gene. Is
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N_Geneseq_36:Q99257  +   10.00  129.16   13.57     2841  ! Yeast coagulation gene FLO8. Y
N_Geneseq_36:T42476  -   10.00  139.37   3.66      645  ! HuntL4 coding sequence. HuntL a
N_Geneseq_36:T45133  +   10.00  141.75   2.70      457  ! Wilms' tumour gene exon 1. Leuk
N_Geneseq_36:T75529  +   10.00  139.50   3.60      633  ! cDNA encoding Wilms' tumour prc
N_Geneseq_36:T97924  +   10.00  120.25   42.57     10366  ! Composite sequence of a novel
N_Geneseq_36:T88434  -   10.00  130.94   10.80     2195  ! Human 5-lipoxygenase gene p
N_Geneseq_36:V05828  +   10.00  120.25   42.57     10366  ! Human huntingtin coding se
N_Geneseq_36:V17757  +   10.00  128.87   14.09     2965  ! Fractionated X irradiation-
N_Geneseq_36:V27112  -   10.00  111.85   125.03    35099  ! Adenovirus 17. Recombinant
N_Geneseq_36:X15842  +   10.00  141.75   2.70      457  ! Nucleotide sequence of the s
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seq_name: N_Geneseq_36:V58452

seq_documentation_block:
ID   V58452 standard; DNA; 3554 BP.
AC   V58452;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69376.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 226-230; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3554 BP;    1170 A;    683 C;    653 G;    1048 T;


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 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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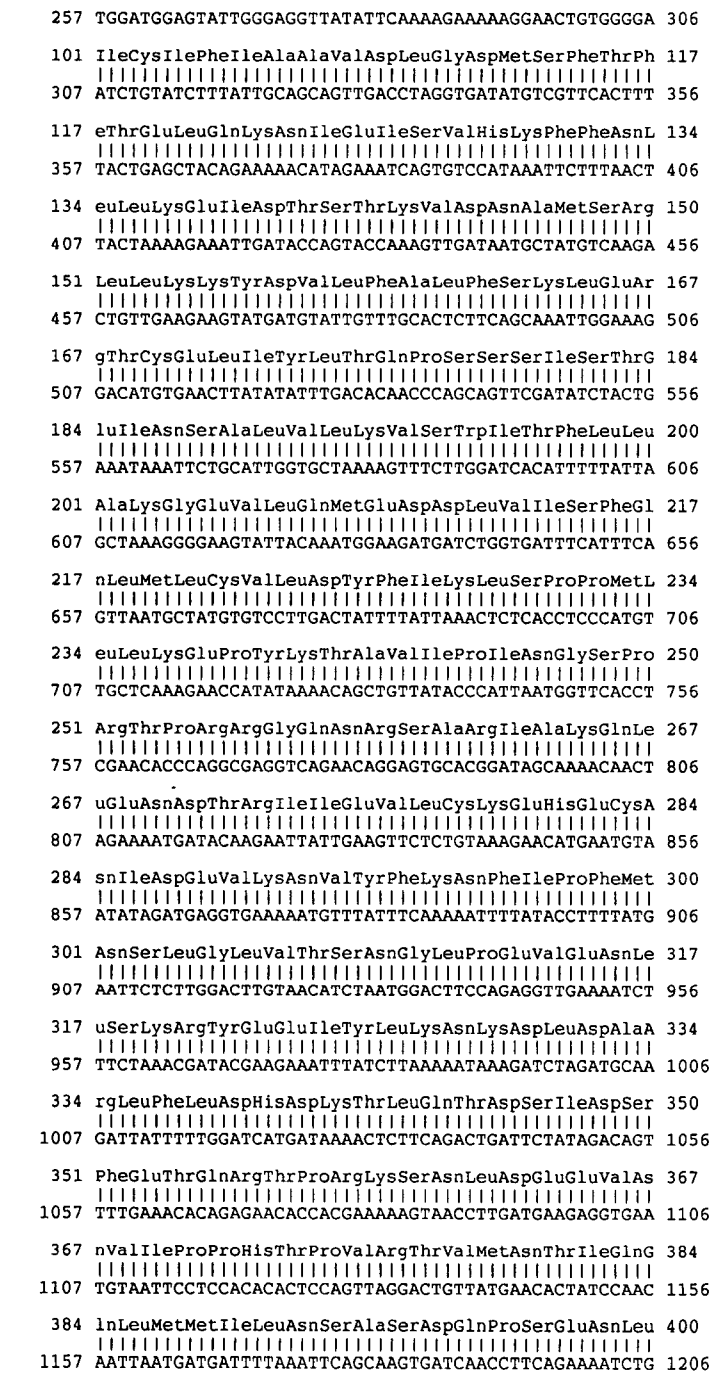
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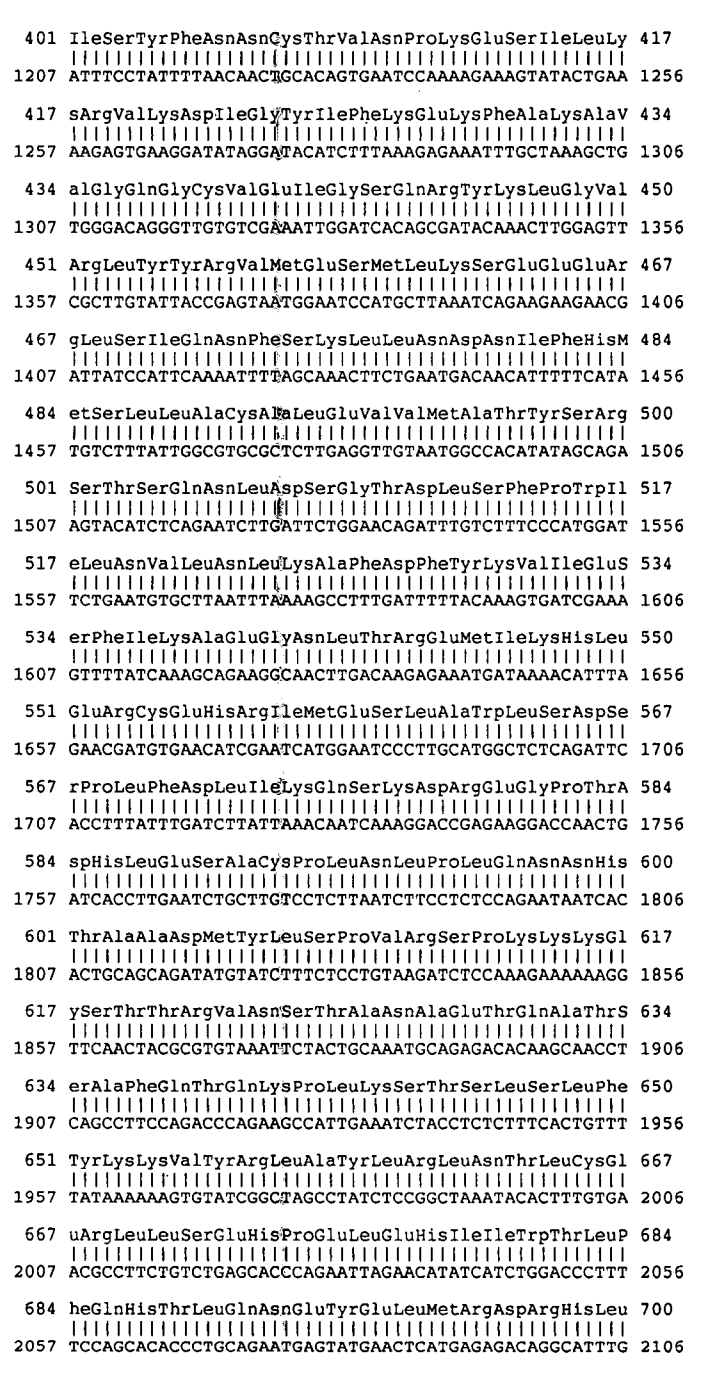
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     107 AGCAGGACAGCGGCCCGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAA 156

      51 GluThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIlePr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     157 GAAACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACC 206

      67 oAspHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerServ 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     207 AGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAAGTTTCATCTG 256

      84 alAspGlyValLeuGlyGlyTyrIleGlnLysLysLysGluLeuTrpGly 100
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101 IleCysIlePheIleAlaAlaValAspLeuGlyAspMetSerPheThrPh 117
307 ATCTGTATCTTTATTGCAGCAGTTGACCTAGGTGATATGTCGTTCACTTT 356
117 eThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnL 134
357 TACTGAGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACT 406
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407 TACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGA 456
151 LeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluAr 167
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201 AlaLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGl 217
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seq_documentation_block:
ID   Q04713 standard; cDNA; 2994 BP.
AC   Q04713;
DT   11-OCT-1990  (first entry)
DE   Cancer supressing gene (CSG).
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   RB; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             139. .2922
FT                   /*tag= a
PN   WO9005180-A.
PD   17-MAY-1990.
PF   30-OCT-1989; 004808.
PR   31-OCT-1988; US-265829.
PA   (REGC) Univ of Caifornia.
PI   Lee WH, Huang HJS;
DR   WPI; 90-178822/23.
DR   P-PSDB; R05305.
PT   Controlling cancer -
PT   by replacing ineffective cancer suppressing gene with cloned,
PT   active gene.
PS   Claim 35; Page 86; 105pp; English.
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
SQ   Sequence   2994 BP;   974 A;   618 C;   593 G;   809 T;
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    179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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    196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
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    213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
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    229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
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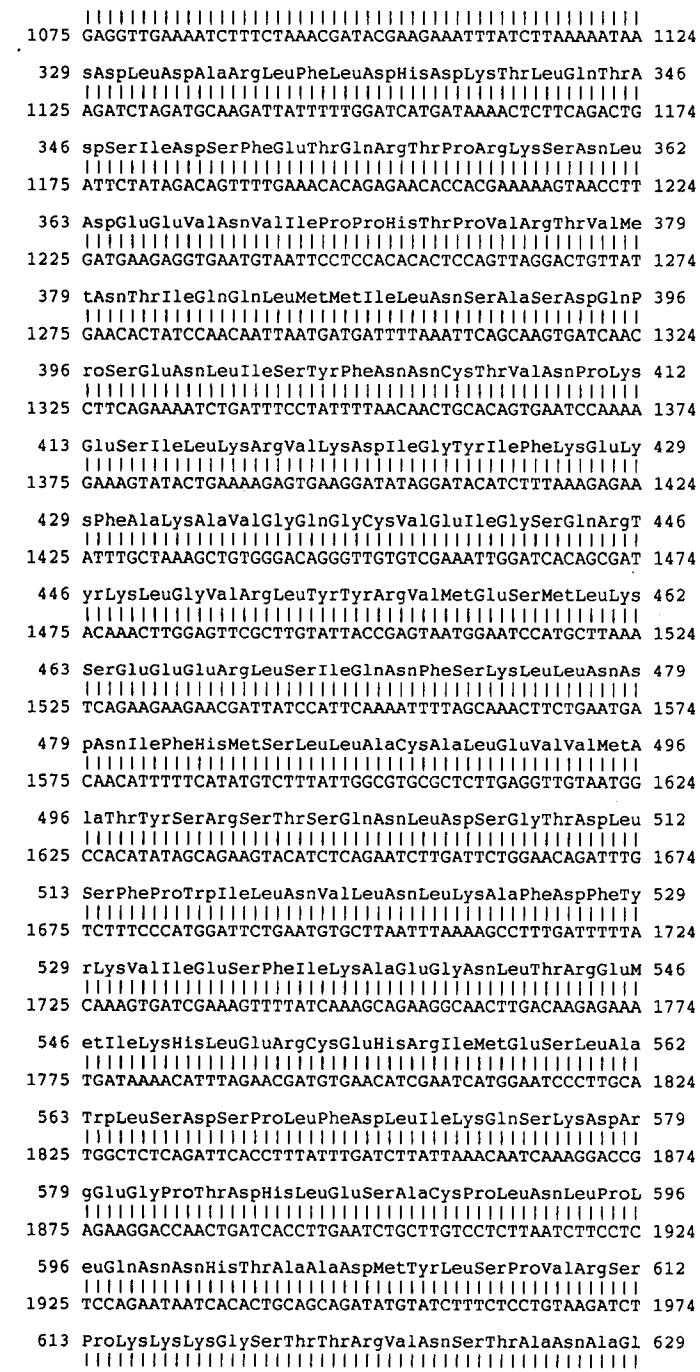
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346 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 362
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DE   Retinoblastoma gene.
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.;
KW   gamete prodn.; ss.
OS   Homo sapiens SR-40 cell line.
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FT                   /note= "Rb protein"
PN   WO9308267-A.
PD   29-APR-1993.
PF   16-OCT-1992; U08918.
PR   17-OCT-1991; US-778510.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Lee EYHP, Lee WH, Wang NP;
DR   WPI; 93-152462/18.
DR   P-PSDB; R36534.
PT   Method of controlling cell cycle progression - uses purified
PT   retinoblastoma protein or fragment, for use in combination with
PT   therapeutic methods to arrest tumorigenesis
PS   Disclosure; Fig 9; 68pp; English.
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumourigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
SQ   Sequence   2994 BP;    974 A;    618 C;    594 G;    808 T;


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     229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
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     246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
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     263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
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seq_name: N_Geneseq_36:Q72690

seq_documentation_block:
ID Q72690 standard; DNA; 3233 BP.
AC Q72690;
DT 01-JUN-1995 (first entry)
DE Retinoblastoma 94kD therapeutic protein encoding DNA.
KW Retinoblastoma gene product; p94RB; tumour suppressor gene; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 19. .2469
FT /*tag= a
PN WO9421115-A.
PD 29-SEP-1994.
PF 24-MAR-1994; U03211.
PR 25-MAR-1993; US-038760.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PI Benedict WF, Xu H, Xu S;
DR WPI; 94-316534/39.
DR P-PSDB; R63564.
PT Broad spectrum tumour suppressor gene - by using retinoblastoma
PT gene product p94RB to suppress abnormal cell proliferation in the
PT treatment of cancer
PS Claim 4; Fig 1; 115pp; English.
CC Q72690 is the fragment of p94RB (a broad-spectrum tumour suppressor
CC gene) which encodes the 94kD therapeutic retinoblastoma protein
CC R63564. Expression of this protein in an abnormally proliferating
CC cell causes that cell to enter a senescent-like state, terminating
CC the proliferation. R63564 also has the advantage of engendering a low
CC incidence of tumour suppressor gene resistance in a population of
CC treated cells.
SQ Sequence 3233 BP; 1086 A; 597 C; 567 G; 983 T;

alignment_scores:
Quality: 816.00 Length: 816
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-51 x Q72690 ..

Align seg 1/1 to: Q72690 from: 1 to: 3233

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    179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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     846 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 862
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2219 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2268

     863 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 879
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2269 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2318

     879 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 896
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2319 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2368

     896 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 912
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2369 AATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2418

     913 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 928
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seq_name: N_Geneseq_36:V58447

seq_documentation_block:

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ID   V58447 standard; DNA; 3461 BP.
AC   V58447;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2700
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69371.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 188-192; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3461 BP;    1141 A;    675 C;    627 G;    1018 T;
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alignment_scores:

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           Quality:  816.00            Length:    816
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

US-09-026-459A-51 x V58447 ..

Align seg 1/1 to: V58447 from: 1 to: 3461

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     250 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 299

     129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     300 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 349

     146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     350 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 399

     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     400 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 449

     179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     450 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 499

     196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     500 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 549

     213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     550 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 599

     229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     600 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 649

     246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     650 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 699

     263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     700 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 749

     279 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 296
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     750 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 799

     296 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     800 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 849

     313 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 329
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 329 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 346
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 900 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 949

 346 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 362
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 950 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 999

 363 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 379
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1000 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 1049

 379 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 396
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1050 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1099

 396 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 412
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1100 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1149

 413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1150 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1199

 429 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 446
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1200 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1249

 446 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 462
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1250 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1299

 463 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 479
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1300 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1349

 479 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 496
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1350 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1399

 496 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 512
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1400 CCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1449

 513 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 529
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1450 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1499

 529 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 546
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1500 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1549

 546 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 562
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1550 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 1599

 563 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 579
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1600 TGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCG 1649

 579 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 596
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1650 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1699

 596 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 612
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1700 TCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1749

 613 ProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGl 629
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1750 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1799

 629 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 646
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1800 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1849

 646 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 662
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1850 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1899

 663 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 679
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1900 AATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATAT 1949

 679 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 696
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1950 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 1999

 696 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 712
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2000 GAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2049

 713 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 729
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 746 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 762
     ||||||||||||||||||||||||||||||||||||||||||||||||||
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 763 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 779
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 779 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 796
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2250 GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCAC 2299

 796 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 812
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2400 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2449

 846 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 862
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 863 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 879
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2500 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2549

 879 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 896
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2550 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2599

 896 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 912
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seq_name: N_Geneseq_36:V58440

seq_documentation_block:
ID   V58440 standard; DNA; 3555 BP.
AC   V58440;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag= a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69364.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Disclosure; Page 121-126; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3555 BP;    1171 A;    684 C;    653 G;    1047 T;


alignment_scores:
           Quality:  816.00            Length:    816
             Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-026-459A-51 x V58440   ..

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     129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
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     393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442

     146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492

     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
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     493 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 542

     179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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     543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592

     196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
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     593 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 642

     213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     643 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 692

     229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     743 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 792

     263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
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     793 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 842

     279 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 296
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     843 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 892

     296 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 312
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     313 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 329
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     993 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 1042

     346 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 362
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     379 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 396
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     396 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 412
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     413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1243 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1292

     429 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 446
         |||||||||||||||||||||||||||||||||||||||||||||||||||
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     446 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 462
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1343 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1392

     463 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 479
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    1393 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1442

     479 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 496
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    1443 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1492

     496 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 512
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     513 SerProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 529
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    1543 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1592

     529 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 546
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1593 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1642

 546 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 562
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1643 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 1692

 563 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 579
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1693 TGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCG 1742

 579 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 596
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1743 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1792

 596 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 612
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1793 TCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1842

 613 ProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGl 629
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1843 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1892

 629 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 646
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1893 GACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1942

 646 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 662
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1943 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1992

 663 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 679
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1993 AATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATAT 2042

 679 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 696
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2043 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 2092

 696 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 712
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2093 GAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2142

 713 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 729
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2143 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAA 2192

 729 sAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysG 746
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2193 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 2242

 746 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 762
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2243 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 2292

 763 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 779
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 779 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 796
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2343 GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCAC 2392

 796 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 812
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2393 CCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCA 2442

 813 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSe 829
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2443 TATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCAAGATC 2492

 829 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 846
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2493 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2542

 846 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 862
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2543 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2592

 863 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 879
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2593 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2642

 879 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 896
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2643 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2692

 896 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 912
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
2693 AATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2742

 913 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 928
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2743 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2790
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seq_name: N_Geneseq_36:V58441

seq_documentation_block:
ID V58441 standard; DNA; 3455 BP.
AC V58441;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2694
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69365.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 142-147; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3455 BP; 1153 A; 631 C; 627 G; 1044 T;

alignment_scores:
Quality: 816.00 Length: 816
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-026-459A-51 x V58441 ..

Align seg 1/1 to: V58441 from: 1 to: 3455

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 244 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 293

 129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 294 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 343
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146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
344 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 393
163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
394 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 443
179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
444 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 493
196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
494 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 543
213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
544 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 593
229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
594 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 643
246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
644 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 693
263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
694 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 743
279 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 296
744 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 793
296 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 312
794 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 843
313 GluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLysAsnLy 329
844 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 893
329 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 346
894 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 943
346 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 362
944 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 993
363 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 379
994 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 1043
379 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 396
1044 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1093
396 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 412
1094 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1143
413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
1144 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1193
429 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 446
1194 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1243
446 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 462
1244 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1293
463 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 479
1294 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1343
479 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 496
1344 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1393
496 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 512
1394 CCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1443
513 SerProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 529
1444 TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTA 1493
529 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 546
1494 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1543
546 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 562
1544 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 1593
563 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 579
1594 TGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCG 1643
579 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 596
1644 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1693
596 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 612
1694 TCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCT 1743
613 ProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGl 629
1744 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1793
629 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 646
1794 GACACAAGCAACCTCAGGCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1843
646 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 662
1844 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1893
663 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 679
1894 AATACACTTTGTGAACGGCTTCTGTCTGAGCACCCAGAATTAGAACATAT 1943
679 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 696
1944 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 1993
696 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 712
1994 GAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGC 2043
713 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 729
2044 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAA 2093
729 sAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysG 746
2094 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 2143
746 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 762

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    2144 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 2193

     763 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 779
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2194 AGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTT 2243

     779 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 796
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    2244 GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCAC 2293

     796 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 812
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     813 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSe 829
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     829 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 846
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     846 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 862
         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2444 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2493

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         |||||||||||||||||||||||||||||||||||||||||||||||||||
    2544 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2593

     896 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 912
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seq_name: N_Geneseq_36:V58442

seq_documentation_block:

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ID   V58442 standard; DNA; 3392 BP.
AC   V58442;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             7. .2641
FT                   /*tag=  a
PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69366.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 150-155; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
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SQ   Sequence   3392 BP;    1137 A;    614 C;    607 G;    1034 T;
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 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

US-09-026-459A-51 x V58442 ..

Align seg 1/1 to: V58442 from: 1 to: 3392

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     181 ATGTCGTTCACTTTTACTGAGCTACAGAAAAACATAGAAATCAGTGTCCA 230

     129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     231 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 280

     146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     281 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 330

     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     331 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 380

     179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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     531 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 580

     246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
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     263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
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     631 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 680

     279 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 296
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     296 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 312
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     781 GAGGTTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAA 830

     329 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 346
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     831 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 880

     346 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 362
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     881 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 930
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 379 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 396
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 981 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1030

 396 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 412
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1031 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1080

 413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1130

 429 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 446
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 446 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 462
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1181 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1230

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seq_documentation_block:
ID   V58443 standard; DNA; 3323 BP.
AC   V58443;
DT   02-DEC-1998  (first entry)
DE   Modified retinoblastoma tumour suppressor gene.
KW   Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW   cellular proliferation inhibitor; ss.
OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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PN   WO9837091-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03041.
PR   20-FEB-1997; US-038118.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Benedict WF, Hu S, Xu H, Zhou Y;
DR   WPI; 98-480788/41.
DR   P-PSDB; W69367.
PT   Retinoblastoma suppressor protein with N-terminal modification -
PT   inhibiting cellular proliferation, particularly cancer
PS   Claim 22; Page 158-162; 249pp; English.
CC   This sequence encodes a modified retinoblastoma tumour suppressor
CC   protein (RTSP) of the invention. The proteins can be used for inhibiting
CC   cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC   can be used for treating diseases characterised by abnormal cellular
CC   proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC   activity than wild type RTSPs.
SQ   Sequence   3323 BP;    1114 A;    605 C;    591 G;    1013 T;


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     162 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 211

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     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
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     179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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seq_name: N_Geneseq_36:V58444

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AC V58444;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2505
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PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69368.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 166-170; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T;

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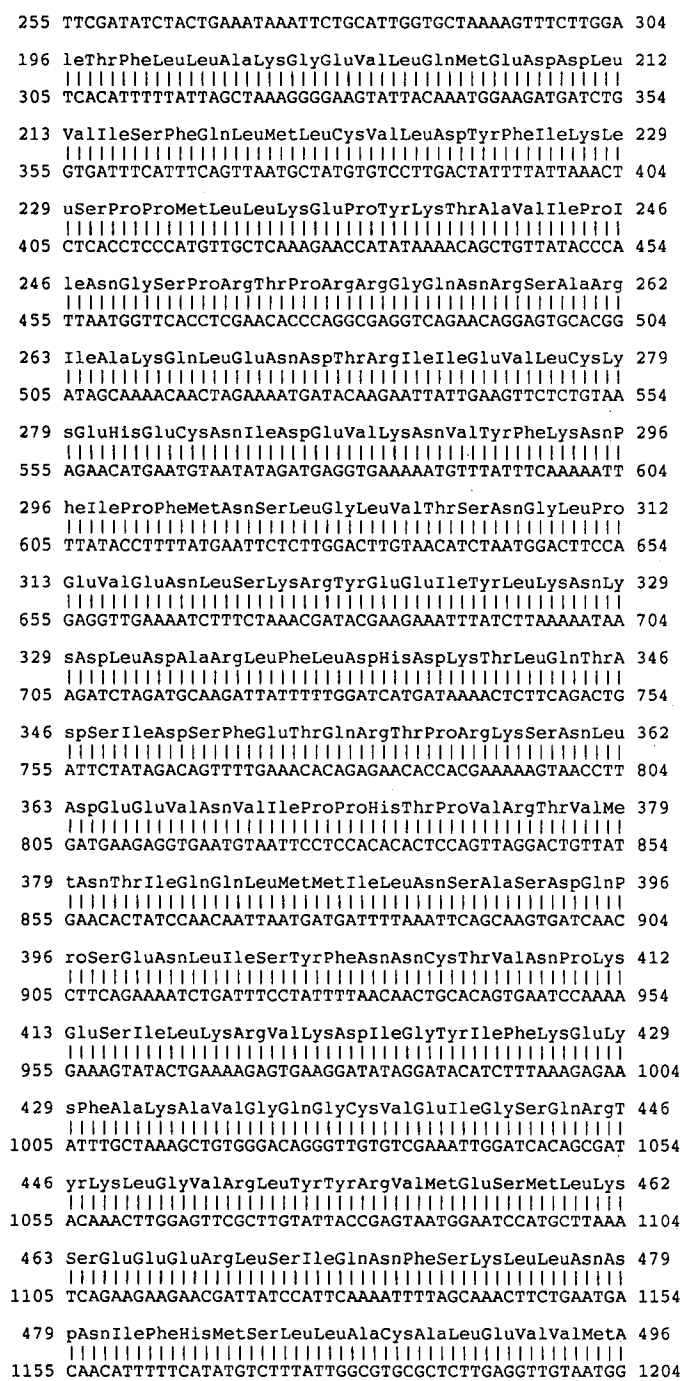
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 146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
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 155 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 204

 163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
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 205 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 254

 179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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255 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 304
196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
305 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 354
213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
355 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 404
229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
405 CTCACCTCCCATGTTGCTCAAAGAACCATATAAAACAGCTGTTATACCCA 454
246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
455 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 504
263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
505 ATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAA 554
279 sGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnP 296
555 AGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATT 604
296 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 312
605 TTATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCA 654
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705 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 754
346 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 362
755 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 804
363 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 379
805 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 854
379 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 396
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2055 GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTTCAC 2104

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seq_name: N_Geneseq_36:V58446

seq_documentation_block:

ID V58446 standard; DNA; 3323 BP.
AC V58446;
DT 02-DEC-1998 (first entry)
DE Modified retinoblastoma tumour suppressor gene.
KW Modified retinoblastoma tumour suppressor; RTSP protein; cancer therapy;
KW cellular proliferation inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 7. .2562
FT /*tag= a
PN WO9837091-A2.
PD 27-AUG-1998.
PF 19-FEB-1998; U03041.
PR 20-FEB-1997; US-038118.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
DR WPI; 98-480788/41.
DR P-PSDB; W69370.
PT Retinoblastoma suppressor protein with N-terminal modification -
PT inhibiting cellular proliferation, particularly cancer
PS Claim 22; Page 180-184; 249pp; English.
CC This sequence encodes a modified retinoblastoma tumour suppressor
CC protein (RTSP) of the invention. The proteins can be used for inhibiting
CC cellular proliferation, when coadministered with a p53 protein. The RTSPs
CC can be used for treating diseases characterised by abnormal cellular
CC proliferation, particularly cancers. The RTSPs have a broader spectrum of
CC activity than wild type RTSPs.
SQ Sequence 3323 BP; 1099 A; 647 C; 588 G; 989 T;

alignment_scores:

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            Quality:  816.00          Length:    816
              Ratio:  1.000             Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:

US-09-026-459A-51 x V58446 ..

Align seg 1/1 to: V58446 from: 1 to: 3323

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     162 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 211

     146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
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     212 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 261

     163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
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     262 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 311

     179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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     312 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 361

     196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
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     229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
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     263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
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 429 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 446
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 446 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 462
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seq_documentation_block:
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AC   V54990;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2793
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
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PA (TEXA) UNIV TEXAS SYSTEM.
PI Hu S, Logothetis CJ, Xu H, Zhou Y;
DR WPI; 98-480796/41.
DR P-PSDB; W71354.
PT New tetracycline responsive expression vectors - used for the
PT tightly controlled expression of genes, such as tumour suppressor
PT genes for treating cancers
PS Disclosure; Pages 145-150; 190pp; English.
CC The present sequence appears in the specification, which describes a
CC tetracycline responsive expression vector (TREV), which contains a
CC sequence encoding a fusion protein comprising a transcriptional
CC transactivation domain (TTD) operatively attached to a tetracycline
CC repressor protein (TRP), the first sequence operatively positioned
CC downstream of a promoter. The vector also contains a cloning site
CC operatively positioned downstream of a basal promoter comprising a
CC tetracycline operator. The TREVs can be used to produce stable cell
CC lines in which gene expression is tightly regulated by tetracycline.
CC They can be used for the production of proteins such as tumour
CC suppressor proteins which can be used for treating diseases characterised
CC by abnormal cellular proliferation, particularly cancers.
SQ Sequence 3555 BP; 1171 A; 684 C; 653 G; 1047 T;

alignment_scores:
Quality: 816.00 Length: 816
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: V54990 from: 1 to: 3555

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 129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
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 393 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 442

 146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
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 443 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 492

 163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
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 179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
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 543 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 592

 196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
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 213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
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AC   V54991;
DT   26-NOV-1998  (first entry)
DE   DNA sequence of the specification.
KW   Minimal promoter; tetracycline responsive expression vector; TREV;
KW   transcriptional transactivation domain; TTD;
KW   tetracycline repressor protein; TRP; tetracycline operator;
KW   production; stable cell line; protein production;
KW   tumour suppressor protein; treatment; cancer; ss.
OS   Unidentified.
FH   Key             Location/Qualifiers
FT   CDS             7. .2457
FT                   /*tag=  a
PN   WO9837185-A2.
PD   27-AUG-1998.
PF   19-FEB-1998; U03092.
PR   20-FEB-1997; US-038755.
PA   (TEXA ) UNIV TEXAS SYSTEM.
PI   Hu S, Logothetis CJ, Xu H, Zhou Y;
DR   WPI; 98-480796/41.
DR   P-PSDB; W71355.
PT   New tetracycline responsive expression vectors - used for the
PT   tightly controlled expression of genes, such as tumour suppressor
PT   genes for treating cancers
PS   Disclosure; Pages 153-157; 190pp; English.
CC   The present sequence appears in the specification, which describes a
CC   tetracycline responsive expression vector (TREV), which contains a
CC   sequence encoding a fusion protein comprising a transcriptional
CC   transactivation domain (TTD) operatively attached to a tetracycline
CC   repressor protein (TRP), the first sequence operatively positioned
CC   downstream of a promoter. The vector also contains a cloning site
CC   operatively positioned downstream of a basal promoter comprising a
CC   tetracycline operator. The TREVs can be used to produce stable cell
CC   lines in which gene expression is tightly regulated by tetracycline.
CC   They can be used for the production of proteins such as tumour
CC   suppressor proteins which can be used for treating diseases characterised
CC   by abnormal cellular proliferation, particularly cancers.
SQ   Sequence   3218 BP;    1080 A;    595 C;    561 G;    982 T;


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1507 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 1556

 629 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 646
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1557 GACACAAGCAACCTCAGGCTTCCAGACCCAGAAGCCATTGAAATCTACCT 1606

 646 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 662
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1607 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 1656

 663 AsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIl 679
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1657 AATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATAT 1706

 679 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 696
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1707 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 1756

 696 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 712
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 713 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 729
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 729 sAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysG 746
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1857 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 1906

 746 luGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGln 762
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1907 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 1956
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     763 ArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLe 779
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     779 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 796
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     796 roLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerPro 812
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     813 TyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArgSe 829
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     829 rArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheG 846
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    2157 AAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCC 2206

     846 lnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSer 862
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    2207 AGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGT 2256

     863 AlaGluGlySerAsnProProLysProLeuLysLysLeuArgPheAspIl 879
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    2257 GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATAT 2306

     879 eGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerL 896
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    2307 TGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGTCCA 2356

     896 ysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 912
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    2357 AATTTCAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAA 2406

      913 LysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 928
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     2407 AAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAA 2454

seq_name: N_Geneseq_36:V40004

seq_documentation_block:
ID   V40004 standard; DNA; 2994 BP.
AC   V40004;
DT   15-FEB-1999  (first entry)
DE   Retinoblastoma protein RB.
KW   Retinoblastoma protein RB; E2F; transcription factor; human;
KW   bladder cancer; restenosis; angioplasty; diabetic retinopathy;
KW   thyroid hyperplasia; Grave's disease; psoriasis;
KW   benign prostatic hypertrophy; Li-Fraumeni syndrome;
KW   peripheral vascular disease; therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             139. .2925
FT                   /*tag=  a
PN   WO9821228-A1.
PD   22-MAY-1998.
PF   13-NOV-1997; U21821.
PR   14-FEB-1997; US-801092.
PR   15-NOV-1996; US-751517.
PA   (CANJ-) CANJI INC.
PI   Antelman D, Gregory RJ, Wills KN;
DR   WPI; 98-297858/26.
DR   P-PSDB; W62465.
PT   New fusion polypeptide of, e.g. transcription factor  - used to
PT   treat, e.g. hyper-proliferative disease such as cancer and
PT   restenosis
PS   Example 1; Fig 2A; 91pp; English.
CC   This nucleotide sequence includes a coding region for retinoblastoma
CC   protein RB (see W62465).  A new claimed polypeptide is a fusion of:
CC   (i) a transcription factor (TF) comprising a DNA binding domain,
CC   and (ii) a retinoblastoma (Rb) polypeptide that includes a growth
CC   suppression domain.  Also new are: (1) a nucleic acid encoding the
CC   fusion protein, and (2) expression vectors containing such DNA.
CC   The fusion protein, particularly expressed from gene therapy
CC   vectors (especially adenovirus vectors), is used to treat
CC   hyperproliferative conditions, specifically cancer (particularly of
CC   the bladder) or restenosis (after angioplasty), but also diabetic
CC   retinopathy, thyroid hyperplasia, Grave's disease, psoriasis,
CC   benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
CC   vascular disease.  Tissue-specific expression of E2F-RB fusions is
CC   provided.  The fusion proteins are more effective in repressing
CC   transcription of the E2F promoter than Rb alone and cause cell-cycle
CC   arrest in a variety of cells.
SQ   Sequence   2994 BP;     974 A;     618 C;     593 G;     809 T;


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            Quality:  816.00              Length:    816
              Ratio:  1.000                Gaps:      0
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      129 sLysPhePheAsnLeuLeuLysGluIleAspThrSerThrLysValAspA 146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      525 TAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATA 574

      146 snAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPhe 162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      575 ATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTC 624

      163 SerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSe 179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      625 AGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAG 674

      179 rSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpI 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      675 TTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGA 724

      196 leThrPheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeu 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      725 TCACATTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTG 774

      213 ValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLe 229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      775 GTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACT 824

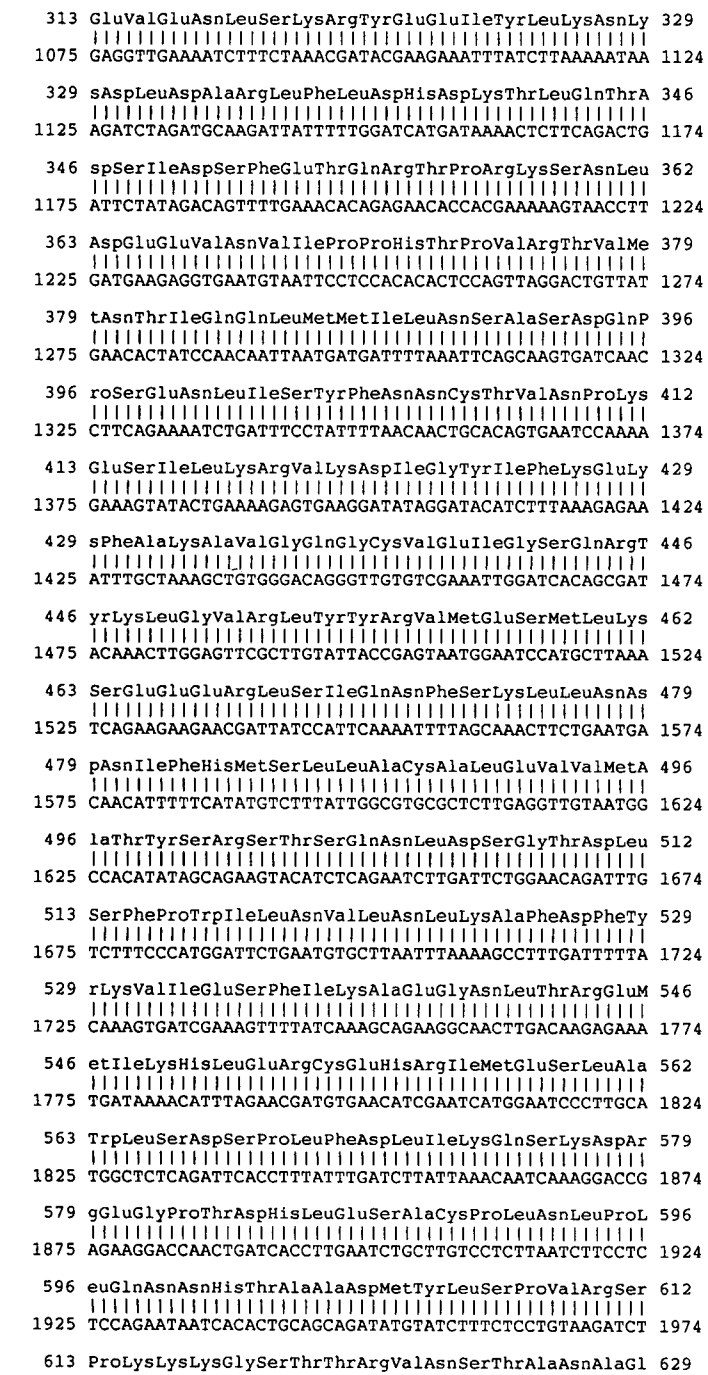
      229 uSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProI 246
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      246 leAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
      875 TTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGG 924

      263 IleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLy 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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      296 heIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuPro 312
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329 sAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrA 346
1125 AGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTG 1174
346 spSerIleAspSerPheGluThrGlnArgThrProArgLysSerAsnLeu 362
1175 ATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTT 1224
363 AspGluGluValAsnValIleProProHisThrProValArgThrValMe 379
1225 GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTAT 1274
379 tAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnP 396
1275 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1324
396 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 412
1325 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1374
413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
1375 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1424
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1875 AGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTAATCTTCCTC 1924
596 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 612
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679 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 696
2175 CATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGA 2224
696 rgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCys 712
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2275 AAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAA 2324
729 sAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysG 746
2325 GGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAG 2374
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2375 AAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAG 2424
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2425 AGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTT 2474
779 uSerProIleProHisIleProArgSerProTyrLysPheProSerSerP 796
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seq_documentation_block:
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AC   X00737;
DT   13-APR-1999  (first entry)
DE   cDNA encoding a retinoblastoma protein designated ppRB-110 or p110-RB.
KW   Retinoblastoma protein; RB protein; ppRB-110; p110-RB; inhibition;
KW   proliferation; cancer; retinoblastoma; secondary osteosarcoma;
KW   breast cancer; small-cell lung cancer; fibrosarcoma; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
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PN   US5851991-A.
PD   22-DEC-1998.
PF   13-SEP-1994; 306513.
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PR   31-AUG-1987; US-091547.
PR   17-SEP-1987; US-098612.
PR   15-OCT-1987; US-108748.
PR   31-OCT-1988; US-265829.
PR   11-JUL-1990; US-550877.
PR   16-JUL-1990; US-553892.
PR   16-JUL-1990; US-553905.
PR   17-OCT-1991; US-778510.
PR   14-JUL-1992; US-914039.
PR   02-OCT-1992; US-956472.
PR   17-JUN-1993; US-079207.
PR   13-SEP-1993; US-121108.
PR   24-SEP-1993; US-126810.
PA   (CANJ-) CANJI INC.
PA   (REGC ) UNIV CALIFORNIA.
PI   Goodrich DW, Johnson D, Lee EY, Lee W, Shepard HM,
PI   Wang NP;
DR   WPI; 99-080477/07.
DR   P-PSDB; W67801.
PT   Inhibition of cancer cell proliferation - with retinoblastoma
PT   protein or polypeptide
PS   Example 1; Fig 2A-K; 72pp; English.
CC   The present sequence encodes a human retinoblastoma (RB) protein
CC   designated ppRB-110 or p110-RB. The protein is used in a method
CC   for inhibiting proliferation of pathologically proliferating cells
CC   lacking endogenous functional retinoblastoma protein. The method
CC   comprises contacting the cells with a polypeptide comprising a 56 kD
CC   C-terminal fragment of retinoblastoma protein. The method is useful
CC   for treating cancers, especially retinoblastoma or secondary
CC   osteosarcoma, breast cancer, small-cell lung cancer or fibrosarcoma.
SQ   Sequence   2995 BP;    975 A;    618 C;    593 G;    809 T;


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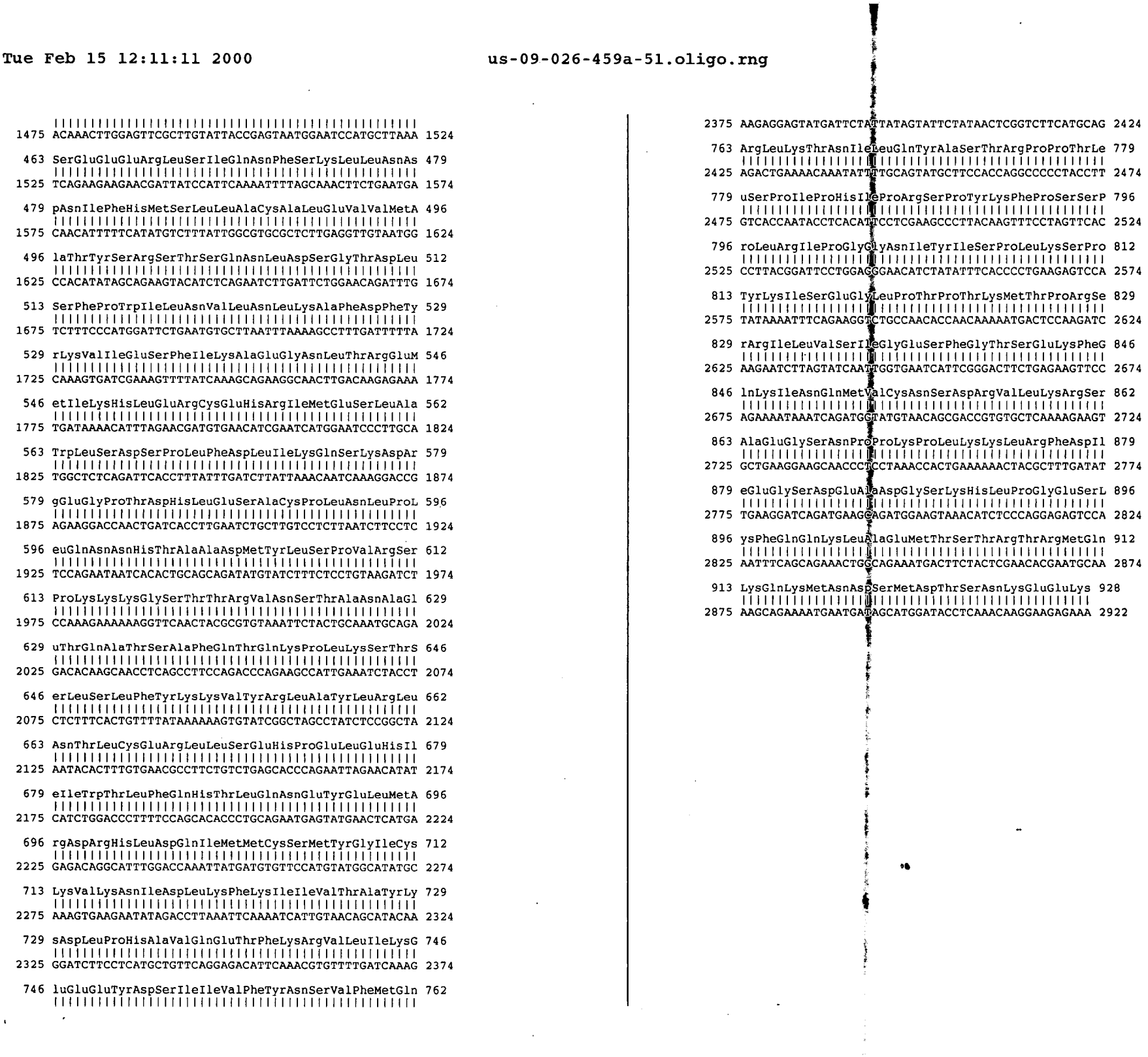
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    1275 GAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAAC 1324

     396 roSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLys 412
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1325 CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAA 1374

     413 GluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGluLy 429
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1375 GAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAA 1424

     429 sPheAlaLysAlaValGlyGlnGlyCysValGluIleGlySerGlnArgT 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1425 ATTTGCTAAAGCTGTGGGACAGGGTTGTGTCGAAATTGGATCACAGCGAT 1474

     446 yrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuLys 462
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1475 ACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAA 1524
463 SerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAs 479
1525 TCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTGAATGA 1574
479 pAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetA 496
1575 CAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATGG 1624
496 laThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeu 512
1625 CCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG 1674
513 SerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTy 529
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529 rLysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluM 546
1725 CAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAA 1774
546 etIleLysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAla 562
1775 TGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCA 1824
563 TrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAr 579
1825 TGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGGACCG 1874
579 gGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProL 596
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596 euGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSer 612
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613 ProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAlaGl 629
1975 CCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGA 2024
629 uThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrS 646
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646 erLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeu 662
2075 CTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTA 2124
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679 eIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetA 696
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713 LysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLy 729
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